

# Package ‘armspp’

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**Title** Adaptive Rejection Metropolis Sampling (ARMS) via 'Rcpp'

**Version** 0.0.2

**Description** An efficient 'Rcpp' implementation of the Adaptive Rejection Metropolis Sampling (ARMS) algorithm proposed by Gilks, W. R., Best, N. G. and Tan, K. K. C. (1995) <doi:10.2307/2986138>. This allows for sampling from a univariate target probability distribution specified by its (potentially unnormalised) log density.

**Depends** R (>= 3.2.3)

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**LinkingTo** Rcpp

**Imports** Rcpp

**RoxygenNote** 6.1.1

**Suggests** knitr, rmarkdown, covr, testthat

**VignetteBuilder** knitr

**NeedsCompilation** yes

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arms

*Adaptive Rejection Metropolis Sampling***Description**

This function performs Adaptive Rejection Metropolis Sampling to sample from a target distribution specified by its (potentially unnormalised) log density. The function constructs a rejection distribution based on piecewise linear functions that envelop the log density of the target.

If the target is log-concave, the `metropolis` parameter can be set to `FALSE`, and an accept-reject sampling scheme is used which yields independent samples.

Otherwise, if `metropolis` is `TRUE`, a Metropolis-Hastings step is used to construct a Markov chain with a stationary distribution matching the target. It is possible in this case for the rejection distribution to be a poor proposal, so users should be careful to check the output matches the desired distribution.

All arguments other than `n_samples`, `include_n_evaluations` and `arguments` can be either vectors or lists as appropriate. If they are vectors, they will be recycled in the same manner as, e.g., `rnorm`. The entries of arguments may be vectors/lists and will also be recycled (see examples).

**Usage**

```
arms(n_samples, log_pdf, lower, upper, previous = (upper + lower)/2,
     initial = lower + (1:n_initial) * (upper - lower)/(n_initial + 1),
     n_initial = 10, convex = 0, max_points = max(2 * n_initial + 1,
     100), metropolis = TRUE, include_n_evaluations = FALSE,
     arguments = list())
```

**Arguments**

<code>n_samples</code>	Number of samples to return.
<code>log_pdf</code>	Potentially unnormalised log density of target distribution. Can also be a list of functions.
<code>lower</code>	Lower bound of the support of the target distribution.
<code>upper</code>	Upper bound of the support of the target distribution.
<code>previous</code>	The previous value of the Markov chain to be used if <code>metropolis = TRUE</code> .
<code>initial</code>	Initial points with which to build the rejection distribution.
<code>n_initial</code>	Number of points used to form <code>initial</code> ; ignored if <code>initial</code> provided.
<code>convex</code>	Convexity adjustment.
<code>max_points</code>	Maximum number of points to allow in the rejection distribution.
<code>metropolis</code>	Whether to use a Metropolis-Hastings step after rejection sampling. Not necessary if the target distribution is log concave.
<code>include_n_evaluations</code>	Whether to return an object specifying the number of function evaluations used.
<code>arguments</code>	List of additional arguments to be passed to <code>log_pdf</code>

**Value**

Vector or matrix of samples if `include_n_evaluations` is `FALSE`, otherwise a list.

**References**

Gilks, W. R., Best, N. G. and Tan, K. K. C. (1995) Adaptive rejection Metropolis sampling. *Applied Statistics*, 44, 455-472.

**See Also**

[http://www1.maths.leeds.ac.uk/~wally.gilks/adaptive.rejection/web\\_page/Welcome.html](http://www1.maths.leeds.ac.uk/~wally.gilks/adaptive.rejection/web_page/Welcome.html)

**Examples**

```
# The normal distribution, which is log concave, so metropolis can be FALSE
result <- arms(
  1000, dnorm, -1000, 1000, metropolis = FALSE,
  arguments = list(log = TRUE), include_n_evaluations = TRUE
)
print(result$n_evaluations)
hist(result$samples, freq = FALSE, br = 20)
curve(dnorm(x), min(result$samples), max(result$samples), col = 'red', add = TRUE)

# Mixture of normals: 0.4 N(-1, 1) + 0.6 N(4, 1). Not log concave.
dnormmixture <- function(x) {
  parts <- log(c(0.4, 0.6)) + dnorm(x, mean = c(-1, 4), log = TRUE)
  log(sum(exp(parts - max(parts)))) + max(parts)
}
samples <- arms(1000, dnormmixture, -1000, 1000)
hist(samples, freq = FALSE)

# List of log pdfs, demonstrating recycling of log_pdf argument
samples <- arms(
  10,
  list(
    function(x) -x ^ 2 / 2,
    function(x) -(x - 10) ^ 2 / 2
  ),
  -1000,
  1000
)
print(samples)

# Another way to achieve the above, this time with recycling in arguments
samples <- arms(
  10, dnorm, -1000, 1000,
  arguments = list(
    mean = c(0, 10), sd = 1, log = TRUE
  )
)
print(samples)
```

arms\_gibbs

*Gibbs sampling using ARMS***Description**

This function uses ARMS (see also [arms](#)) to sample from a multivariate target distribution specified by its (potentially unnormalised) log density using Gibbs sampling. The function updates each argument to the log pdf in turn using ARMS, returning a matrix of samples.

The arguments to this function have the same meaning as for [arms](#), except here they are recycled along the dimension of previous, rather than from sample to sample.

**Usage**

```
arms_gibbs(n_samples, previous, log_pdf, lower, upper, initial = NULL,
           n_initial = 10, convex = 0, max_points = 100, metropolis = TRUE,
           include_n_evaluations = FALSE, show_progress = FALSE)
```

**Arguments**

n_samples	Number of samples to return.
previous	Starting value for the Gibbs sampler. Vectors of this length are passed to log_pdf as the first argument.
log_pdf	Potentially unnormalised log density of target distribution.
lower	Lower bound of the support of the target distribution.
upper	Upper bound of the support of the target distribution.
initial	Initial points with which to build the rejection distribution.
n_initial	Number of points used to form initial; ignored if initial provided.
convex	Convexity adjustment.
max_points	Maximum number of points to allow in the rejection distribution.
metropolis	Whether to use a Metropolis-Hastings step after rejection sampling. Not necessary if the target distribution is log concave.
include_n_evaluations	Whether to return an object specifying the number of function evaluations used.
show_progress	If TRUE, a progress bar is shown.

**Value**

Matrix of samples if include\_n\_evaluations is FALSE, otherwise a list.

**References**

Gilks, W. R., Best, N. G. and Tan, K. K. C. (1995) Adaptive rejection Metropolis sampling. Applied Statistics, 44, 455-472.

**See Also**

[http://www1.maths.leeds.ac.uk/~wally.gilks/adaptive.rejection/web\\_page/Welcome.html](http://www1.maths.leeds.ac.uk/~wally.gilks/adaptive.rejection/web_page/Welcome.html)

**Examples**

```
# The classic 8schools example from RStan
# https://github.com/stan-dev/rstan/wiki/RStan-Getting-Started
schools_data <- list(
  J = 8,
  y = c(28, 8, -3, 7, -1, 1, 18, 12),
  sigma = c(15, 10, 16, 11, 9, 11, 10, 18)
)

log_pdf <- function(params, p) {
  mu <- params[1]
  tau <- params[2]
  eta <- params[3 : (3 + schools_data$J - 1)]
  output <- (
    sum(dnorm(eta, 0, 1, log = TRUE)) +
    sum(dnorm(
      schools_data$y,
      mu + tau * eta,
      schools_data$sigma,
      log = TRUE
    ))
  )
  return(output)
}

x_start <- c(0, 0, rep(0, schools_data$J))
names(x_start) <- c(
  'mu',
  'tau',
  paste0('eta', 1 : schools_data$J)
)

samples <- arms_gibbs(
  250,
  x_start,
  log_pdf,
  c(-1000, 0, rep(-1000, schools_data$J)),
  1000,
  metropolis = FALSE
)
print(colMeans(samples[51 : 250, ]))
```

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