

# Package: ramcmc (via r-universe)

November 2, 2024

**Title** Robust Adaptive Metropolis Algorithm

**Version** 0.1.2

**Date** 2021-10-06

**Description** Function for adapting the shape of the random walk Metropolis proposal as specified by robust adaptive Metropolis algorithm by Vihola (2012) <[doi:10.1007/s11222-011-9269-5](https://doi.org/10.1007/s11222-011-9269-5)>. The package also includes fast functions for rank-one Cholesky update and downdate. These functions can be used directly from R or the corresponding C++ header files can be easily linked to other R packages.

**License** GPL (>= 2)

**BugReports** <https://github.com/helske/ramcmc/issues>

**Suggests** testthat, knitr, rmarkdown

**Imports** Rcpp (>= 0.12.8)

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 5.0.1

**VignetteBuilder** knitr

**Repository** <https://helske.r-universe.dev>

**RemoteUrl** <https://github.com/helske/ramcmc>

**RemoteRef** HEAD

**RemoteSha** 09aa27a675b38cecd19cb274d0fa63d4955594d0

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 adapt\_S

*Update the Proposal of RAM Algorithm*


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### Description

Given the lower triangular matrix  $S$  obtained from the Cholesky decomposition of the shape of the proposal distribution, function `adapt_S` updates  $S$  according to the RAM algorithm.

### Usage

```
adapt_S(S, u, current, n, target = 0.234, gamma = 2/3)
```

### Arguments

<code>S</code>	A lower triangular matrix corresponding to the Cholesky decomposition of the scale of the proposal distribution.
<code>u</code>	A vector with with length matching with the dimensions of $S$ .
<code>current</code>	The current acceptance probability.
<code>n</code>	Scaling parameter corresponding to the current iteration number.
<code>target</code>	The target acceptance rate. Default is 0.234.
<code>gamma</code>	Scaling parameter. Default is $2/3$ .

### Value

If the resulting matrix is positive definite, an updated value of  $S$ . Otherwise original  $S$  is returned.

### Note

If the downdating would result non-positive definite matrix, no adaptation is performed.

### References

Matti Vihola (2012). "Robust adaptive Metropolis algorithm with coerced acceptance rate". *Statistics and Computing*, 22: 997. doi:10.1007/s11222-011-9269-5

### Examples

```
# sample from standard normal distribution
# use proposals from the uniform distribution on
# interval (-s, s), where we adapt s

adapt_mcmc <- function(n = 10000, s) {
  x <- numeric(n)
  loglik_old <- dnorm(x[1], log = TRUE)
  for (i in 2:n) {
    u <- s * runif(1, -1, 1)
    prop <- x[i] + u
```

```

loglik <- dnorm(prop, log = TRUE)
accept_prob <- min(1, exp(loglik - loglik_old))
if (runif(1) < accept_prob) {
  x[i] <- prop
  loglik_old <- loglik
} else {
  x[i] <- x[i - 1]
}
# Adapt only during the burn-in
if (i < n/2) {
  s <- adapt_S(s, u, accept_prob, i)
}
}
list(x = x[(n/2):n], s = s)
}

out <- adapt_mcmc(1e5, 2)
out$s
hist(out$x)
# acceptance rate:
1 / mean(rle(out$x)$lengths)

```

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chol\_downdate

*Rank-one Downdate of Cholesky Decomposition*


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### Description

Given the lower triangular matrix  $L$  obtained from the Cholesky decomposition of  $A$ , function `chol_downdate` updates  $L$  such that it corresponds to the decomposition of  $A - u*u'$  (if such decomposition exists).

### Usage

```
chol_downdate(L, u)
```

### Arguments

$L$                     A lower triangular matrix. Strictly upper diagonal part is not referenced.  
 $u$                     A vector with with length matching with the dimensions of  $L$ .

### Value

Updated  $L$ .

### Note

The function does not check that the resulting matrix is positive semidefinite.

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`chol_update`*Rank-one Update of Cholesky Decomposition*

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**Description**

Given the lower triangular matrix  $L$  obtained from the Cholesky decomposition of  $A$ , function `chol_update` updates  $L$  such that it corresponds to the decomposition of  $A + u*u'$ .

**Usage**

```
chol_update(L, u)
```

**Arguments**

`L` A lower triangular matrix. Strictly upper diagonal part is not referenced.  
`u` A vector with with length matching with the dimensions of  $L$ .

**Value**

Updated  $L$ .

**Examples**

```
L <- matrix(c(4,3,0,5), 2, 2)
u <- c(1, 2)
chol_update(L, u)
t(chol(L %*% t(L) + u %*% t(u)))
```

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