

Package: Rtwalk (via r-universe)

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Type Package

Title An MCMC Sampler Using the t-Walk Algorithm

Version 2.0.1

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Description Implements the t-walk algorithm, a general-purpose, self-adjusting Markov Chain Monte Carlo (MCMC) sampler for continuous distributions as described by Christen & Fox (2010) <doi:10.1214/10-BA603>. The t-walk requires no tuning and is robust for a wide range of target distributions, including high-dimensional and multimodal problems. This implementation includes an option for running multiple chains in parallel to accelerate sampling and facilitate convergence diagnostics.

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Encoding UTF-8

RoxygenNote 7.3.2

Imports parallel, stats, utils, graphics, grDevices, coda

Suggests mvtnorm, devtools, roxygen2, knitr, rmarkdown, ellipse,

VignetteBuilder knitr

URL <https://github.com/rodrigorsqt3/Rtwalk>

BugReports <https://github.com/rodrigorsqt3/Rtwalk/issues>

Repository <https://rodrigorsqt3.r-universe.dev>

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calculate_diagnostics *Calculate MCMC diagnostics*

Description

Computes posterior summaries (mean, SD, quantiles) and effective sample sizes after discarding a burn-in fraction.

Usage

```
calculate_diagnostics(  
  samples,  
  burnin_frac = 0.2,  
  param_names = NULL,  
  title = ""  
)
```

Arguments

samples	Matrix of MCMC samples (iterations x parameters).
burnin_frac	Fraction of samples to discard as burn-in.
param_names	Optional character vector of parameter names.
title	Optional title for printed output.

Value

A data frame with posterior summaries and effective sample sizes.

Examples

```
log_post <- function(x) dnorm(x, log = TRUE)  
res <- twalk(log_post, n_iter = 2000, x0 = -2, xp0 = 2)  
calculate_diagnostics(  
  res$all_samples,  
  burnin_frac = 0.2,  
  param_names = "theta",  
  title = "Standard normal"  
)
```

twalk

*Run the t-walk MCMC Algorithm***Description**

This function implements the t-walk algorithm by Christen & Fox (2010), a general-purpose MCMC sampler that does not require manual tuning. The function can run multiple independent MCMC chains in parallel to accelerate execution and facilitate convergence diagnostics.

Usage

```
twalk(log_posterior, n_iter, x0, xp0, n_chains = 1, n_cores = NULL, ...)
```

Arguments

<code>log_posterior</code>	A function that takes a parameter vector as its first argument and returns the scalar log posterior density. Additional arguments can be passed to this function via <code>'...'</code> .
<code>n_iter</code>	The number of iterations to run for each chain.
<code>x0</code>	A numeric vector with the initial values for the first point (<code>'x'</code>).
<code>xp0</code>	A numeric vector with the initial values for the second point (<code>'x'</code>).
<code>n_chains</code>	The number of independent MCMC chains to run. Defaults to <code>'1'</code> , which runs a single chain sequentially. If greater than 1, parallel mode is activated.
<code>n_cores</code>	The number of CPU cores to use in parallel mode. If <code>'NULL'</code> (default), it will attempt to use all available cores minus one.
<code>...</code>	Additional arguments to be passed to the <code>'log_posterior'</code> function.

Value

A list containing:

<code>all_samples</code>	A matrix with the combined samples from all chains.
<code>acceptance_rate</code>	The average acceptance rate across all chains.
<code>total_iterations</code>	The total number of samples generated (<code>n_iter * n_chains</code>).
<code>n_dim</code>	The dimension of the parameter space.
<code>individual_chains</code>	If <code>'n_chains > 1'</code> , a list containing the raw results from each separate chain, useful for diagnostics like R-hat.

Examples

```
# Example 1: Sampling from a Bivariate Normal (sequential mode)
# The 'mvtnorm' package is required for this example
if (requireNamespace("mvtnorm", quietly = TRUE)) {
  log_post <- function(x) {
    mvtnorm::dmvnorm(x, mean = c(0, 0), sigma = matrix(c(1, 0.8, 0.8, 1), 2, 2), log = TRUE)
  }

  # Run with fewer iterations for a quick example
  # Set a seed for reproducibility
  set.seed(123)
  result_seq <- twalk(log_posterior = log_post, n_iter = 5000,
                    x0 = c(-1, 1), xp0 = c(1, -1))

  plot(result_seq$all_samples, pch = '.', main = "t-walk Samples (Sequential)")
}

# Example 2: The same problem in parallel (will run faster)
# Using 2 chains. n_iter is now per chain.
if (requireNamespace("mvtnorm", quietly = TRUE)) {
  set.seed(123)
  result_par <- twalk(log_posterior = log_post, n_iter = 2500,
                    x0 = c(-1, 1), xp0 = c(1, -1), n_chains = 2)

  plot(result_par$all_samples, pch = '.', main = "t-walk Samples (Parallel)")
}
```

visualize_results

Visualize MCMC results

Description

Produces trace plots, marginal densities and joint plots depending on the dimension of the parameter space.

Usage

```
visualize_results(
  samples,
  true_values = NULL,
  title = "Results",
  burnin_frac = 0.2,
  true_covariance = NULL,
  show_acf = TRUE
)
```

Arguments

<code>samples</code>	Matrix of MCMC samples.
<code>true_values</code>	Optional vector of true parameter values.
<code>title</code>	Plot title.
<code>burnin_frac</code>	Burn-in fraction.
<code>true_covariance</code>	Optional true covariance matrix.
<code>show_acf</code>	Logical; whether to display autocorrelation plots.

Examples

```
log_post <- function(x) dnorm(x, log = TRUE)
res <- twalk(log_post, n_iter = 2000, x0 = -2, xp0 = 2)
visualize_results(
  res$all_samples,
  true_values = 0,
  title = "Standard normal"
)
```

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