

Package: linconGaussR (via r-universe)

September 3, 2024

Type Package

Title Sampling Multivariate Normal Distribution under Linear Constraints

Version 0.1

Date 2021-10-25

Maintainer Yunyi Shen <yshen99@wisc.edu>

Description Sample truncated multivariate Normal distribution following Gessner, A., Kanjilal, O., & Hennig, P. (2019). Integrals over Gaussians under Linear Domain Constraints. 108. <[arxiv:1910.09328](https://arxiv.org/abs/1910.09328)>.

License GPL-3

Imports Rcpp (>= 1.0.7), MASS

LinkingTo Rcpp, RcppArmadillo

URL <https://github.com/YunyiShen/linconGaussR>

BugReports <https://github.com/YunyiShen/linconGaussR/issues>

RoxygenNote 7.1.1

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

RemoteUrl <https://github.com/yunyishen/lincongaussr>

RemoteRef HEAD

RemoteSha 668b4f7f0e8ab993b0b7d48e57e2ccde8a70997e

Contents

linconGauss	2
Index	4

linconGauss	<i>Sample Gaussian distribution with linear constraints Taking truncated sample of Gaussian distribution over a linear constraint domain.</i>
-------------	---

Description

Sample Gaussian distribution with linear constraints Taking truncated sample of Gaussian distribution over a linear constraint domain.

Usage

```
linconGauss(
  n,
  A,
  b,
  Sigma,
  mu,
  x_init = NULL,
  intersection = TRUE,
  n_retry_init = 1000,
  nskip = 5
)
```

Arguments

n	number of samples to take
A	a matrix with M by D dimensions, the linear constraints, such that $Ax+b \geq 0$
b	the offset of the linear constraints with dimension M such that $Ax+b \geq 0$
Sigma	covariance matrix of the Gaussian
mu	mean vector of the Gaussian
x_init	the sample to start with, if NULL, a sample will be drawn using rejection method
intersection	bool whether sample from the intersection or the union of the linear constraints, default true, sample from the intersection
n_retry_init	how many times to try finding a initial value
nskp	how many sample to skip during the sampling routine

Value

a matrix with truncated sample, row as samples

Examples

```
my_sample <- linconGauss(100, diag(2),c(0,0),diag(2),c(0,0))
MASS_sample <- MASS::mvrnorm(1000,c(0,0),diag(2))
plot(MASS_sample)
points(my_sample,col = "red")
abline(h=0)
abline(v=0)
```

Index

linconGauss, [2](#)