

An R Package for Fast Sampling from the von Mises–Fisher Distribution

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Introduction

The package **vMF** simulates von Mises-Fisher distribution (\mathcal{M}). Unlike the package **movMF** (Hornik and Grün, 2014), which simulates and estimates mixtures of \mathcal{M} , **vMF** performs fast sampling as its source code is written in C++. **vMF** also computes the density and the normalization constant of \mathcal{M} .

The von Mises-Fisher distribution is used to model coordinates on a hypersphere of dimension $p \geq 2$. Roughly speaking, it is the equivalent of the normal distribution on a hypersphere. As the normal distribution, \mathcal{M} is characterized by two parameters. The location (or mean directional) parameter $\boldsymbol{\mu}$ around which draws will be concentrated and the intensity parameter η which measures the intensity of concentration of the draws around $\boldsymbol{\mu}$. The higher η , the more the draws are concentrated around $\boldsymbol{\mu}$. Compared to the normal distribution, $\boldsymbol{\mu}$ is similar to the mean parameter of the normal distribution and $1/\eta$ is similar to the standard deviation.

There are several definitions of the density function of \mathcal{M} . In this package, the density is normalized by the uniform distribution without loss of generality. This is also the case in Mardia and Jupp (2009) and Hornik and Grün (2013).

Let $\mathbf{z} \sim \mathcal{M}(\eta, \boldsymbol{\mu})$. The density of \mathbf{z} is given by

$$f_p(\mathbf{z}|\eta, \boldsymbol{\mu}) = C_p(\eta)e^{\eta\mathbf{z}'\boldsymbol{\mu}},$$

where $C_p(x) = \left(\frac{x}{2}\right)^{\frac{p}{2}-1} \frac{1}{\Gamma(\frac{p}{2}) I_{\frac{p}{2}-1}(x)}$ is the normalization constant and $I_1(\cdot)$ the Bessel function of the first kind defined by:

$$I_\alpha(x) = \sum_{m=0}^{\infty} \frac{\left(\frac{x}{2}\right)^{2m+\alpha}}{m! \Gamma(m+\alpha+1)}.$$

The normalization with respect to the uniform distribution implies $C_p(0) = 1$.

Simulation from von Mises Fisher distribution

The following algorithm provides a rejection sampling scheme for drawing a sample from \mathcal{M} with mean directional parameter $\boldsymbol{\mu} = (0, \dots, 0, 1)$ and concentration (intensity) parameter $\eta \geq 0$ (see Section 2.1 in Hornik and Grün, 2014).

- Step 1. Calculate b using * Step 1. Calculate b using

$$b = \frac{p-1}{2\eta + \sqrt{2\eta^2 + (p-1)^2}}.$$

Let $x_0 = (1-b)/(1+b)$ and $c = \eta x_0 + (p-1) \log(1-x_0^2)$.

- Step 2. Generate $Z \sim \text{Beta}((p-1)/2, (p-1)/2)$ and $U \sim \text{Unif}([0, 1])$ and calculate

$$W = \frac{1 - (1+b)Z}{1 - (1-b)Z}.$$

- Step 3. If

$$\eta W + (p-1) \log(1 - x_0 W) - c < \log(U),$$

go to step 2.

- Step 4. Generate a uniform $(d-1)$ -dimensional unit vector \mathbf{V} and return

$$\mathbf{X} = \left(\sqrt{1 - W^2} \mathbf{V}', W \right)'$$

The uniform $(d-1)$ -dimensional unit vector \mathbf{V} can be generated by simulating $d-1$ independent standard normal random variables and normalizing them so as $\|\mathbf{V}\|_2 = 1$. To get sampling from \mathcal{M} with arbitrary mean direction parameter $\boldsymbol{\mu}$, \mathbf{X} is multiplied from the left with a matrix where the first $d-1$ columns consist of unitary basis vectors of the subspace orthogonal to $\boldsymbol{\mu}$ and the last column is equal to $\boldsymbol{\mu}$.

Comparison of vMF and movMF

In this section, I compare **vMF** and **movMF**.

```
library(rbenchmark)

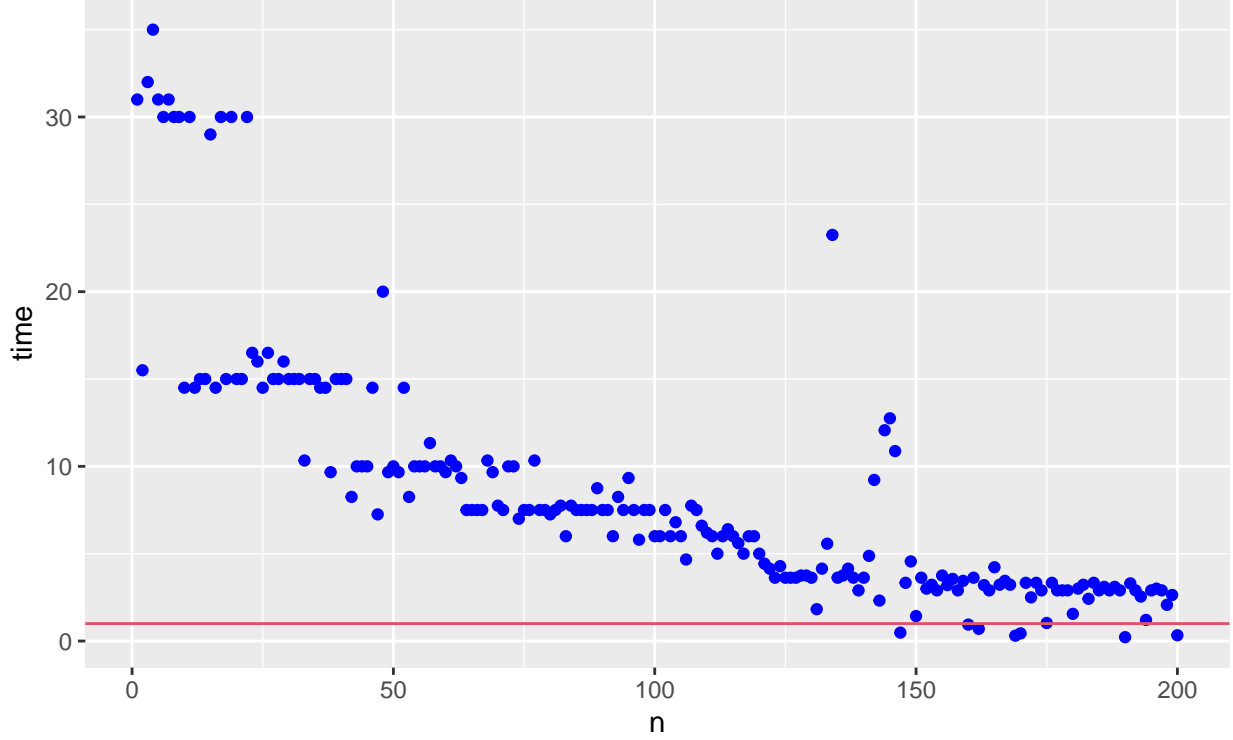
fcompare <- function(n) {
  benchmark("vMF" = rvMF(n, c(1, 0, 0)), "movMF" = rmovMF(1, c(1, 0, 0)))
}

fcompare(1)
#>   test replications elapsed relative user.self sys.self user.child sys.child
#> 2 movMF           100    0.024         24    0.024         0         0         0
#> 1  vMF           100    0.001          1    0.001         0         0         0
fcompare(10)
#>   test replications elapsed relative user.self sys.self user.child sys.child
#> 2 movMF           100    0.025        12.5    0.024         0         0         0
#> 1  vMF           100    0.002          1.0    0.002         0         0         0
fcompare(100)
#>   test replications elapsed relative user.self sys.self user.child sys.child
#> 2 movMF           100    0.025         3.571    0.025         0         0         0
#> 1  vMF           100    0.007          1.000    0.008         0         0         0
```

vMF performs over **movMF**. The performance of **vMF** is much better when only few simulations are performed. When the sample is too large, the two package require approximately the same running time.

```
out <- unlist(lapply(1:200, function(x) fcompare(x)$elapsed[1]/fcompare(x)$elapsed[2]))
```

```
library(ggplot2)
ggplot(data = data.frame(n = 1:200, time = out), aes(x = n, y = time)) +
  geom_point(col = "blue") + geom_hline(yintercept = 1, col = 2)
```



Many papers use simulations from the von-Mises Fisher distribution in a Markov Chain Monte Carlo (MCMC) process. A single draw is performed at each iteration of the MCMC. This is for example the case in [Boucher and Houndetoungan \(2022\)](#), [Breza et al. \(2020\)](#), [McCormick and Zheng \(2015\)](#). In such a simulation context, using **vMF** would take much less time than **movMF**. For example, I consider the process $(\mathbf{z}_t)_{t \in \mathbb{N}}$ which follows a random walk of the von-Mises Fisher distribution. The first variable, \mathbf{z}_0 , is randomly set on a 4-dimensional hypersphere and $\mathbf{z}_t \sim \mathcal{M}(1, \mathbf{z}_{t-1}) \forall t > 0$. Simulating this process has about the same complexity as using von-Mises Fisher drawings in an MCMC.

```
set.seed(123)
P <- 4
initial <- rmovMF(1, rep(0, P))
# Fonction based on vMF to simulate theta
SamplevMF <- function(n) {
  output <- matrix(0, n + 1, P)
  output[1, ] <- initial
  for (i in 1:n) {
    output[i + 1, ] <- rvMF(1, output[i,])
  }
  return(output)
}

# Fonction based on movMF to simulate theta
SamplemovMF <- function(n){
  output <- matrix(0, n + 1, P)
  output[1, ] <- initial
  for (i in 1:n) {
    output[i + 1, ] <- rmovMF(1, output[i,])
  }
  return(output)
}
benchmark("vMF" = SamplevMF(1000), "movMF" = SamplemovMF(1000))
```

```
#>      test replications elapsed relative user.self sys.self user.child sys.child
#> 2 movMF           100  35.605   51.902   35.260    0.032         0         0
#> 1  vMF            100   0.686    1.000    0.643    0.044         0         0
```

The comparison of the running times **vMF** is less time-consuming

References

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- Breza, E., Chandrasekhar, A. G., McCormick, T. H., and Pan, M. (2020). Using aggregated relational data to feasibly identify network structure without network data. *American Economic Review*, 110(8):2454–84.
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