An R Package for Fast Sampling from 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 $\mathcal{M}$, **vFM** performs fast sampling as its source code is written in C++. **vFM** 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 $C_p(x) = \left(\frac{x}{2}\right)^{\frac{p}{2}-1} \frac{1}{\Gamma\left(\frac{p}{2}\right) I_{\frac{p}{2}-1}(x)}$ is the normalization constant and $I_{.}(.)$ 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 $\boldsymbol{\mu} = (0, ..., 0, 1)$ 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 $c = \eta x_0 + (p-1)\log\left(1 - x_0^2\right)$.

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

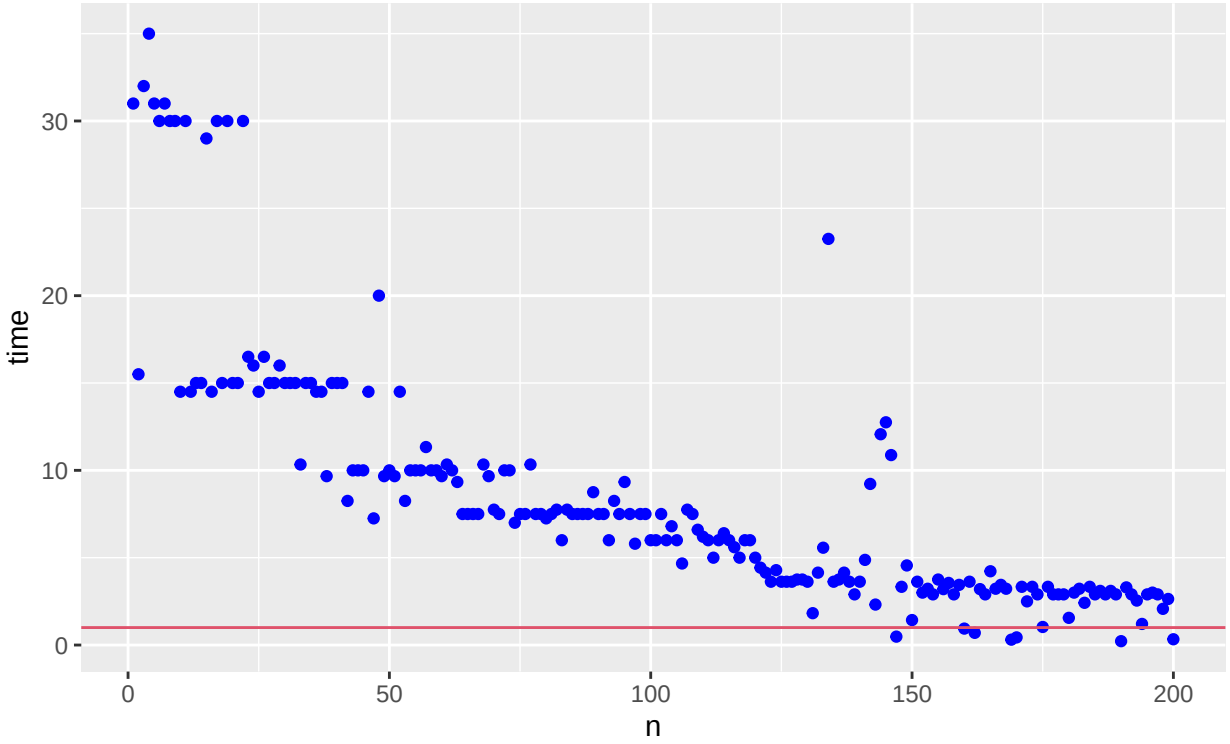
In this section, I compare **vMF** and **movMF**.

```
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   0.018        9     0.017        0          0         0
#> 1   vMF          100   0.002        1     0.001        0          0         0
fcompare(10)
#>    test replications elapsed relative user.self sys.self user.child sys.child
#> 2 movMF          100   0.017       17     0.017        0          0         0
#> 1   vMF          100   0.001        1     0.002        0          0         0
fcompare(100)
#>    test replications elapsed relative user.self sys.self user.child sys.child
#> 2 movMF          100   0.017      3.4     0.017        0          0         0
#> 1   vMF          100   0.005      1.0     0.005        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 randowmly 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

Boucher, V. and Houndetoungan, E. A. (2022). Estimating peer effects using partial network data.

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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