

# Package ‘mig’

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**Type** Package

**Title** Multivariate Inverse Gaussian Distribution

**Version** 1.0

**Description** Provides utilities for estimation for the multivariate inverse Gaussian distribution of Miani (2003) <[doi:10.1081/STA-120025379](https://doi.org/10.1081/STA-120025379)>, including random vector generation and explicit estimators of the location vector and scale matrix. The package implements kernel density estimators discussed in Belzile, Desgagnes, Genest and Ouimet (2024) <[doi:10.48550/arXiv.2209.04757](https://doi.org/10.48550/arXiv.2209.04757)> for smoothing multivariate data on half-spaces.

**BugReports** <https://github.com/lbelzile/mig/issues>

**Imports** statmod, TruncatedNormal (>= 2.3), Rcpp (>= 1.0.12)

**Depends** R (>= 2.10)

**Suggests** numDeriv, tinytest, knitr, rmarkdown, minqa

**LinkingTo** Rcpp, RcppArmadillo

**Encoding** UTF-8

**LazyData** true

**License** MIT + file LICENSE

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**NeedsCompilation** yes

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**Repository** CRAN

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dmig	<i>Multivariate inverse Gaussian distribution</i>
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### Description

The density of the MIG model is

$$f(\mathbf{x} + \mathbf{a}) = (2\pi)^{-d/2} \boldsymbol{\beta}^\top \boldsymbol{\xi} |\boldsymbol{\Omega}|^{-1/2} (\boldsymbol{\beta}^\top \mathbf{x})^{-(1+d/2)} \exp \left\{ -\frac{(\mathbf{x} - \boldsymbol{\xi})^\top \boldsymbol{\Omega}^{-1} (\mathbf{x} - \boldsymbol{\xi})}{2\boldsymbol{\beta}^\top \mathbf{x}} \right\}$$

for points in the d-dimensional half-space  $\{\mathbf{x} \in \mathbb{R}^d : \boldsymbol{\beta}^\top (\mathbf{x} - \mathbf{a}) \geq 0\}$

### Usage

```
dmig(x, xi, Omega, beta, shift, log = FALSE)

rmig(n, xi, Omega, beta, shift, method = c("invsim", "bm"), timeinc = 0.001)

pmig(q, xi, Omega, beta, log = FALSE, method = c("sov", "mc"), B = 10000L)
```

### Arguments

x	n by d matrix of quantiles
xi	d vector of location parameters $\boldsymbol{\xi}$ , giving the expected value
Omega	d by d positive definite scale matrix $\boldsymbol{\Omega}$
beta	d vector $\boldsymbol{\beta}$ defining the half-space through $\boldsymbol{\beta}^\top \boldsymbol{\xi} > 0$
shift	d translation for the half-space $\mathbf{a}$
log	logical; if TRUE, returns log probabilities
n	number of observations
method	string; one of inverse system (invsim, default), Brownian motion (bm)
timeinc	time increment for multivariate simulation algorithm based on the hitting time of Brownian motion, default to 1e-3.
q	n by d matrix of quantiles
B	number of Monte Carlo replications for the SOV estimator

**Details**

Observations are generated using the representation as the first hitting time of a hyperplane of a correlated Brownian motion.

**Value**

for `dmig`, the (log)-density  
 for `rmig`, an  $n$  vector if  $d=1$  (univariate) or an  $n$  by  $d$  matrix if  $d > 1$   
 an  $n$  vector of (log) probabilities

**Author(s)**

Frederic Ouimet (`bm`), Leo Belzile (`invsim`)  
 Leo Belzile

**Examples**

```
# Density evaluation
x <- rbind(c(1, 2), c(2,3), c(0,-1))
beta <- c(1, 0)
xi <- c(1, 1)
Omega <- matrix(c(2, -1, -1, 2), nrow = 2, ncol = 2)
dmig(x, xi = xi, Omega = Omega, beta = beta)
# Random number generation
d <- 5L
beta <- runif(d)
xi <- rexp(d)
Omega <- matrix(0.5, d, d) + diag(d)
samp <- rmig(n = 1000, beta = beta, xi = xi, Omega = Omega)
mle <- fit_mig(samp, beta = beta, method = "mle")
set.seed(1234)
d <- 2L
beta <- runif(d)
Omega <- rWishart(n = 1, df = 2*d, Sigma = matrix(0.5, d, d) + diag(d))[,1]
xi <- rexp(d)
q <- mig::rmig(n = 10, beta = beta, Omega = Omega, xi = xi)
pmig(q, xi = xi, beta = beta, Omega = Omega)
```

fit\_mig

*Fit multivariate inverse Gaussian distribution***Description**

Fit multivariate inverse Gaussian distribution

**Usage**

```
fit_mig(x, beta, method = c("mle", "mom"), shift)
```

**Arguments**

x	n by d matrix of quantiles
beta	d vector $\beta$ defining the half-space through $\beta^\top \xi > 0$
method	string, one of <code>mle</code> for maximum likelihood estimation, or <code>mom</code> for method of moments.
shift	d translation for the half-space $a$

**Value**

a list with components:

- xi: estimate of the expectation or location vector
- Omega: estimate of the scale matrix

geomagnetic

*Magnetic storms***Description**

Absolute magnitude of 373 geomagnetic storms lasting more than 48h with absolute magnitude (dst) larger than 100 in 1957-2014.

**Format**

a vector of size 373

**Note**

For a detailed article presenting the derivation of the Dst index, see <http://wdc.kugi.kyoto-u.ac.jp/dstdir/dst2/onDst.pdf>

**Source**

Aki Vehtari

**References**

World Data Center for Geomagnetism, Kyoto, M. Nose, T. Iyemori, M. Sugiura, T. Kamei (2015), *Geomagnetic Dst index*, doi:10.17593/14515-74000.

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mig\_kdens*Multivariate inverse Gaussian kernel density estimator*

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**Description**

Given a matrix of new observations, compute the density of the multivariate inverse Gaussian mixture defined by assigning equal weight to each component where  $\xi$  is the location parameter.

**Usage**

```
mig_kdens(x, newdata, Omega, beta, log = FALSE)
```

**Arguments**

x	n by d matrix of quantiles
newdata	matrix of new observations at which to evaluated the kernel density
Omega	d by d positive definite scale matrix $\Omega$
beta	d vector $\beta$ defining the half-space through $\beta^\top \xi > 0$
log	logical; if TRUE, returns log probabilities

**Value**

value of the (log)-density at newdata

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mig\_kdens\_bandwidth*Optimal scale matrix for MIG kernel density estimation*

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**Description**

Given an n sample from a multivariate inverse Gaussian distribution on the half-space defined by  $\{x \in \mathbb{R}^d : \beta^\top x > 0\}$ , the function computes the bandwidth (type="isotropic") or scale matrix that minimizes the asymptotic mean integrated squared error away from the boundary. The latter depend on the true unknown density, which is replaced using as plug-in a MIG distribution evaluated at the maximum likelihood estimator. The integral or the integrated squared error are obtained by Monte Carlo integration with N simulations

**Usage**

```
mig_kdens_bandwidth(
  x,
  beta,
  shift,
  method = c("amise", "lcv", "lscv", "rlcv"),
  type = c("isotropic", "full"),
```

```

approx = c("mig", "tnorm"),
transformation = c("none", "scaling", "spherical"),
N = 10000L,
buffer = 0.25,
pointwise = NULL,
maxiter = 2000L,
...
)

```

## Arguments

<code>x</code>	an n by d matrix of observations
<code>beta</code>	d vector defining the half-space
<code>shift</code>	location vector for translating the half-space. If missing, defaults to zero
<code>method</code>	estimation criterion, either <code>amise</code> for the expression that minimizes the asymptotic integrated squared error, <code>lcv</code> for likelihood (leave-one-out) cross-validation, <code>lscv</code> for least-square cross-validation or <code>r1cv</code> for robust cross validation of Wu (2019)
<code>type</code>	string indicating whether to compute an isotropic model or estimate the optimal scale matrix via optimization
<code>approx</code>	string; distribution to approximate the true density function $f(x)$ ; either <code>mig</code> for multivariate inverse Gaussian, or <code>tnorm</code> for truncated Gaussian.
<code>transformation</code>	string for optional scaling of the data before computing the bandwidth. Either standardization to unit variance <code>scaling</code> , spherical transformation to unit variance and zero correlation ( <code>spherical</code> ), or <code>none</code> (default).
<code>N</code>	integer number of simulations to evaluate the integrals of the MISE by Monte Carlo
<code>buffer</code>	double indicating the buffer from the halfspace
<code>pointwise</code>	if <code>NULL</code> , evaluates the mean integrated squared error, otherwise a d vector to evaluate the bandwidth or scale pointwise
<code>maxiter</code>	integer; max number of iterations in the call to <code>optim</code> .
<code>...</code>	additional parameters, currently ignored

## Value

a d by d scale matrix

## References

- Wu, X. (2019). Robust likelihood cross-validation for kernel density estimation. *Journal of Business & Economic Statistics*, 37(4), 761–770. doi:[10.1080/07350015.2018.1424633](https://doi.org/10.1080/07350015.2018.1424633) Bowman, A.W. (1984). An alternative method of cross-validation for the smoothing of density estimates, *Biometrika*, 71(2), 353–360. doi:[10.1093/biomet/71.2.353](https://doi.org/10.1093/biomet/71.2.353) Rudemo, M. (1982). Empirical choice of histograms and kernel density estimators. *Scandinavian Journal of Statistics*, 9(2), 65–78. http://www.jstor.org/stable/4615859

**mig\_lcv***Likelihood cross-validation for kernel density estimation with MIG***Description**

Given a data matrix over a half-space defined by `beta`, compute the log density using leave-one-out cross validation, taking in turn an observation as location vector and computing the density of the resulting mixture.

**Usage**

```
mig_lcv(x, beta, Omega)
```

**Arguments**

<code>x</code>	$n$ by $d$ matrix of quantiles
<code>beta</code>	$d$ vector $\beta$ defining the half-space through $\beta^\top \xi > 0$
<code>Omega</code>	$d$ by $d$ positive definite scale matrix $\Omega$

**Value**

the value of the likelihood cross-validation criterion

**mig\_rlcv***Robust likelihood cross-validation for kernel density estimation***Description**

Given a data matrix over a half-space defined by `beta`, compute the log density using leave-one-out cross validation, taking in turn an observation as location vector and computing the density of the resulting mixture.

**Usage**

```
mig_rlcv(x, beta, Omega, xsamp, dxsamp)
```

**Arguments**

<code>x</code>	$n$ by $d$ matrix of quantiles
<code>beta</code>	$d$ vector $\beta$ defining the half-space through $\beta^\top \xi > 0$
<code>Omega</code>	$d$ by $d$ positive definite scale matrix $\Omega$
<code>xsamp</code>	matrix of points at which to evaluate the integral
<code>dxsamp</code>	density of points

**Value**

the value of the likelihood cross-validation criterion

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