

# Package ‘covsim’

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**Type** Package

**Title** VITA and IG Simulation for Given Covariance and Marginals

**Version** 0.1.0

**Description** User specifies population covariance matrix. Marginal information may be fully specified, for which the package implements the VITA (VIne-To-Anything) algorithm. Groenneberg and Foldnes (2017) <doi:10.1007/s11336-017-9569-6>. Alternatively, marginal skewness and kurtosis may be specified, for which the package implements the IG (independent generator) algorithm. Foldnes and Ols-son (2016) <doi:10.1080/00273171.2015.1133274>.

**License** GPL (>= 2)

**Depends** R (>= 3.1.0)

**Imports** rvinecopulib (>= 0.5.1.1.0), lavaan (>= 0.6-5), nleqslv, PearsonDS, MASS, stats, Rcpp, gsl

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

**NeedsCompilation** no

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**Repository** CRAN

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rIG

*Simulation of non-normal data*

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### Description

Using the IG method to simulate non-normal data

### Usage

```
rIG(N, sigma.target, skewness, excesskurtosis, reps = 1, typeA = "symm")
```

### Arguments

N	Number of observations to simulate.
sigma.target	Target population covariance matrix
skewness	Target skewness
excesskurtosis	Target excess kurtosis
reps	Number of simulated samples
typeA	Symmetrical (default) or triangular A matrix

### Value

A list of simulated samples

### Author(s)

Njål Foldnes (<njal.foldnes@gmail.com>)

### References

Foldnes, N. and Olson, U. H. (2016). A simple simulation technique for nonnormal data with prespecified skewness, kurtosis, and covariance matrix. *Multivariate behavioral research*, 51(2-3), 207-219

### Examples

```
set.seed(1234)
model <- '
# measurement model
ind60 =~ x1 + x2 + x3
dem60 =~ y1 + y2 + y3 + y4
dem65 =~ y5 + y6 + y7 + y8
# regressions
dem60 ~ ind60
dem65 ~ ind60 + dem60
# residual correlations
y1 ~~ y5
```

```

y2 ~~ y4 + y6
y3 ~~ y7
y4 ~~ y8
y6 ~~ y8'
fit <- lavaan::sem(model, data=lavaan::PoliticalDemocracy)
population.sigma <- lavaan::lavInspect(fit, "sigma.hat")
population.skew <- c(0, 0, 0, 0, 1, 1, 1, 1, 2,2,2 )
population.excesskurt <- c( 1 , 1, 1, 1, 3, 3, 3, 3, 7, 7, 7)
my.samples <- rIG(N=10^3, sigma=population.sigma,
  skewness=population.skew,
  excesskurt=population.excesskurt,
  reps=5)

```

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vita

*Calibrate a regular vine*


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## Description

vita implements the VITA (VIne-To-Anything) algorithm. Covariance matrix and margins are specified, and vita calibrates the pair-copulas in each node of the tree to match the target covariance.

## Usage

```

vita(
  margins,
  sigma.target,
  vc = NULL,
  family_set = c("clayton", "gauss", "joe", "gumbel", "frank"),
  Nmax = 10^6,
  numrootpoints = 10,
  conflevel = 0.995,
  numpoints = 4,
  verbose = TRUE,
  cores = parallel::detectCores()
)

```

## Arguments

- |              |                                                                                                                                                                                                                 |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| margins      | A list where each element corresponds to a margin. Each margin element is a list containing the distribution family ("distr") and additional parameters. Must be a distribution available in the stats package. |
| sigma.target | The target covariance matrix that is to be matched. The diagonal elements must contain the variances of marginal distributions.                                                                                 |
| vc           | A vine dist object as specified by the rvinecopulib package. This object specifies the vine that is to be calibrated. If not provided, a D-vine is assumed.                                                     |

family_set	A vector of one-parameter pair-copula families that is to be calibrated at each node in the vine. Possible entries are "gauss", "clayton", "joe", "gumbel" and "frank". Calibration of pair-copula families is attempted in the order provided.
Nmax	The sample size used for calibration. Reduce for faster calibration, at the cost of precision.
numrootpoints	The number of estimated roots at the initial calibration stage, which determines a search interval where Nmax samples are drawn
confllevel	Confidence level for determining search interval
numpoints	The number of samples drawn with size Nmax, to determine the root within search interval To increase precision increase this number. To calibrate faster (but less precisely), may be reduced to a number no lower than 2
verbose	If TRUE, outputs details of calibration of each bicopula
cores	Number of cores to use. If larger than 1, computations are done in parallel. May be determined with parallel:detectCores()

### Value

If a feasible solution was found, a vine to be used for simulation

### References

Grønneberg, S and Foldnes, N. (2017). Covariance model simulation using regular vines. *Psychometrika*, 82(4), 1035-1051

### Examples

```
set.seed(1)# define a target covariance. 3 dimensions.
sigma.target <- cov(MASS::mvrnorm(10, mu=rep(0,3), Sigma=diag(1, 3)))

#normal margins that match the covariances:
marginsnorm <- lapply(X=sqrt(diag(sigma.target)),function(X) list(distr="norm", sd=X) )

#calibrate with a default D-vine, with rather low precision (default Nmax is 10^6)
# if cores=1 is removed, all cores are used, with a speed gain
calibrated.vine <- vita(marginsnorm, sigma.target =sigma.target, Nmax=10^5, cores=1)
#check
#round(cov(rvinecopulib::rvine(10^5, calibrated.vine))-sigma.target, 3)

#margins are normal but dependence structure is not
#pairs(rvinecopulib::rvine(500, calibrated.vine))
```

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