Package: ar.matrix (via r-universe)

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Type Package

Title Simulate Auto Regressive Data from Precision Matrices

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Description Using sparse precision matrices and Cholesky factorization simulates data that is auto-regressive.

Depends R (>= 3.3.0)

Imports MASS, Matrix, sparseMVN, sp

Suggests ggplot2, leaflet

BugReports https://github.com/nmmarquez/ar.matrix/issues

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Repository https://nmmarquez.r-universe.dev

RemoteUrl https://github.com/nmmarquez/ar.matrix

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Contents

Q.AR1 — *Precision matrix for an AR1 process*

Description

Functions for creating precision matricies and observations of an AR1 process

Usage

```
Q.AR1(M, sigma, rho, sparse=TRUE, vcov=FALSE)

r.AR1(n, M, sigma, rho)
```

Arguments

`M`	int > 0, number of elements in the AR1 process.
`sigma`	float > 0, pairwise observation standard deviation.
`rho`	float >= 0 & < 1, how correlated pairwise observations are. The function will still run with values outside of the range [0,1) however the stability of the simulation results are not gaurunteed.
`sparse`	bool Should the matrix be of class 'dsCMatrix'
`vcov`	bool If the vcov matrix should be returned instead of the precision matrix.
`n`	int > 0, number of observations to simulate from the GMRF.

Value

Q.AR1 returns either a precision or variance-covariance function with a AR1 structure.

r.AR1 retrurns a matrix with n rows which are the n observations of a Gaussian Markov random field AR1 process.

Examples

```
require("ggplot2")
# simulate AR1 GMRF
obs <- r.AR1(100, M=30, sigma=1, rho=.98)
# resulting matrix is n x M
dim(obs)
# subtract off the first time point to more easily observe correlation
obs_adj <- obs - obs[,1]
# move objects to a data frame
ar1_df <- data.frame(obs=c(t(obs_adj)), realization=rep(1:100, each=30),
```

```
                     time=rep(1:30, 100))
# plot each realization
ggplot(data=ar1_df, aes(time, obs, group=realization, color=realization)) +
    geom_line()
```

Q.iid *Precision matrix for a IID process*

Description

Functions for creating precision matricies and observations of a independent identically distributed GMRF process.

Usage

```
Q.iid(M, sigma, sparse=TRUE,  vcov=FALSE)

r.iid(n, M, sigma)
```

Arguments

M	int > 0, number of elements in the process.
sigma	float > 0, standard deviat
sparse	bool Should the matrix be of class 'dsCMatrix'
vcov	bool If the vcov matrix should be returned instead of the precision matrix.
n	int > 0, number of observations to simulate from the GMRF.

Value

Q.iid returns either a precision or variance-covariance function with iid structure.

r.iid retrurns a matrix with n rows which are the n observations of a Gaussian Markov random field iid process.

Examples

```
require("leaflet")
require("sp")

# simulate iid data and attach to spatial polygons data frame
US.df@data$data <- c(r.iid(1, M=nrow(US.graph), sigma=1))

# color palette of data
pal <- colorNumeric(palette="YlGnBu", domain=US.df@data$data)

# see map
map1<-leaflet() %>%
```

```
    addProviderTiles("CartoDB.Positron") %>%
    addPolygons(data=US.df, fillColor=~pal(data), color="#b2aeae",
                fillOpacity=0.7, weight=0.3, smoothFactor=0.2) %>%
    addLegend("bottomright", pal=pal, values=US.df$data, title="", opacity=1)
map1
```

Q.lCAR *Precision matrix for a pCAR process*

Description

Functions for creating precision matricies and observations of a Leroux CAR(lCAR) process as defined in MacNab 2011. The matrix defines the precision of estimates when observations share connections which are conditionally auto-regressive(CAR).

Usage

```
Q.lCAR(graph, sigma, rho, sparse=TRUE, vcov=FALSE)

r.lCAR(n, graph, sigma, rho)
```

Arguments

graph	matrix, square matrix indicating where two observations are connected (and therefore conditionally auto-regressive).
sigma	float > 0, process standard derviation see MacNab 2011.
rho	float >= 0 & < 1, how correlated neighbors are. The function will still run with values outside of the range [0,1) however the stability of the simulation results are not gaurunteed. see MacNab 2011.
sparse	bool Should the matrix be of class 'dsCMatrix'
vcov	bool If the vcov matrix should be returned instead of the precision matrix.
n	int > 0, number of observations to simulate from the GMRF.

Value

Q.lCAR returns either a precision or variance-covariance function with a lCAR structure.

r.lCAR retrurns a matrix with n rows which are the n observations of a Gaussian Markov random field lCAR process.

References

Y.C. MacNab On Gaussian Markov random fields and Bayesian disease mapping. Statistical Methods in Medical Research. 2011.

Examples

```
require("leaflet")
require("sp")

# simulate lCAR data and attach to spatial polygons data frame
US.df@data$data <- c(r.lCAR(1, graph=US.graph, sigma=1, rho=.99))

# color palette of data
pal <- colorNumeric(palette="YlGnBu", domain=US.df@data$data)

# see map
map1<-leaflet() %>%
    addProviderTiles("CartoDB.Positron") %>%
    addPolygons(data=US.df, fillColor=~pal(data), color="#b2aeae",
                fillOpacity=0.7, weight=0.3, smoothFactor=0.2) %>%
    addLegend("bottomright", pal=pal, values=US.df$data, title="", opacity=1)
map1
```

Q.mBYM *Modified Precision matrix for a BYM process*

Description

EXPIREMENTAL. Functions for creating precision matricies and observations of a modified BYM process as defined in MacNab 2011. The matrix defines the precision of estimates when observations share connections which are conditionally auto-regressive(CAR). Because the precision matrix is not symetric the process is not a true GMRF.

Usage

```
Q.mBYM(graph, sigma, rho, vcov=FALSE)

r.mBYM(n, graph, sigma, rho)
```

Arguments

graph	matrix, square matrix indicating where two observations are connected (and therefore conditionally auto-regressive).
sigma	float > 0, process standard derviation see MacNab 2011.
rho	float >= 0 & < 1, how correlated neighbors are. The function will still run with values outside of the range [0,1) however the stability of the simulation results are not gaurunteed. see MacNab 2011.
vcov	bool If the vcov matrix should be returned instead of the precision matrix.
n	int > 0, number of observations to simulate from the GMRF.

Value

Q.mBYM returns either a precision or variance-covariance function with a modified BYM structure.

r.mBYM retrurns a matrix with n rows which are the n observations of a pseudo Gaussian Markov random field of a modified BYM process.

References

Y.C. MacNab On Gaussian Markov random fields and Bayesian disease mapping. Statistical Methods in Medical Research. 2011.

Examples

```
## Not run:
require("leaflet")
require("sp")

# simulate mBYM data and attach to spatial polygons data frame
US.df@data$data <- c(r.mBYM(1, graph=US.graph, sigma=1, rho=.99))

# color palette of data
pal <- colorNumeric(palette="YlGnBu", domain=US.df@data$data)

# see map
map1<-leaflet() %>%
    addProviderTiles("CartoDB.Positron") %>%
    addPolygons(data=US.df, fillColor=~pal(data), color="#b2aeae",
                fillOpacity=0.7, weight=0.3, smoothFactor=0.2) %>%
    addLegend("bottomright", pal=pal, values=US.df$data, title="", opacity=1)
map1

## End(Not run)
```

Q.pCAR *Precision matrix for a pCAR process*

Description

Functions for creating precision matricies and observations of a proper CAR(pCAR) process as defined in MacNab 2011. The matrix defines the precision of estimates when observations share connections which are conditionally auto-regressive(CAR).

Usage

```
Q.pCAR(graph, sigma, rho, sparse=TRUE, vcov=FALSE)

r.pCAR(n, graph, sigma, rho)
```

Arguments

graph	matrix, square matrix indicating where two observations are connected (and therefore conditionally auto-regressive).
sigma	float > 0, process standard derviation see MacNab 2011.
rho	float >= 0 & < 1, how correlated neighbors are. The function will still run with values outside of the range [0,1) however the stability of the simulation results are not gaurunteed. see MacNab 2011.
sparse	bool Should the matrix be of class 'dsCMatrix'
vcov	bool If the vcov matrix should be returned instead of the precision matrix.
n	int > 0, number of observations to simulate from the GMRF.

Value

Q.pCAR returns either a precision or variance-covariance function with a pCAR structure.

r.pCAR retrurns a matrix with n rows which are the n observations of a Gaussian Markov random field pCAR process.

References

Y.C. MacNab On Gaussian Markov random fields and Bayesian disease mapping. Statistical Methods in Medical Research. 2011.

Examples

```
require("leaflet")
require("sp")

# simulate pCAR data and attach to spatial polygons data frame
US.df@data$data <- c(r.pCAR(1, graph=US.graph, sigma=1, rho=.99))

# color palette of data
pal <- colorNumeric(palette="YlGnBu", domain=US.df@data$data)

# see map
map1<-leaflet() %>%
    addProviderTiles("CartoDB.Positron") %>%
    addPolygons(data=US.df, fillColor=~pal(data), color="#b2aeae",
                fillOpacity=0.7, weight=0.3, smoothFactor=0.2) %>%
    addLegend("bottomright", pal=pal, values=US.df$data, title="", opacity=1)
map1
```

Q.RW1 *Precision matrix for an RW1 process*

Description

Functions for creating precision matricies and observations of an RW1 process

Usage

```
Q.RW1(M, sigma, sparse=TRUE)

r.RW1(n, M, sigma)
```

Arguments

M	int > 0, number of elements in the RW1 process.
sigma	float > 0, pairwise observation standard deviation.
sparse	bool Should the matrix be of class 'dsCMatrix'
n	int > 0, number of observations to simulate from the GMRF.

Value

Q.RW1 returns a precision matrix with a RW1 structure.

r.RW1 retrurns a matrix with n rows which are the n observations of an Intrinsic Gaussian Markov random field RW1 process.

Examples

```
require("ggplot2")
# simulate RW1 GMRF
obs <- r.RW1(100, M=30, sigma=1)
# resulting matrix is n x M
dim(obs)
# subtract off the first time point to more easily observe correlation
obs_adj <- obs - obs[,1]
# move objects to a data frame
rw1_df <- data.frame(obs=c(t(obs_adj)), realization=rep(1:100, each=30),
                     time=rep(1:30, 100))
# plot each realization
ggplot(data=rw1_df, aes(time, obs, group=realization, color=realization)) +
    geom_line()
```

Q.RW2 *Precision matrix for an RW2 process*

Description

Functions for creating precision matricies and observations of an RW2 process

Usage

```
Q.RW2(M, sigma, sparse=TRUE)

r.RW2(n, M, sigma)
```

Arguments

M	int > 0, number of elements in the RW2 process.
sigma	float > 0, pairwise observation standard deviation.
sparse	bool Should the matrix be of class 'dsCMatrix'
n	int > 0, number of observations to simulate from the GMRF.

Value

Q.RW2 returns a precision matrix with a RW2 structure.

r.RW2 retrurns a matrix with n rows which are the n observations of an Intrinsic Gaussian Markov random field RW2 process.

Examples

```
require("ggplot2")
# simulate RW2 GMRF
obs <- r.RW2(100, M=30, sigma=1)
# resulting matrix is n x M
dim(obs)
# move objects to a data frame
RW2_df <- data.frame(obs=c(t(obs)), realization=rep(1:100, each=30),
                     time=rep(1:30, 100))
# plot each realization
ggplot(data=RW2_df, aes(time, obs, group=realization, color=realization)) +
    geom_line()
```

sim.AR *Simulate correlated data from a precision matrix.*

Description

Takes in a square precision matrix, which ideally should be sparse and using Choleski factorization simulates data from a mean 0 process where the inverse of the precision matrix represents the variance-covariance of the points in the process. The resulting simulants represent samples of a Gaussian Markov random field (GMRF).

Usage

```
sim.AR(n, Q)
```

Arguments

n	int > 0, number of observations to simulate from the GMRF.
Q	matrix, a square precision matrix.

Value

Matrix object, matrix where each row is a single obsrevation from a GMRF with covariance structure Q^-1.

Examples

```
require("ggplot2")

# simulate 2D ar1 process
# pairwise correlation
rho <- .95
# pairwise variance
sigma <- .5

# 2 dimensions of simulations
years <- 20
ages <- 10

# kronnecker product to get joint covariance
Q2D <- kronecker(Q.AR1(M=years, sigma, rho), Q.AR1(M=ages, sigma, rho))

# simulate the data and place it in a data frame
Q2D.df <- data.frame(obs=c(sim.AR(1, Q2D)), age=rep(1:ages, years),
                     year=rep(1:years, each=ages))

# graph results
ggplot(data=Q2D.df, aes(year, obs, group=age, color=age)) + geom_line()
```

sim.GMRF *Simulate correlated data from a precision matrix.*

Description

Takes in a square precision matrix of a gaussian Markov random field, which ideally should be sparse, and using algorithm 3.1 from Gaussian Markov Random Fields by Rue & Held simulates data from a mean 0 process where the inverse of the precision matrix represents the variance-covariance of the points in the process. The resulting simulants represent samples of a Gaussian Markov random field (GMRF).

Usage

```
sim.GMRF(n, Q, tol = 1e-12)
```

Arguments

n	int > 0, number of observations to simulate from the GMRF.
Q	matrix, a square precision matrix of a GMRF.
tol	numeric, The tolerance for the removal of zero eigenvalues.

Value

Matrix object, matrix where each row is a single obsrevation from a GMRF with precision structure Q.

References

Rue, H. Held, L. Gaussian Markov Random Fields: Theory and Applications. Chapman and Hall. 2005.

Examples

```
require("ggplot2")

# simulate 2D rw1 process
# pairwise variance
sigma <- .5

# 2 dimensions of simulations
years <- 20
ages <- 10

# kronnecker product to get joint precision
Q2D <- kronecker(Q.RW1(M=years, sigma), Q.RW1(M=ages, sigma))

# simulate the data and place it in a data frame
Q2D.df <- data.frame(obs=c(sim.GMRF(1, Q2D)), age=rep(1:ages, years),
```

```
                    year=rep(1:years, each=ages))

# graph results
ggplot(data=Q2D.df, aes(year, obs, group=age, color=age)) + geom_line()
```

US.df *Spatial Polygons Data Frame of Counties for Several States*

Description

Spatial Polygons data frame with 475 counties from the US states Louisiana, Texas, Mississippi, & Arkansas. FIPS codes for the state and county are provided in the data frame.

US.graph *Matrix of Shared Boundaries Between US.df Counties*

Description

A 475x475 matrix where the index corresponds to a row in the US.df Spatial Polygons data frame and the index of the matrix at row i column j is 1 when US.df[i,] and US.df[j,] share a border and 0 when they do not.

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