Package 'dyads'

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Type Package

Title Dyadic Network Analysis

Version 1.1.2

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Depends R (>= 3.0.0), mvtnorm, stats, MASS

Description Contains functions for the MCMC simulation of dyadic network models j2 (Zijlstra, 2017, <doi:10.1080/0022250X.2017.1387858>) and p2 (Van Duijn, Snijders & Zijlstra, 2004, <doi: 10.1046/j.0039-0402.2003.00258.x>) as described in Zijlstra, Van Duijn & Snijders (2009) <doi: 10.1348/000711007X255336>.

License GPL (>= 2)

NeedsCompilation no

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R topics documented:

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dyads-package   *dyads*

Description

Package for Dyadic Network Analysis.

Details

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Package:	dyads
Type:	Package
Title:	Dyadic Network Analysis
Version:	1.1.2
Date:	2019-04-10
Author:	Bonne J.H. Zijlstra <B.J.H.Zijlstra@uva.nl>
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Depends:	R (>= 3.0.0), mvtnorm, stats, MASS
Description:	Contains functions for the MCMC simulation of dyadic network models j2 (Zijlstra, 2017, <doi:10.1080/00222
License:	GPL (>= 2)

Index of help topics:

```
dyads-package            dyads
j2                       MCMC estimates for the j2 model
p2                       MCMC estimates for the p2 model
```

Includes functions for estimation of the p2 model (van Duijn, Snijders and Zijlstra (2004) <doi:10.1046/j.0039-0402.2003.00258.x>), more specifically the adaptive random walk algorithm (Zijlstra, van Duijn and Snijders (2009) <doi:10.1348/000711007X255336>), and for the estimation of the j2 model (Zijlstra (in press) <doi:10.1080/0022250X.2017.1387858>).

Author(s)

Bonne J.H. Zijlstra Maintainer: Bonne J.H. Zijlstra <B.J.H.Zijlstra@uva.nl>

References

Zijlstra, B.J.H., Duijn, M.A.J. van, and Snijders, T.A.B. (2009). MCMC estimation for the p_2 network regression model with crossed random effects. *British Journal of Mathematical and Statistical Psychology*, 62, 143-166. Zijlstra, B.J.H. (2017). Regression of directed graphs on independent effects for density and reciprocity. *Journal of Mathematical Sociology*, 41(4), 185-192..

Examples

```
# create a very small network with covariates for illustrative purposes
S <- c(1,0,1,0,1,1,0,1,0,1)
REC <- (S*-1)+1
D1 <- matrix(c(0,1,0,1,0,1,0,1,0,1,
               0,0,0,1,0,1,0,1,0,1,
               1,1,0,0,1,0,0,0,0,0,
               1,1,1,0,1,0,0,0,0,1,
               1,0,1,0,0,1,1,0,1,0,
               0,0,0,0,0,0,1,1,1,1,
               0,0,0,0,0,1,0,1,0,1,
               1,0,0,0,0,1,1,0,1,1,
               0,1,0,1,0,1,0,1,0,0,
               1,0,1,1,1,0,0,0,0,0), ncol=10)
```

```
D2 <- abs(matrix(rep(S,10), byrow = FALSE, ncol= 10) -
           matrix(rep(REC,10), byrow = TRUE, ncol= 10))
R <- D1*t(D1)
Y <- matrix(c(0,1,1,1,1,1,0,0,1,1,
              0,0,0,1,1,1,0,0,1,0,
              1,1,0,1,1,1,0,0,1,1,
              1,1,1,0,1,1,0,1,1,0,
              1,1,1,1,0,1,1,0,1,1,
              0,1,1,1,1,0,1,1,1,0,
              1,0,1,0,1,1,0,1,0,1,
              0,1,1,1,0,1,1,0,1,1,
              1,0,1,0,1,0,1,1,0,1,
              1,1,1,0,0,1,1,1,1,0), ncol=10)

# estimate p2 model
p2(Y,sender= ~ S, receiver =  ~ REC, density = ~ D1 + D2, reciprocity= ~ R,
   burnin = 100, sample = 400, adapt = 10)
# Notice: burn-in, sample size and number of adaptive sequenses are
# much smaller than recommended to keep computation time low.
# recommended code:

p2(Y,sender= ~ S, receiver =  ~ REC, density = ~ D1 + D2, reciprocity= ~ R)
```

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j2   *MCMC estimates for the j2 model*

Description

Estimates j2 model parameters as described in Zijlstra (in press) <doi:10.1080/0022250X.2017.1387858>.

Usage

```
j2(net, sender = NULL, receiver = NULL , density = NULL, reciprocity = NULL,
burnin = NULL, sample = NULL, adapt= NULL, center = NULL, seed = NULL)
```

Arguments

net	Directed dichotomous n*n network (digraph).
sender	Optional sender covariates of lenght n.
receiver	Optinal receiver covariates of length n.
density	Optional density covariates of dimensions n*n.
reciprocity	Optional symmetric reciprocity covariates of dimensions n*n.
burnin	Optional specification of number of burn-in iterations (default is 10000).
sample	Optional specification of number of MCMC samples (default is 40000).
adapt	Optional number of adaptive sequenses (default is 100).
center	Optional boolean argument for centering predictors (default is TRUE).
seed	Optonal specification of random seed (delfault is 1).

Value

Returns a matrix with MCMC means, standard deviations, quantiles and effective sample sizes for j2 parameters.

Author(s)

Bonne J.H. Zijlstra <b.j.h.zijlstra@uva.nl>

References

Zijlstra, B.J.H. (in press). Regression of directed graphs on independent effects for density and reciprocity. *Journal of Mathematical Sociology*.

Examples

```
# create a very small network with covariates for illustrative purposes
S <- c(1,0,1,0,1,1,0,1,0,1)
REC <- c(0,0,1,1,0,0,1,1,0,0)
D1 <- matrix(c(0,1,0,1,0,1,0,1,0,0,
               0,0,1,1,0,1,0,1,0,1,
               1,1,0,0,1,0,0,0,0,0,
               1,1,1,0,1,0,0,0,0,1,
               1,0,1,0,0,1,1,0,1,1,
               0,0,0,0,0,0,1,1,1,1,
               0,0,0,0,0,1,0,1,0,1,
               1,0,0,0,0,1,1,0,1,1,
               0,1,0,1,0,1,0,1,0,0,
               0,0,1,1,1,0,0,0,0,0), ncol=10)
D2 <- abs(matrix(rep(S,10), byrow = FALSE, ncol= 10) -
            matrix(rep(REC,10), byrow = TRUE, ncol= 10))
R <- D1*t(D1)
Y <- matrix(c(0,0,1,1,1,1,0,0,1,1,
              0,0,0,1,1,1,0,0,1,0,
              1,1,0,1,1,1,0,0,1,1,
              0,1,1,0,1,1,0,1,1,0,
              1,1,1,1,0,1,1,0,1,1,
              0,1,1,1,1,0,1,1,1,0,
              1,0,1,0,1,1,0,1,0,1,
              0,1,1,1,0,1,1,0,1,1,
              1,0,1,0,1,0,1,1,0,1,
              1,1,1,0,0,1,1,1,1,0), ncol=10)

# estimate j2 model
j2(Y,sender= ~ S, receiver =  ~ REC, density = ~ D1 + D2, reciprocity= ~ R,
   burnin = 100, sample = 400, adapt = 10)
# notice: burn-in, sample size and number of adaptive sequenses are
# much smaller than recommended to keep computation time low.
# recommended code:

j2(Y,sender= ~ S, receiver =  ~ REC, density = ~ D1 + D2, reciprocity= ~ R)
```

| p2 | *MCMC estimates for the p2 model* |

Description

Estimates p2 model parameters with the adaptive random walk algorithm as described in Zijlstra, Van Duijn and Snijders (2009) <doi: 10.1348/000711007X255336>.

Usage

```
p2(net, sender = NULL, receiver = NULL, density = NULL, reciprocity = NULL,
burnin = NULL, sample = NULL, adapt = NULL, seed = NULL)
```

Arguments

net	Directed dichotomous n*n network (digraph).
sender	Optional sender covariates of lenght n.
receiver	Optinal receiver covariates of length n.
density	Optional density covariates of dimensions n*n.
reciprocity	Optional symmetric reciprocity covariates of dimensions n*n.
burnin	Optional specification of number of burn-in iterations (default is 10000).
sample	Optional specification of number of MCMC samples (default is 40000).
adapt	Optional number of adaptive sequenses (default is 100).
seed	Optonal specification of random seed (delfault is 1).

Value

Returns a matrix with MCMC means, standard deviations, quantiles and estimated effective sample sizes for p2 parameters.

Author(s)

Bonne J.H. Zijlstra <b.j.h.zijlstra@uva.nl>

References

Zijlstra, B.J.H., Duijn, M.A.J. van, and Snijders, T.A.B. (2009). MCMC estimation for the p_2 network regression model with crossed random effects. *British Journal of Mathematical and Statistical Psychology*, 62, 143-166.

Examples

```
# create a very small network with covariates for illustrative purposes
S <- c(1,0,1,0,1,1,0,1,0,1)
REC <- (S*-1)+1
D1 <- matrix(c(0,1,0,1,0,1,0,1,0,1,
               0,0,0,1,0,1,0,1,0,1,
               1,1,0,0,1,0,0,0,0,0,
               1,1,1,0,1,0,0,0,0,1,
               1,0,1,0,0,1,1,0,1,0,
               0,0,0,0,0,0,1,1,1,1,
               0,0,0,0,0,1,0,1,0,1,
               1,0,0,0,0,1,1,0,1,1,
               0,1,0,1,0,1,0,1,0,0,
               1,0,1,1,1,0,0,0,0,0), ncol=10)
D2 <- abs(matrix(rep(S,10), byrow = FALSE, ncol= 10) -
          matrix(rep(REC,10), byrow = TRUE, ncol= 10))
R <- D1*t(D1)
Y <- matrix(c(0,1,1,1,1,1,0,0,1,1,
              0,0,0,1,1,1,0,0,1,0,
              1,1,0,1,1,1,0,0,1,1,
              1,1,1,0,1,1,0,1,1,0,
              1,1,1,1,0,1,1,0,1,1,
              0,1,1,1,1,0,1,1,1,0,
              1,0,1,0,1,1,0,1,0,1,
              0,1,1,1,0,1,1,0,1,1,
              1,0,1,0,1,0,1,1,0,1,
              1,1,1,0,0,1,1,1,1,0), ncol=10)

# estimate p2 model
p2(Y,sender= ~ S, receiver =  ~ REC, density = ~ D1 + D2, reciprocity= ~ R,
   burnin = 100, sample = 400, adapt = 10)
# Notice: burn-in, sample size and number of adaptive sequenses are
# much smaller than recommended to keep computation time low.
# recommended code:

p2(Y,sender= ~ S, receiver =  ~ REC, density = ~ D1+ D2, reciprocity= ~ R)
```

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