

Package ‘dyads’

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Type Package

Title Dyadic Network Analysis

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Depends R (>= 3.0.0)

Imports stats, CholWishart, MASS, RcppZiggurat, Rfast, mvtnorm

Suggests plyr

Description Contains functions for the MCMC simulation of dyadic network models j2 (Zijlstra, 2017, <[doi:10.1080/0022250X.2017.1387858](https://doi.org/10.1080/0022250X.2017.1387858)>) and p2 (Van Duijn, Snijders & Zijlstra, 2004, <[doi:10.1046/j.0039-0402.2003.00258.x](https://doi.org/10.1046/j.0039-0402.2003.00258.x)>), the multilevel p2 model (Zijlstra, Van Duijn & Snijders (2009) <[doi:10.1348/000711007X255336](https://doi.org/10.1348/000711007X255336)>), and the bidirectional (multilevel) counterpart of the the multilevel p2 model as described in Zijlstra, Van Duijn & Snijders (2009) <[doi:10.1348/000711007X255336](https://doi.org/10.1348/000711007X255336)>, the (multilevel) b2 model.

License GPL (>= 2)

NeedsCompilation no

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dyads-package	<i>dyads</i>
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Description

Package for Dyadic Network Analysis.

Details

Package: dyads
 Type: Package
 Title: Dyadic Network Analysis
 Version: 1.2.1
 Date: 2022-08-16
 Author: Bonne J.H. Zijlstra <B.J.H.Zijlstra@uva.nl>
 Maintainer: Bonne J.H. Zijlstra <B.J.H.Zijlstra@uva.nl>
 Depends: R (>= 3.0.0)
 Imports: stats, CholWishart, MASS, RcppZiggurat, Rfast, mvtnorm
 Suggests: plyr
 Description: Contains functions for the MCMC simulation of dyadic network models j2 (Zijlstra, 2017, <doi:10.1080/0022250X.2017.1387858>), and for their bidirectional counterpart, b2.
 License: GPL (>= 2)

Index of help topics:

b2ML	MCMC estimates for the (multilevel) b2 model
dyads-package	dyads
j2	MCMC estimates for the j2 model
p2	MCMC estimates for the p2 model
p2ML	MCMC estimates for the (multilevel) p2 model

Includes functions for estimation of the (multilevel) 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>), for the estimation of the j2 model (Zijlstra (2017) <doi:10.1080/0022250X.2017.1387858>), and for their bidirectional counterpart, b2.

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,
              1,1,1,0,0,1,1,1,0,0), 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 sequences are
# much smaller than recommended to keep computation time low.
# recommended code:
## Not run:
p2(Y,sender= ~ S, receiver = ~ REC, density = ~ D1 + D2, reciprocity= ~ R)

## End(Not run)

```

Description

Estimates the (multilevel) b2 model parameters, which is the bidirectional counterpart of the multilevel p2 model as described in Zijlstra, Van Duijn and Snijders (2006) <doi: 10.1027/1614-2241.2.1.42>.

Usage

```
b2ML(nets, actor = NULL, density = NULL, adapt = NULL, burnin = NULL, center = NULL,
     separate = NULL, densVar = NULL, seed = NULL)
```

Arguments

nets	List with n dichotomous symmetric dependent networks.
actor	Optional matrix with a stacked actor covariate, corresponding to the n networks. Multiple actor covariates can be added as a formula object, see example below
density	Optional matrix with symmetric a stacked density covariate, with dimensions similar to the n dependent networks. Multiple density covariates can be added as a formula object, see example below
adapt	Optional number of adaptive sequenses (default is 100).
burnin	Optional specification of number of burn-in iterations (default is 5000).
center	Optional argument for centering predictors (default is TRUE).
separate	Optional argument for estimating separate coefficients for the n dependent networks (default is FALSE).
densVar	Optional argument for estimating density variance at the network level (default is TRUE).
seed	Optional specification of random seed (default is 1).

Value

Returns a fitted model of class b2ML, to be opened with the function summary().

Author(s)

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

References

Zijlstra, B. J., Van Duijn, M. A., & Snijders, T. A. (2006). The Multilevel p2 Model A random effects model for the analysis of multiple social networks. *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences*, 2(1), 42.

Examples

```
# create two very small networks with covariates for illustrative purposes
Y1 <- matrix(c( 0,1,1,1,1,1,1,1,0,
               1,0,1,0,1,1,1,1,1,
               1,1,0,0,1,1,1,1,0,1,
               1,0,0,0,1,0,0,1,0,0,
               1,1,1,1,0,1,1,0,1,1,
               1,1,1,0,1,0,1,0,1,1,
               1,1,1,0,1,1,0,1,1,1,
               1,1,1,1,0,0,1,0,0,1,
               1,1,0,0,1,1,1,0,0,1,
```

```

      0,1,1,0,1,1,1,1,0), ncol=10)
Y2 <- matrix(c( 0,0,1,0,1,1,0,1,0,0,
               0,0,0,0,0,0,0,1,1,0,
               1,0,0,1,0,1,0,1,0,0,
               0,0,1,0,0,0,1,1,0,0,
               1,0,0,0,0,0,1,1,0,0,
               1,0,1,0,0,0,1,1,0,0,
               0,0,0,1,1,1,0,1,0,0,
               1,1,1,1,1,1,0,0,1,
               0,1,0,0,0,0,0,0,0,0,
               0,0,0,0,0,0,0,1,0,0), ncol=10)
Y <- list(Y1, Y2)
Aa1 <- c(1,0,1,0,1,1,0,1,0,1)
Aa2 <- c(1,0,0,1,0,0,1,1,0,1)
Aa <- list(Aa1, Aa2)
Aat <- do.call(plyr::rbind.fill.matrix, Aa)
Ab1 <- c(0,0,0,0,0,0,0,0,0,0)
Ab2 <- c(1,1,1,1,1,1,1,1,1,1)
Ab <- list(Ab1, Ab2)
Abt <- do.call(plyr::rbind.fill.matrix, Ab)
Da1 <- abs(matrix(rep(Aa1,10), byrow = FALSE, ncol= 10) -
             matrix(rep(Aa1,10), byrow = TRUE, ncol= 10))
Da2 <- abs(matrix(rep(Aa2,10), byrow = FALSE, ncol= 10) -
             matrix(rep(Aa2,10), byrow = TRUE, ncol= 10))
Da <- list(Da1, Da2)
Dat <- do.call(plyr::rbind.fill.matrix, Da)

# estimate b2 model for two networks
M1 <- b2ML(Y,actor= ~ Aat + Abt, density = ~ Dat, adapt = 10, burnin = 100, densVar = FALSE)
summary(M1)
# Notice: burn-in, and number of adaptive sequenses are
# much smaller than recommended to keep computation time low.
# recommended code:
## Not run:
M1 <- b2ML(Y,actor= ~ Aat + Abt, density = ~ Dat, densVar = FALSE)
summary(M1)

## End(Not run)

# estimate b2 model for a single network
M2 <- b2ML(list(Y[[1]]),actor= ~ Aat[1:10,], density = ~ Dat[1:10,], adapt = 10, burnin = 100,
densVar = FALSE)
summary(M2)
# Notice: burn-in, and number of adaptive sequenses are
# much smaller than recommended to keep computation time low.
# recommended code:
## Not run:
M2 <- b2ML(list(Y[[1]]),actor= ~ Aat[1:10,], density = ~ Dat[1:10,], densVar = FALSE)
summary(M2)

## End(Not run)

```

j2

*MCMC estimates for the j2 model***Description**

Estimates j2 model parameters as described in Zijlstra (2017) <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 length n.
receiver	Optional 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 sequences (default is 100).
center	Optional boolean argument for centering predictors (default is TRUE).
seed	Optional specification of random seed (default 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. (2017). Regression of directed graphs on independent effects for density and reciprocity. *The Journal of Mathematical Sociology* 41 (4).

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:
## Not run:
j2(Y,sender= ~ S, receiver = ~ REC, density = ~ D1 + D2, reciprocity= ~ R)

## End(Not run)
```

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 length n.
receiver	Optional 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	Optional specification of random seed (default 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:
## Not run:
p2(Y,sender= ~ S, receiver = ~ REC, density = ~ D1+ D2, reciprocity= ~ R)

## End(Not run)

```

p2ML

*MCMC estimates for the (multilevel) p2 model***Description**

Estimates the (multilevel) p2 model parameters,as described in Zijlstra, Van Duijn and Snijders (2006) <doi: 10.1027/1614-2241.2.1.42>.

Usage

```
p2ML(nets, sender = NULL, receiver = NULL, density =~ 1, reciprocity =~ 1,
    adapt = NULL, burnin = NULL, center = NULL, separate= NULL, seed = NULL)
```

Arguments

nets	List with n dichotomous dependent directed networks.
sender	Optional matrix with a stacked actor-level sender covariate, corresponding to the n networks. Multiple sender covariates can be added as a formula object, see example below
receiver	Optional matrix with a stacked actor-level receiver covariate, corresponding to the n networks. Multiple receiver covariates can be added as a formula object
density	Optional stacked matrix with a density covariate, with dimensions similar to the n dependent networks. Multiple density covariates can be added as a formula object, see example below
reciprocity	Optional stacked matrix with a symmetric reciprocity covariate, with dimensions similar to the n dependent networks. Multiple reciprocity covariates can be added as a formula object
adapt	Optional number of adaptive sequenses (default is 125).

burnin	Optional specification of number of burn-in iterations (default is 2500).
center	Optional argument for centering predictors (default is TRUE).
separate	Optional argument for estimating separate coefficients for the n dependent networks (default is FALSE).
seed	Optional specification of random seed (default is 1).

Value

Returns a fitted model of class 2ML, to be opened with the function `summary()`.

Author(s)

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

References

Zijlstra, B. J., Van Duijn, M. A., & Snijders, T. A. (2006). The Multilevel p2 Model A random effects model for the analysis of multiple social networks. *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences*, 2(1), 42.

Examples

```
# create two very small networks with covariates for illustrative purposes
Y1 <- 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)
Y2 <- matrix(c(0,0,1,0,1,0,0,1,0,0,
              0,0,0,0,0,0,0,1,1,0,
              0,0,0,1,0,1,0,1,0,1,
              0,0,1,0,0,0,1,1,0,0,
              1,0,0,1,0,0,1,0,0,1,
              0,0,1,0,0,0,1,1,0,0,
              0,1,0,0,1,0,0,0,0,0,
              1,0,1,0,1,1,1,0,0,1,
              0,1,0,1,0,0,0,0,0,0,
              0,1,0,1,0,0,0,1,0,0), ncol=10)
Y <- list(Y1, Y2)
Sa1 <- c(1,0,1,0,1,1,0,1,0,1)
Sa2 <- c(1,0,0,1,0,0,1,1,0,1)
Sa <- list(Sa1, Sa2)
Sat <- Rat <- do.call(plyr::rbind.fill.matrix, Sa)
Sb1 <- c(0,1,1,0,1,0,1,0,1,0)
Sb2 <- c(1,0,1,0,0,1,0,1,0,1)
Sb <- list(Sb1, Sb2)
```

```
Sbt <- do.call(ply::rbind.fill.matrix, Sb)
Da1 <- abs(matrix(rep(Sa1,10), byrow = FALSE, ncol= 10) -
            matrix(rep(Sa1,10), byrow = TRUE, ncol= 10))
Da2 <- abs(matrix(rep(Sa2,10), byrow = FALSE, ncol= 10) -
            matrix(rep(Sa2,10), byrow = TRUE, ncol= 10))
Da <- list(Da1, Da2)
Dat <- do.call(ply::rbind.fill.matrix, Da)

# estimate p2 model for two networks
M1 <- p2ML(Y, sender= ~ Sat + Sbt, receiver= ~ Rat, density = ~ Dat, adapt = 10, burnin = 100)
summary(M1)
# Notice: burn-in, and number of adaptive sequenses are
# much smaller than recommended to keep computation time low.
# recommended code:
## Not run:
M1 <- p2ML(Y, sender= ~ Sat + Sbt, receiver= ~ Rat, density = ~ Dat)
summary(M1)

## End(Not run)

# estimate p2 model for a single network
M2 <- p2ML(list(Y[[1]]), sender= ~ Sat[1:10,] + Sbt[1:10,], receiver= ~ Rat[1:10,],
           density = ~ Dat[1:10,], adapt = 10, burnin = 100)
summary(M2)
# Notice: burn-in, and number of adaptive sequenses are
# much smaller than recommended to keep computation time low.
# recommended code:
## Not run:
M2 <- p2ML(list(Y[[1]]), sender= ~ Sat[1:10,] + Sbt[1:10,], receiver= ~ Rat[1:10,],
           density = ~ Dat[1:10,])
summary(M2)

## End(Not run)
```

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