Package ‘dyads’
March 28, 2019

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>
Maintainer Bonne J.H. Zijlstra <B.J.H.Zijlstra@uva.nl>
Depends R (>= 3.0.0), mvtnorm, stats, MASS
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
Date/Publication 2019-03-28 10:00:12 UTC

R topics documented:

- dyads-package
- j2
- p2

Index

<table>
<thead>
<tr>
<th>dyads-package</th>
<th>dyads</th>
</tr>
</thead>
</table>

Description

Package for Dyadic Network Analysis.

Details
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>
Maintainer: Bonne J.H. Zijlstra <B.J.H.Zijlstra@uva.nl>
Depends: R (>= 3.0.0), mvtnorm, stats, MASS
License: GPL (>= 2)

Index of help topics:

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


Author(s)

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

References


Examples

# create a very small network with covariates for illustrative purposes
S <- c(1,0,1,0,1,0,1,0,1)
REC <- (S==1)+1
D1 <- matrix(c(0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1), ncol=10)
`j2 <- abs(matrix(rep(S,10), byrow = FALSE, ncol= 10) -
         matrix(rep(REC,10), byrow = TRUE, ncol= 10))
R <- D1*t(D1)
Y <- matrix(c(0,1,1,1,1,0,0,1,1,
           0,0,1,1,0,0,1,0,
           1,1,0,1,1,0,0,1,1,
           1,1,1,0,1,0,1,1,0,
           1,1,1,0,1,1,0,1,1,
           0,1,1,1,0,1,1,1,0,
           1,0,1,0,1,0,1,0,1,
           0,1,1,0,1,0,1,0,1,
           1,0,1,0,1,0,1,0,1,
           1,1,1,0,0,1,1,1,0), 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 sequences are
# much smaller than recommended to keep computation time low.
# recommended code:

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

---

### j2

MCMC estimates for the j2 model

**Description**


**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


Examples

```r
# create a very small network with covariates for illustrative purposes
S <- c(1,0,1,0,1,0,1,0,1,0)
REC <- c(0,0,1,0,0,1,1,0,0,0)
D1 <- matrix(c(0,1,0,1,0,1,1,0,1,0,0,0,1,1,0,1,0,1,0,0,1,1,0,0,1,1,0,0,1,1,0,0,1,0,0,1,0,0,1,1,1,1,1,0,0,0,0,0,0), 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,
              0,0,1,1,1,1,0,0,1,1,
              1,0,1,1,1,1,0,0,1,1,
              0,1,1,1,1,1,0,0,1,1,
              1,1,1,1,1,1,0,0,1,1,
              0,1,1,1,1,1,0,0,1,1,
              1,0,1,1,1,1,0,0,1,1,
              0,1,1,1,1,1,0,0,1,1,
              1,0,1,1,1,1,0,0,1,1,
              1,1,1,1,1,1,0,0,1,1), 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 sequences are
# much smaller than recommended to keep computation time low.
# recommended code:

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

Examples

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

# estimate pR model
pR(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:

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

*Topic j2 model, p2 model
   dyads-package, 1

*Topic j2 model
   j2, 3

*Topic p2 model
   p2, 5

 dyads (dyads-package), 1
 dyads-package, 1

 j2, 3

 p2, 5