Package 'NBR'

August 3, 2020

Type Package

Title Network-Based R-Statistics using Mixed Effects Models

Version 0.1.3

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Description An implementation of network-based statistics in R using mixed effects models. Theoretical background for Network-Based Statistics can be found in Zalesky et al. (2010) <doi:10.1016/j.neuroimage.2010.06.041>. For Mixed Effects Models check the R package <https://CRAN.R-project.org/package=nlme>.

Depends R (>= 2.10)

License GPL-3

Encoding UTF-8

LazyData true

Imports nlme, parallel, stats

RoxygenNote 7.0.2

Suggests graphics, knitr, lattice, rmarkdown

VignetteBuilder knitr

Language en-US

NeedsCompilation no

Repository CRAN

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R topics documented:

`frontal2D` *Frontal lobe functional connectivity in ADHD*

Description

A dataset containing the functional connectivity between frontal lobe areas of the brain in 24 control and 24 patients with Attention-Deficit/Hyperactivity Disorder (ADHD).

Usage

```
frontal2D
```

Format

A data frame with 48 rows and 381 variables:

Group Diagnostic group factor, control or patient.

Sex Factor, female (F) or male (M).

Age Chronological age in years, numeric.

FAG.FAD Functional connectivity between FAG and FAD regions, numeric

FAG.F1G Functional connectivity between FAG and F1G regions, numeric

FAD.F1G Functional connectivity between FAD and F1G regions, numeric

FAG.F1D Functional connectivity between FAG and F1D regions, numeric

FAD.F1D Functional connectivity between FAD and F1D regions, numeric

F1G.F1D Functional connectivity between F1G and F1D regions, numeric

FAG.F1OG Functional connectivity between FAG and F1OG regions, numeric

FAD.F1OG Functional connectivity between FAD and F1OG regions, numeric

F1G.F1OG Functional connectivity between F1G and F1OG regions, numeric

F1D.F1OG Functional connectivity between F1D and F1OG regions, numeric

FAG.F1OD Functional connectivity between FAG and F1OD regions, numeric

FAD.F1OD Functional connectivity between FAD and F1OD regions, numeric

F1G.F1OD Functional connectivity between F1G and F1OD regions, numeric

F1D.F1OD Functional connectivity between F1D and F1OD regions, numeric

F1OG.F1OD Functional connectivity between F1OG and F1OD regions, numeric

FAG.F2G Functional connectivity between FAG and F2G regions, numeric

FAD.F2G Functional connectivity between FAD and F2G regions, numeric

F1G.F2G Functional connectivity between F1G and F2G regions, numeric

F1D.F2G Functional connectivity between F1D and F2G regions, numeric

F1OG.F2G Functional connectivity between F1OG and F2G regions, numeric

F1OD.F2G Functional connectivity between F1OD and F2G regions, numeric

FAG.F2D Functional connectivity between FAG and F2D regions, numeric

FAD.F2D Functional connectivity between FAD and F2D regions, numeric

F1G.F2D Functional connectivity between F1G and F2D regions, numeric

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F1OD.ORD Functional connectivity between F1OD and ORD regions, numeric
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F2D.ORD Functional connectivity between F2D and ORD regions, numeric
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F1D.SMAG Functional connectivity between F1D and SMAG regions, numeric
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F1D.COBG Functional connectivity between F1D and COBG regions, numeric

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F3OG.COBG Functional connectivity between F3OG and COBG regions, numeric

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FAD.COBD Functional connectivity between FAD and COBD regions, numeric
F1G.COBD Functional connectivity between F1G and COBD regions, numeric
F1D.COBD Functional connectivity between F1D and COBD regions, numeric
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F2D.COBD Functional connectivity between F2D and COBD regions, numeric
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ORD.COBD Functional connectivity between ORD and COBD regions, numeric
SMAG.COBD Functional connectivity between SMAG and COBD regions, numeric
SMAD.COBD Functional connectivity between SMAD and COBD regions, numeric
COBG.COBD Functional connectivity between COBG and COBD regions, numeric
FAG.FMG Functional connectivity between FAG and FMG regions, numeric
FAD.FMG Functional connectivity between FAD and FMG regions, numeric
F1G.FMG Functional connectivity between F1G and FMG regions, numeric
F1D.FMG Functional connectivity between F1D and FMG regions, numeric
F1OG.FMG Functional connectivity between F1OG and FMG regions, numeric
F1OD.FMG Functional connectivity between F1OD and FMG regions, numeric
F2G.FMG Functional connectivity between F2G and FMG regions, numeric
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SMAD.FMG Functional connectivity between SMAD and FMG regions, numeric

COBG.FMG Functional connectivity between COBG and FMG regions, numeric

COBD.FMG Functional connectivity between COBD and FMG regions, numeric

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COBD.FMD Functional connectivity between COBD and FMD regions, numeric

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ORD.FMOG Functional connectivity between ORD and FMOG regions, numeric
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SMAD.FMOG Functional connectivity between SMAD and FMOG regions, numeric
COBG.FMOG Functional connectivity between COBG and FMOG regions, numeric
COBD.FMOG Functional connectivity between COBD and FMOG regions, numeric
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SMAD.FMOD Functional connectivity between SMAD and FMOD regions, numeric
COBG.FMOD Functional connectivity between COBG and FMOD regions, numeric
COBD.FMOD Functional connectivity between COBD and FMOD regions, numeric
FMG.FMOD Functional connectivity between FMG and FMOD regions, numeric
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F1OD.GRG Functional connectivity between F1OD and GRG regions, numeric
F2G.GRG Functional connectivity between F2G and GRG regions, numeric
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F3OD.GRG Functional connectivity between F3OD and GRG regions, numeric
ORG.GRG Functional connectivity between ORG and GRG regions, numeric
ORD.GRG Functional connectivity between ORD and GRG regions, numeric
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SMAD.GRG Functional connectivity between SMAD and GRG regions, numeric
COBG.GRG Functional connectivity between COBG and GRG regions, numeric
COBD.GRG Functional connectivity between COBD and GRG regions, numeric
FMG.GRG Functional connectivity between FMG and GRG regions, numeric
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FMOG.GRG Functional connectivity between FMOG and GRG regions, numeric
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ORD.GRD Functional connectivity between ORD and GRD regions, numeric

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GRG.GRD Functional connectivity between GRG and GRD regions, numeric

Details

Data was taken from the ADHD200 dataset and variables were manipulated in order to be different of the original data. Functional connectivity was measured as the Pearson correlation between the average fMRI signal from the regions of interest (ROI), i.e., 28 anatomical areas of the frontal lobe. Thus, a total of 378 pairwise connections are contained in the dataset.

Source

https://fcon_1000.projects.nitrc.org/indi/adhd200/

nbr_lm *Network-based R-statistics using Linear Model*

Description

This function computes the specified linear model (LM) for each edge in the network, and calculates the family wise error (FWE) p-value for the size of the clusters of connected edges that are individually below the P threshold (*thrP*), or above the T threshold (*thrT*). FWE estimation is based on the null distribution of the maximum size of sets of connected edges (defined as above), obtained with *nperm* permutations of the original data.

Usage

```
nbr_lm(net, nnodes, idata, mod, diag = FALSE, nperm,
       thrP = 0.05, thrT = NULL, cores = NULL,
       nudist = FALSE, expList = NULL, verbose = TRUE,
       ...)
```

Arguments

net	3D volume (2D matrices for each observation) or 2D matrix of edges as columns.
nnodes	Number of network nodes.
idata	Matrix or data.frame including independent variables of interest of the model.
mod	Model, specify as a string, e.g., "~Group + Age".
diag	Logical indicating if matrix diagonal is to be included in the analysis (default: FALSE).
nperm	Number of permutations.
thrP	Individual edge p-value threshold (if NULL, thrT should be given).
thrT	Individual edge T-value threshold (if NULL, thrP should be given).
cores	Number of selected cores for parallel computing (default: NULL).
nudist	Logical indicating if null distribution should be returned (default: FALSE).
expList	Character string adding variable names to the varlist of 'clusterExport' (default: NULL).
verbose	Logical indicating if messages should be printed (default: TRUE).
...	Additional arguments to be passed to the low level 'lm' function.

Details

It's VERY IMPORTANT when giving *net* as a 2D matrix or data.frame, to be completely sure that column distribution fits that of the upper triangle indices of an *nnodes* * *nnodes* matrix. This may be verified through the edge indices, e.g., "which(upper.tri(matrix(nrow = nnodes, ncol = nnodes)), arr.ind = T)" (see vignette NBR-LME for more details).

Regarding *nperm*, I suggest first setting it to small values (5 or 10) in order to test that everything runs fine. After that, set *nperm* to 1000 or larger number to decrease the margin of error of the FWE p-value (see https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Randomise/Theory#Conditional_Monte_Carlo_Permutation_Tests to explore the behavior of FWE p-value as a function of *nperm*).

Value

List containing the observed statistics and their corresponding FWE p-values, if requested by *nudist* it will return the null distribution.

1. Observed statistics for every individual edge: corresponding subset of connected nodes and strength for each model term.
2. FWE for components: binary and strength sum, with their corresponding FWE p-value.
3. Null Distribution: maximal component size and strength for each permutation. Only returned if *nudist* is TRUE.

Examples

```
data(frontal2D)

nbr_result <- nbr_lm(net = frontal2D[,-(1:3)], nnodes = 28,
  idata = frontal2D[,1:3], mod = "~ Group + Sex * Age",
  thrP = NULL, thrT = 4, nperm = 5)
show(nbr_result)
```

---

nbr_lme *Network-based R-statistics using Mixed Effects Models*

Description

This function computes the specified (non)linear mixed models (LME) for each edge in the network, and calculates the family wise error (FWE) p-value for the size of the clusters of connected edges that are individually below the P threshold (*thrP*), or above the T threshold (*thrT*). FWE estimation is based on the null distribution of the maximum size of sets of connected edges (defined as above), obtained with *nperm* permutations of the original data.

Usage

```
nbr_lme(net, nnodes, idata, mod, rdm, diag = FALSE,
        nperm, thrP = 0.05, thrT = NULL, cores = NULL,
        nudist = FALSE, expList = NULL, verbose = TRUE,
        ...)
```

Arguments

net	3D volume (2D matrices for each observation) or 2D matrix of edges as columns.
nnodes	Number of network nodes.
idata	Matrix or data.frame including independent variables of interest of the model.
mod	Fixed effects, specify as a string, e.g., "~Session + Sex".
rdm	Random effects, specify as a string, e.g., "~1+Sessionlid".
diag	Logical indicating if matrix diagonal is to be included in the analysis (default: FALSE).
nperm	Number of permutations.
thrP	Individual edge p-value threshold (if NULL, thrT should be given).
thrT	Individual edge T-value threshold (if NULL, thrP should be given).
cores	Number of selected cores for parallel computing (default: NULL).
nudist	Logical indicating if null distribution should be returned (default: FALSE).
expList	Character string adding variable names to the varlist of 'clusterExport' (default: NULL).
verbose	Logical indicating if messages should be printed (default: TRUE).
...	Additional arguments to be passed to the low level 'lm' function.

Details

It's VERY IMPORTANT when giving *net* as a 2D matrix or data.frame, to be completely sure that column distribution fits that of the upper triangle indices of an *nnodes* * *nnodes* matrix. This may be verified through the edge indices, e.g., "which(upper.tri(matrix(nrow = nnodes, ncol = nnodes)), arr.ind = T)" (see vignette NBR-LME for more details).

Regarding *nperm*, I suggest first setting it to small values (5 or 10) in order to test that everything runs fine. After that, set *nperm* to 1000 or larger number to decrease the margin of error of the FWE p-value (see https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Randomise/Theory#Conditional_Monte_Carlo_Permutation_Tests to explore the behavior of FWE p-value as a function of *nperm*).

Value

List containing the observed statistics and their corresponding FWE p-values, if requested by *nudist* it will return the null distribution.

1. Observed statistics for every individual edge: corresponding subset of connected nodes and strength for each model term.
2. FWE for components: binary and strength sum, with their corresponding FWE p-value.
3. Null Distribution: maximal component size and strength for each permutation. Only returned if *nudist* is TRUE.

Examples

```
data(voles)

nbr_result <- nbr_lme(net = voles[,-(1:3)], nnodes = 16,
  idata = voles[,1:3], mod = "~ Session*Sex",
  rdm = "~ 1+Session|id", nperm = 5,
  na.action = na.exclude
  )
show(nbr_result)
```

---

nbr_lme_aov *Network-based R-statistics using Mixed Effects Models ANOVA*

Description

This function computes the specified (non)linear mixed models (LME) ANOVA for each edge in the network, and calculates the family wise error (FWE) p-value for the size of the clusters of connected edges that are individually below the P threshold (*thrP*), or above the F threshold (*thrF*). FWE estimation is based on the null distribution of the maximum size of sets of connected edges (defined as above), obtained with *nperm* permutations of the original data.

Usage

```
nbr_lme_aov(net, nnodes, idata, mod, rdm, diag = FALSE,
            nperm, thrP = 0.05, thrF = NULL, cores = NULL,
            nudist = FALSE, expList = NULL,
            verbose = TRUE, ...)
```

Arguments

net	3D volume (2D matrices for each observation) or 2D matrix of edges as columns.
nnodes	Number of network nodes.
idata	Matrix or data.frame including independent variables of interest of the model.
mod	Fixed effects, specify as a string, e.g., "~Session + Sex".
rdm	Random effects, specify as a string, e.g., "~1+Sessionlid".
diag	Logical indicating if matrix diagonal is to be included in the analysis (default: FALSE).
nperm	Number of permutations.
thrP	Individual edge p-value threshold (if NULL, thrF should be given).
thrF	Individual edge F-value threshold (if NULL, thrP should be given).
cores	Number of selected cores for parallel computing (default: NULL).
nudist	Logical indicating if null distribution should be returned (default: FALSE).

`expList`	Character string adding variable names to the varlist of 'clusterExport' (default: NULL).
`verbose`	Logical indicating if messages should be printed (default: TRUE).
`...`	Additional arguments to be passed to the low level 'lm' function.

Details

It's VERY IMPORTANT when giving *net* as a 2D matrix or data.frame, to be completely sure that column distribution fits that of the upper triangle indices of an *nnodes* * *nnodes* matrix. This may be verified through the edge indices, e.g., "which(upper.tri(matrix(nrow = nnodes, ncol = nnodes)), arr.ind = T)" (see vignette NBR-LME for more details).

Regarding *nperm*, I suggest first setting it to small values (5 or 10) in order to test that everything runs fine. After that, set *nperm* to 1000 or larger number to decrease the margin of error of the FWE p-value (see https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Randomise/Theory#Conditional_Monte_Carlo_Permutation_Tests to explore the behavior of FWE p-value as a function of *nperm*).

Value

List containing the observed statistics and their corresponding FWE p-values, if requested by *nudist* it will return the null distribution.

1. Observed statistics for every individual edge: corresponding subset of connected nodes and strength for each model term.
2. FWE for components: binary and strength sum, with their corresponding FWE p-value.
3. Null Distribution: maximal component size and strength for each permutation. Only returned if *nudist* is TRUE.

Examples

```
data(voles)

nbr_result <- nbr_lme_aov(net = voles[,-(1:3)],
  nnodes = 16, idata = voles[,1:3],
  mod = "~ Session*Sex",
  rdm = "~ 1+Session|id",
  nperm = 5, na.action = na.exclude
  )
show(nbr_result)
```

nbr_lm_aov *Network-based R-statistics using Linear Model ANOVA*

Description

This function computes the specified linear model (LM) ANOVA for each edge in the network, and calculates the family wise error (FWE) p-value for the size of the clusters of connected edges that are individually below the P threshold (*thrP*), or above the F threshold (*thrF*). FWE estimation is based on the null distribution of the maximum size of sets of connected edges (defined as above), obtained with *nperm* permutations of the original data.

Usage

```
nbr_lm_aov(net, nnodes, idata, mod, diag = FALSE, nperm,
           thrP = 0.05, thrF = NULL, cores = NULL,
           nudist = FALSE, expList = NULL,
           verbose = TRUE, ...)
```

Arguments

net	3D volume (2D matrices for each observation) or 2D matrix of edges as columns.
nnodes	Number of network nodes.
idata	Matrix or data.frame including independent variables of interest of the model.
mod	Model, specify as a string, e.g., "~Group + Age".
diag	Logical indicating if matrix diagonal is to be included in the analysis (default: FALSE).
nperm	Number of permutations.
thrP	Individual edge p-value threshold (if NULL, thrF should be given).
thrF	Individual edge F-value threshold (if NULL, thrP should be given).
cores	Number of selected cores for parallel computing (default: NULL).
nudist	Logical indicating if null distribution should be returned (default: FALSE).
expList	Character string adding variable names to the varlist of 'clusterExport' (default: NULL).
verbose	Logical indicating if messages should be printed (default: TRUE).
...	Additional arguments to be passed to the low level 'lm' function.

Details

It's VERY IMPORTANT when giving *net* as a 2D matrix or data.frame, to be completely sure that column distribution fits that of the upper triangle indices of an *nnodes* * *nnodes* matrix. This may be verified through the edge indices, e.g., "which(upper.tri(matrix(nrow = nnodes, ncol = nnodes)), arr.ind = T)" (see vignette NBR-LME for more details).

Regarding *nperm*, I suggest first setting it to small values (5 or 10) in order to test that everything runs fine. After that, set *nperm* to 1000 or larger number to decrease the margin of error of the FWE p-value (see https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Randomise/Theory#Conditional_Monte_Carlo_Permutation_Tests to explore the behavior of FWE p-value as a function of *nperm*).

Value

List containing the observed statistics and their corresponding FWE p-values, if requested by *nudist* it will return the null distribution.

1. Observed statistics for every individual edge: corresponding subset of connected nodes and strength for each model term.
2. FWE for components: binary and strength sum, with their corresponding FWE p-value.
3. Null Distribution: maximal component size and strength for each permutation. Only returned if *nudist* is TRUE.

Examples

```
data(frontal2D)

ncores <- 2
library(parallel)
if(detectCores() < ncores) ncores <- NULL
nbr_result <- nbr_lm_aov(net = frontal2D[,-(1:3)],
  nnodes = 28, idata = frontal2D[,1:3],
  mod = "~ Group + Sex * Age",
  thrP = 0.01, nperm = 5, cores = ncores)
show(nbr_result)
```

---

voles *Prairie voles functional connectivity*

Description

A dataset containing the functional connectivity between 16 brain areas of 32 prairie voles in three different sessions.

Usage

```
voles
```

Format

A data.frame with 96 rows and 123 variables:

id Subject ID, factor.

Sex Factor: female (F) or male (M).

Session Factor: 1st, 2nd, or 3rd.

ACC.AON Functional connectivity between ACC and AON regions, numeric

ACC.BLA Functional connectivity between ACC and BLA regions, numeric

AON.BLA Functional connectivity between AON and BLA regions, numeric

ACC.BNST Functional connectivity between ACC and BNST regions, numeric

AON.BNST Functional connectivity between AON and BNST regions, numeric

BLA.BNST Functional connectivity between BLA and BNST regions, numeric

ACC.LS Functional connectivity between ACC and LS regions, numeric

AON.LS Functional connectivity between AON and LS regions, numeric

BLA.LS Functional connectivity between BLA and LS regions, numeric

BNST.LS Functional connectivity between BNST and LS regions, numeric

ACC.MeA Functional connectivity between ACC and MeA regions, numeric

AON.MeA Functional connectivity between AON and MeA regions, numeric

BLA.MeA Functional connectivity between BLA and MeA regions, numeric

BNST.MeA Functional connectivity between BNST and MeA regions, numeric

LS.MeA Functional connectivity between LS and MeA regions, numeric

ACC.MOB Functional connectivity between ACC and MOB regions, numeric

AON.MOB Functional connectivity between AON and MOB regions, numeric

BLA.MOB Functional connectivity between BLA and MOB regions, numeric

BNST.MOB Functional connectivity between BNST and MOB regions, numeric

LS.MOB Functional connectivity between LS and MOB regions, numeric

MeA.MOB Functional connectivity between MeA and MOB regions, numeric

ACC.mPFC Functional connectivity between ACC and mPFC regions, numeric

AON.mPFC Functional connectivity between AON and mPFC regions, numeric

BLA.mPFC Functional connectivity between BLA and mPFC regions, numeric

BNST.mPFC Functional connectivity between BNST and mPFC regions, numeric

LS.mPFC Functional connectivity between LS and mPFC regions, numeric

MeA.mPFC Functional connectivity between MeA and mPFC regions, numeric

MOB.mPFC Functional connectivity between MOB and mPFC regions, numeric

ACC.NAcc Functional connectivity between ACC and NAcc regions, numeric

AON.NAcc Functional connectivity between AON and NAcc regions, numeric

BLA.NAcc Functional connectivity between BLA and NAcc regions, numeric

BNST.NAcc Functional connectivity between BNST and NAcc regions, numeric

LS.NAcc Functional connectivity between LS and NAcc regions, numeric
MeA.NAcc Functional connectivity between MeA and NAcc regions, numeric
MOB.NAcc Functional connectivity between MOB and NAcc regions, numeric
mPFC.NAcc Functional connectivity between mPFC and NAcc regions, numeric
ACC.PVN Functional connectivity between ACC and PVN regions, numeric
AON.PVN Functional connectivity between AON and PVN regions, numeric
BLA.PVN Functional connectivity between BLA and PVN regions, numeric
BNST.PVN Functional connectivity between BNST and PVN regions, numeric
LS.PVN Functional connectivity between LS and PVN regions, numeric
MeA.PVN Functional connectivity between MeA and PVN regions, numeric
MOB.PVN Functional connectivity between MOB and PVN regions, numeric
mPFC.PVN Functional connectivity between mPFC and PVN regions, numeric
NAcc.PVN Functional connectivity between NAcc and PVN regions, numeric
ACC.RSC Functional connectivity between ACC and RSC regions, numeric
AON.RSC Functional connectivity between AON and RSC regions, numeric
BLA.RSC Functional connectivity between BLA and RSC regions, numeric
BNST.RSC Functional connectivity between BNST and RSC regions, numeric
LS.RSC Functional connectivity between LS and RSC regions, numeric
MeA.RSC Functional connectivity between MeA and RSC regions, numeric
MOB.RSC Functional connectivity between MOB and RSC regions, numeric
mPFC.RSC Functional connectivity between mPFC and RSC regions, numeric
NAcc.RSC Functional connectivity between NAcc and RSC regions, numeric
PVN.RSC Functional connectivity between PVN and RSC regions, numeric
ACC.VP Functional connectivity between ACC and VP regions, numeric
AON.VP Functional connectivity between AON and VP regions, numeric
BLA.VP Functional connectivity between BLA and VP regions, numeric
BNST.VP Functional connectivity between BNST and VP regions, numeric
LS.VP Functional connectivity between LS and VP regions, numeric
MeA.VP Functional connectivity between MeA and VP regions, numeric
MOB.VP Functional connectivity between MOB and VP regions, numeric
mPFC.VP Functional connectivity between mPFC and VP regions, numeric
NAcc.VP Functional connectivity between NAcc and VP regions, numeric
PVN.VP Functional connectivity between PVN and VP regions, numeric
RSC.VP Functional connectivity between RSC and VP regions, numeric
ACC.VTA Functional connectivity between ACC and VTA regions, numeric
AON.VTA Functional connectivity between AON and VTA regions, numeric
BLA.VTA Functional connectivity between BLA and VTA regions, numeric

BNST.VTA Functional connectivity between BNST and VTA regions, numeric
LS.VTA Functional connectivity between LS and VTA regions, numeric
MeA.VTA Functional connectivity between MeA and VTA regions, numeric
MOB.VTA Functional connectivity between MOB and VTA regions, numeric
mPFC.VTA Functional connectivity between mPFC and VTA regions, numeric
NAcc.VTA Functional connectivity between NAcc and VTA regions, numeric
PVN.VTA Functional connectivity between PVN and VTA regions, numeric
RSC.VTA Functional connectivity between RSC and VTA regions, numeric
VP.VTA Functional connectivity between VP and VTA regions, numeric
ACC.Dent Functional connectivity between ACC and Dent regions, numeric
AON.Dent Functional connectivity between AON and Dent regions, numeric
BLA.Dent Functional connectivity between BLA and Dent regions, numeric
BNST.Dent Functional connectivity between BNST and Dent regions, numeric
LS.Dent Functional connectivity between LS and Dent regions, numeric
MeA.Dent Functional connectivity between MeA and Dent regions, numeric
MOB.Dent Functional connectivity between MOB and Dent regions, numeric
mPFC.Dent Functional connectivity between mPFC and Dent regions, numeric
NAcc.Dent Functional connectivity between NAcc and Dent regions, numeric
PVN.Dent Functional connectivity between PVN and Dent regions, numeric
RSC.Dent Functional connectivity between RSC and Dent regions, numeric
VP.Dent Functional connectivity between VP and Dent regions, numeric
VTA.Dent Functional connectivity between VTA and Dent regions, numeric
ACC.HipD Functional connectivity between ACC and HipD regions, numeric
AON.HipD Functional connectivity between AON and HipD regions, numeric
BLA.HipD Functional connectivity between BLA and HipD regions, numeric
BNST.HipD Functional connectivity between BNST and HipD regions, numeric
LS.HipD Functional connectivity between LS and HipD regions, numeric
MeA.HipD Functional connectivity between MeA and HipD regions, numeric
MOB.HipD Functional connectivity between MOB and HipD regions, numeric
mPFC.HipD Functional connectivity between mPFC and HipD regions, numeric
NAcc.HipD Functional connectivity between NAcc and HipD regions, numeric
PVN.HipD Functional connectivity between PVN and HipD regions, numeric
RSC.HipD Functional connectivity between RSC and HipD regions, numeric
VP.HipD Functional connectivity between VP and HipD regions, numeric
VTA.HipD Functional connectivity between VTA and HipD regions, numeric
Dent.HipD Functional connectivity between Dent and HipD regions, numeric
ACC.HipV Functional connectivity between ACC and HipV regions, numeric

AON.HipV Functional connectivity between AON and HipV regions, numeric

BLA.HipV Functional connectivity between BLA and HipV regions, numeric

BNST.HipV Functional connectivity between BNST and HipV regions, numeric

LS.HipV Functional connectivity between LS and HipV regions, numeric

MeA.HipV Functional connectivity between MeA and HipV regions, numeric

MOB.HipV Functional connectivity between MOB and HipV regions, numeric

mPFC.HipV Functional connectivity between mPFC and HipV regions, numeric

NAcc.HipV Functional connectivity between NAcc and HipV regions, numeric

PVN.HipV Functional connectivity between PVN and HipV regions, numeric

RSC.HipV Functional connectivity between RSC and HipV regions, numeric

VP.HipV Functional connectivity between VP and HipV regions, numeric

VTA.HipV Functional connectivity between VTA and HipV regions, numeric

Dent.HipV Functional connectivity between Dent and HipV regions, numeric

HipD.HipV Functional connectivity between HipD and HipV regions, numeric

Details

Data is based on an experiment of social bonding in prairie voles. Functional connectivity was measured as the Pearson correlation between the average fMRI signal from the regions of interest (ROI) within 16 anatomical areas of brain. Then, a total of 120 pairwise connections are contained in the dataset. NOTE: This is not the original data of the study!

Source

https://www.biorxiv.org/content/10.1101/752345v2

Index