

Package ‘manynet’

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Title Many Ways to Make, Modify, Mark, and Measure Myriad Networks

Version 1.7.1

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Description Many tools for making, modifying, marking, measuring, and motifs and memberships of many different types of networks. All functions operate with matrices, edge lists, and 'igraph', 'network', and 'tidygraph' objects, on directed, multiplex, multimodal, signed, and other networks. The package includes functions for importing and exporting, creating and generating networks, modifying networks and node and tie attributes, and describing networks with sensible defaults.

URL <https://stocnet.github.io/manynet/>

BugReports <https://github.com/stocnet/manynet/issues>

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Contents

data_overview	4
fict_actually	5
fict_friends	6
fict_greys	7
fict_lotr	8
fict_marvel	9
fict_potter	11
fict_starwars	12
fict_thrones	14
glossary	15
interface	15
irps_911	16
irps_blogs	17
irps_books	18
irps_nuclear	20
irps_revere	21
irps_usgeo	22
irps_wwi	23
ison_adolescents	24
ison_algebra	25
ison_brandes	26
ison_dolphins	27
ison_emotions	28
ison_hightech	29
ison_judo_moves	31
ison_karateka	32
ison_koenigsberg	33
ison_laterals	34
ison_lawfirm	37
ison_monks	38
ison_networkers	39
ison_physicians	41
ison_southern_women	44
make_cran	45
make_create	47
make_ego	49
make_explicit	50

make_learning	51
make_mnet	53
make_motifs	54
make_play	55
make_random	58
make_read	60
make_stochastic	62
make_write	64
manip_as	65
manip_changes	68
manip_correlation	70
manip_deformat	71
manip_direction	72
manip_from	74
manip_info	75
manip_levels	76
manip_miss	77
manip_nodes	78
manip_paths	80
manip_permutation	83
manip_preformat	84
manip_project	85
manip_reformat	87
manip_scope	88
manip_split	90
manip_ties	92
mark_core	93
mark_diff	96
mark_features	97
mark_format	99
mark_is	100
mark_nodes	102
mark_select	104
mark_ties	105
mark_tie_select	106
mark_triangles	107
measure_attributes_nodes	108
measure_attributes_ties	109
measure_central_between	110
measure_central_close	113
measure_central_degree	117
measure_central_eigen	121
measure_closure	124
measure_cohesion	126
measure_diffusion_infection	128
measure_diffusion_net	129
measure_diffusion_node	132
measure_features	134

measure_heterogeneity	138
measure_hierarchy	141
measure_holes	143
measure_periods	145
measure_properties	146
member_brokerage	147
member_cliques	148
member_community_hier	150
member_community_non	152
member_components	155
member_diffusion	156
member_equivalence	158
model_cluster	160
model_kselect	161
motif_brokerage	162
motif_diffusion	163
motif_net	165
motif_node	167
tutorials	169

Index 170

data_overview	<i>Obtain overview of available network data</i>
---------------	--

Description

This function makes it easy to get an overview of available data:

- `table_data()` returns a tibble with details of the network datasets included in the packages.

Usage

```
table_data(..., pkg = c("manynet", "migraph"))
```

Arguments

...	Network marks, e.g. directed, twomode, or signed, that are used to filter the results.
pkg	String, name of the package.

Examples

```
table_data()
# to obtain list of all e.g. directed networks:
table_data(pkg = "manynet", directed)
# to obtain overview of unique datasets:
table_data() %>%
  dplyr::distinct(directed, weighted, twomode, signed,
                 .keep_all = TRUE)
```

fict_actually	<i>Two-mode network of Love Actually characters and their scene appearances (Robinson 2015)</i>
---------------	---

Description

Love Actually is a 2003 British romantic comedy film. David Robinson's data is a two-mode network of 20 characters and their appearances across 76 scenes, as parsed from the script.

Added to this are multiplex, one-mode networks of character relationships, including "romantic", "family", "friendship", and "professional" ties. These were added by Korakot Janteerasakul from the following source: [https://en.wikipedia.org/wiki/Love_Actually#/media/File:Love_Actually_\(2003\)_Interconnections.svg](https://en.wikipedia.org/wiki/Love_Actually#/media/File:Love_Actually_(2003)_Interconnections.svg).

Usage

```
data(fict_actually)
```

Format

```
#> -- # Love actually interactions -----
#> # A labelled, multiplex, two-mode network of 20 characters and 76 scenes and
#> 162 appearance, 3 family, 7 friendship, 10 professional, and 7 romance ties
#>
#> -- Nodes
#> # A tibble: 96 x 6
#>   type name Actor Gender Nationality Occupation
#>   <lg1> <chr> <chr> <chr> <chr> <chr>
#> 1 FALSE Aurelia Lúcia Moniz Female Portuguese Assistant
#> 2 FALSE Billy Bill Nighy Male British Singer
#> 3 FALSE Colin Kris Marshall Male British Travels to America
#> 4 FALSE Daniel Liam Neeson Male British Widower
#> 5 FALSE Harry Alan Rickman Male British Agency Director
#> 6 FALSE John Martin Freeman Male British Nude stand-in
#> # i 90 more rows
#>
#> -- Ties
#> # A tibble: 189 x 3
#>   from to type
#>   <int> <int> <chr>
#> 1 1 7 romance
#> 2 1 51 appearance
#> 3 1 57 appearance
#> 4 1 58 appearance
#> 5 1 63 appearance
#> 6 1 95 appearance
#> # i 183 more rows
#>
```

Author(s)

David Robinson

References

Robinson, David. 2015. "Analyzing networks of characters in 'Love Actually'". <http://varianceexplained.org/r/love-actually-network/>

fict_friends	<i>One-mode undirected Friends character scene co-appearances (McNulty, 2020)</i>
--------------	---

Description

One-mode network collected by [McNulty \(2020\)](#) on the connections between the Friends TV series characters from Seasons 1 to 10. The `fict_friends` is an undirected network containing connections between characters organised by season number, which is reflected in the tie attribute 'wave'. The network contains 650 nodes. Each tie represents the connection between a character pair (appear in the same scene), and the 'weight' of the tie is the number of scenes the character pair appears in together. For all networks, characters are named (eg. Phoebe, Ross, Rachel).

Usage

```
data(fict_friends)
```

Format

```
#> -- # Friends network -----
#> # A labelled, weighted, undirected network of 650 characters and 2976 scene
#> co-appearance ties
#>
#> -- Nodes
#> # A tibble: 650 x 1
#>   name
#>   <chr>
#> 1 Actor
#> 2 Alan
#> 3 Andrea
#> 4 Angela
#> 5 Aunt Iris
#> 6 Aunt Lillian
#> # i 644 more rows
#>
#> -- Ties
#> # A tibble: 2,976 x 3
#>   from   to weight
#>   <int> <int> <dbl>
```

```
#> 1      8      9      3
#> 2      4     10      1
#> 3      8     12      1
#> 4      9     12      1
#> 5      2     14      1
#> 6      3     14      1
#> # i 2,970 more rows
#>
```

References

McNulty, K. (2020). *Network analysis of Friends scripts.*

fict_greys	<i>One-mode undirected network of characters hook-ups on Grey's Anatomy TV show</i>
------------	---

Description

Grey's Anatomy is an American medical drama television series running on ABC since 2005. It focuses on the personal and professional lives of surgical interns, residents, and attendings at Seattle Grace Hospital, later renamed as the Grey Sloan Memorial Hospital. [Gary Weissman](#) collected data on the sexual contacts between characters on the television show through observation of the story lines in the episodes and fan pages, and this data was extended by [Benjamin Lind](#) including nodal attributes:

- 'name': first and, where available, surname
- 'sex': F for female and M for male
- 'race': White, Black, or Other
- 'birthyear': year born (some missing data)
- 'position': "Chief", "Attending", "Resident", "Intern", "Nurse", "Non-Staff", "Other"
- 'season': season that the character joined the show
- 'sign': character's astrological starsign, if known

The data is current up to (I think?) season 10?

Usage

```
data(fict_greys)
```

Format

```

#> -- # Grey's Anatomy -----
#> # A labelled, undirected network of 53 characters and 56 hook-up ties
#>
#> -- Nodes
#> # A tibble: 53 x 7
#>   name          sex  race  birthyear position  season sign
#>   <chr>         <chr> <chr>    <dbl> <chr>    <dbl> <chr>
#> 1 Addison Montgomery F    White    1967 Attending    1 Libra
#> 2 Adele Webber      F    Black    1949 Non-Staff     2 Leo
#> 3 Teddy Altman      F    White    1969 Attending    6 Pisces
#> 4 Amelia Shepherd  F    White    1981 Attending    7 Libra
#> 5 Arizona Robbins   F    White    1976 Attending    5 Leo
#> 6 Rebecca Pope     F    White    1975 Non-Staff     3 Gemini
#> # i 47 more rows
#>
#> -- Ties
#> # A tibble: 56 x 2
#>   from  to
#>   <int> <int>
#> 1     5  47
#> 2    21  47
#> 3     5  46
#> 4     5  41
#> 5    18  41
#> 6    21  41
#> # i 50 more rows
#>

```

Author(s)

Gary Weissman and Benjamin Lind

fict_lotr

One-mode network of Lord of the Rings character interactions

Description

The Lord of the Rings is a beloved, epic high fantasy novel written by J.R.R. Tolkien. This is a network of 36 Lord of the Rings book characters and 66 interactional relationships.

The ties are unweighted and concern only interaction. Interaction can be cooperative or conflictual.

In addition, the race of these characters has been coded, though not without debate. The most contentious is the coding of Tom Bombadil and Goldberry as Maiar, presumably coded as such to avoid having categories of one.

Usage

```
data(fict_lotr)
```

Format

```
#> -- # Lord of the Rings -----
#> # A labelled, complex, undirected network of 36 characters and 66 interaction
#> ties
#>
#> -- Nodes
#> # A tibble: 36 x 2
#>   name      Race
#>   <chr>    <chr>
#> 1 Aragorn  Human
#> 2 Beregond Human
#> 3 Bilbo    Hobbit
#> 4 Celeborn Elf
#> 5 Denethor Human
#> 6 Elladan Elf
#> # i 30 more rows
#>
#> -- Ties
#> # A tibble: 66 x 2
#>   from  to
#>   <int> <int>
#> 1     1   7
#> 2     1   8
#> 3     5   9
#> 4     1  10
#> 5     3  10
#> 6     9  10
#> # i 60 more rows
#>
```

fict_marvel

Multiplex two-mode affiliation and one-mode signed relationship network of Marvel comic book characters (Yuksel 2017)

Description

This multiplex network contains two types of ties related to the Marvel *comic book* universe. The "affiliation" ties offer a two-mode affiliation network of 53 Marvel comic book characters and their affiliations to 141 teams. The "relationship" ties offer a one-mode signed network of friendships and enmities between the 53 Marvel comic book characters. Friendships are indicated by a positive sign in the tie `sign` attribute, whereas enmities are indicated by a negative sign in this edge attribute.

Usage

```
data(fict_marvel)
```

Format

```
#>
#> -- # Marvel universe -----
#> # A labelled, complex, multiplex, signed, two-mode network of 53 characters and
#> 141 teams and 683 affiliation, and 558 relationship ties
#>
#> -- Nodes
#> # A tibble: 194 x 11
#>   type name          Gender Appearances Attractive Rich Intellect Omnilingual
#>   <lg1> <chr>         <chr>         <int>      <int> <int>      <int>      <int>
#> 1 FALSE Abomination   Male           427        0     0         1         1
#> 2 FALSE Ant-Man       Male           589        1     0         1         0
#> 3 FALSE Apocalypse   Male          1207        0     0         1         1
#> 4 FALSE Beast         Male          7609        1     0         1         0
#> 5 FALSE Black Panther Male           2189        1     1         1         0
#> 6 FALSE Black Widow Female          2907        1     0         1         0
#> # i 188 more rows
#> # i 3 more variables: PowerOrigin <chr>, UnarmedCombat <int>, ArmedCombat <int>
#>
#> -- Ties
#> # A tibble: 1,241 x 4
#>   from to type          sign
#>   <int> <int> <chr>         <dbl>
#> 1     1     1 relationship   -1
#> 2     1     4 relationship   -1
#> 3     1    11 relationship   -1
#> 4     1    12 relationship   -1
#> 5     1    23 relationship   -1
#> 6     1    24 relationship   -1
#> # i 1,235 more rows
#>
```

Details

Additional nodal variables have been coded and included by Dr Umut Yuksel:

- **Gender:** binary character, 43 "Male" and 10 "Female"
- **PowerOrigin:** binary character, 2 "Alien", 1 "Cyborg", 5 "God/Eternal", 22 "Human", 1 "Infection", 16 "Mutant", 5 "Radiation", 1 "Robot"
- **Appearances:** integer, in how many comic book issues they appeared in
- **Attractive:** binary integer, 41 1 (yes) and 12 0 (no)
- **Rich:** binary integer, 11 1 (yes) and 42 0 (no)
- **Intellect:** binary integer, 39 1 (yes) and 14 0 (no)

- **Omnilingual:** binary integer, 8 1 (yes) and 45 0 (no)
- **UnarmedCombat:** binary integer, 51 1 (yes) and 2 0 (no)
- **ArmedCombat:** binary integer, 25 1 (yes) and 28 0 (no)

See also <https://graphics.straitstimes.com/STI/STIMEDIA/Interactives/2018/04/marvel-cinematic-universe-whos-who-interactive/index.html>.

Source

Umut Yuksel, 31 March 2017

fict_potter	<i>Six complex one-mode support data in Harry Potter books (Bossaert and Meidert 2013)</i>
-------------	--

Description

Goele Bossaert and Nadine Meidert coded peer support ties among 64 characters in the Harry Potter books. Each author coded four of seven books using NVivo, with the seventh book coded by both and serving to assess inter-rater reliability. The first six books concentrated on adolescent interactions, were studied in their paper, and are made available here. The peer support ties mean voluntary emotional, instrumental, or informational support, or praise from one living, adolescent character to another within the book's pages. In addition, nodal attributes name, schoolyear (which doubles as their age), gender, and their house assigned by the sorting hat are included.

Usage

```
data(fict_potter)
```

Format

```
#> -- # Harry Potter support network -----
#> # A longitudinal, labelled, complex, directed network of 64 students and 544
#> support arcs over 6 waves
#>
#> -- Nodes
#> # A tibble: 64 x 5
#>   name          schoolyear gender house      active
#>   <chr>          <int> <chr> <chr>    <logi>
#> 1 Adrian Pucey      1989 male  Slytherin TRUE
#> 2 Alicia Spinnet    1989 female Gryffindor TRUE
#> 3 Angelina Johnson  1989 female Gryffindor TRUE
#> 4 Anthony Goldstein 1991 male  Ravenclaw TRUE
#> # i 60 more rows
#>
#> -- Changes
#> # A tibble: 81 x 4
```

```

#>   time node var   value
#>   <int> <int> <chr> <lg1>
#> 1     2     9 active TRUE
#> 2     2    21 active TRUE
#> 3     2    35 active TRUE
#> 4     2    39 active FALSE
#> # i 77 more rows
#>
#> -- Ties
#> # A tibble: 544 x 3
#>   from to wave
#>   <int> <int> <dbl>
#> 1    11  11     1
#> 2    11  25     1
#> 3    11  26     1
#> 4    11  44     1
#> # i 540 more rows
#>

```

References

Bossaert, Goele and Nadine Meidert (2013). "'We are only as strong as we are united, as weak as we are divided'. A dynamic analysis of the peer support networks in the Harry Potter books." *Open Journal of Applied Sciences*, 3(2): 174-185. doi:10.4236/ojapps.2013.32024

fict_starwars

Seven one-mode Star Wars character interactions (Gabasova 2016)

Description

One-mode network dataset collected by Gabasova (2016) on the interactions between Star Wars characters in each movie from Episode 1 ("The Phantom Menace") to Episode 7 ("The Force Awakens"). The data was constructed by parsing the scripts, as described in <https://evelinag.com/blog/2015/12-15-star-wars-social-network/index.html>.

Characters are named (eg. R2-D2, Anakin, Chewbacca) and the following node attributes are provided where available: height, mass, hair color, skin color, eye color, birth year, sex, homeworld, and species. The node attribute 'faction' has also been added, denoting the faction (eg. Jedi, Rebel Alliance, etc) that Star Wars characters belong to in each episode (coding completed by Yichen Shen, Tiphaine Aeby, and James Hollway).

Weighted ties represent the number of times characters speak within the same scene of each film, indicated by the wave (1-7).

Change in the composition of the network is tracked by the variable 'active', though several other variables also change (mostly as Anakin becomes *spoiler alert*).

Usage

```
data(fict_starwars)
```

Format

```

#> -- # Star Wars network data -----
#> # A longitudinal, labelled, complex, weighted, directed network of 110
#> characters and 563 interaction arcs over 7 waves
#>
#> -- Nodes
#> # A tibble: 110 x 12
#>   name          species homeworld sex  height hair_color eye_color skin_color
#>   <chr>          <chr>   <chr>   <chr> <int> <chr>      <chr>    <chr>
#> 1 Admiral Ackbar Mon Cala male   180 none    orange  brown mot~
#> 2 Admiral Statura Human   Garel  male   172 black   brown  light
#> 3 Anakin         Human   Tatooine male   188 blond  blue   fair
#> 4 Bail Organa    Human   Alderaan male   191 black   brown  tan
#> # i 106 more rows
#> # i 4 more variables: birth_year <dbl>, mass <dbl>, faction <chr>, active <lgl>
#>
#> -- Changes
#> # A tibble: 184 x 4
#>   time node var  value
#>   <int> <int> <chr> <chr>
#> 1     2     7 active TRUE
#> 2     2    10 active TRUE
#> 3     2    11 active FALSE
#> 4     2    13 active FALSE
#> # i 180 more rows
#>
#> -- Ties
#> # A tibble: 563 x 4
#>   from  to weight wave
#>   <int> <int> <int> <int>
#> 1    80  73     11     1
#> 2    80  79     14     1
#> 3    80   3     16     1
#> 4    80 106      3     1
#> # i 559 more rows
#>

```

Details

The network for each episode may be extracted and used separately, eg. `to_time(fict_starwars, 1)` for Episode 1.

References

Gabasova, Evelina. 2016. *Star Wars social network (Version 1.0.1)*. Zenodo. doi:10.5281/zenodo.1411479

fict_thrones

*One-mode Game of Thrones kinship (Glander 2017)***Description**

The original dataset was put together by Erin Pierce and Ben Kahle for an assignment for a course on Bayesian statistics. The data included information on when characters died in the Song of Ice and Fire books, and some predictive factors such as whether they were nobles, married, etc. Shirin Glander extended this data set on character deaths in the TV series Game of Thrones with the kinship relationships between the characters, by scraping "A Wiki of Ice and Fire" and adding missing information by hand. There is certainly more that can be done here.

Usage

```
data(fict_thrones)
```

Format

```
#> -- # Game of Thrones Kinship -----
#> # A labelled, multiplex, directed network of 208 characters and 404 kinship
#> arcs
#>
#> -- Nodes
#> # A tibble: 208 x 10
#>   name          culture house popularity Gender title birth death noble married
#>   <chr>         <fct>  <chr>      <dbl> <chr>  <chr> <int> <int> <lgl> <lgl>
#> 1 Alys Arryn    <NA>   House~    0.0803 female ""      NA    NA FALSE TRUE
#> 2 Elys Waynwood <NA>   House~    0.0702 female "Ser"   NA    NA TRUE  TRUE
#> 3 Jasper Arryn <NA>   House~    0.0435 male   "Eyr~  NA    NA TRUE  FALSE
#> 4 Jeyne Royce  <NA>   House~    0      female <NA>   NA    NA NA    NA
#> 5 Jon Arryn    Valemen House~    0.836  male   "Eyr~  217   298 TRUE  TRUE
#> 6 Lysa Arryn   <NA>   House~    0      female "Lad~  266   300 TRUE  TRUE
#> # i 202 more rows
#>
#> -- Ties
#> # A tibble: 404 x 3
#>   from  to type
#>   <int> <int> <chr>
#> 1     1   2 spouse
#> 2     2   1 spouse
#> 3     3   1 parent
#> 4     3   5 parent
#> 5     4   5 spouse
#> 6     5   4 spouse
#> # i 398 more rows
#>
```

References

- Pierce, Erin, and Ben Kahle. 2015. "[Bayesian Survival Analysis in A Song of Ice and Fire](#)".
- Glander, Shirin. 2017. "[Network analysis of Game of Thrones](#)".

glossary	<i>Adding network glossary items</i>
----------	--------------------------------------

Description

This function adds a glossary item, useful in tutorials.

Usage

```
gloss(text, ref = NULL)

print_glossary()

clear_glossary()
```

Arguments

text	The text to appear.
ref	The name of the glossary item to index. If NULL, then the function will search the glossary for 'text' instead.

interface	<i>Console command line interface</i>
-----------	---------------------------------------

Description

These functions wrap {cli} functions and elements to build an attractive command line interface (CLI).

If you wish to receive fewer messages in the console, run `options(snet_verbosity = 'quiet')`.

Usage

```
snet_info(..., .envir = parent.frame())

snet_minor_info(..., .envir = parent.frame())

snet_warn(..., .envir = parent.frame())

snet_abort(..., .envir = parent.frame())
```

```
snet_success(..., .envir = parent.frame())
snet_prompt(..., .envir = parent.frame())
snet_unavailable(..., .envir = parent.frame())
snet_progress_step(..., .envir = parent.frame())
snet_progress_along(..., .envir = parent.frame())
snet_progress_seq(..., .envir = parent.frame())
snet_progress_nodes(..., .envir = parent.frame())
```

Arguments

...	One or more character strings. For most of these functions, if multiple strings are passed these will be pasted together.
.envir	This argument is just to inherit the parent frame in the (likely) event that the function is used within another function.

irps_911

One-mode multiplex network of relationships between 9/11 hijackers (Krebs 2002)

Description

This network records two different types of relationships between and surrounding the hijackers of four planes in the United States on September 11, 2001, culminating in those planes crashing into four locations: New York's World Trade Center (North and South buildings), as well as the Pentagon and a location in Somerset County, Pennsylvania.

The hijackers were members of al-Qaeda. Valdis Krebs collected further information from newspapers on the broader network of associates of these hijackers, reflecting on the challenges of collecting this information even after the fact.

The data includes two types of ties: "trust"ed prior contacts among the hijackers, and "association" ties among the hijackers but also their broader associates. All associates are named, along with a logical vector about whether they were a hijacker or not, and if so which their (eventual) target was.

Usage

```
data(irps_911)
```

Format

```

#> -- # 911 Terrorist network -----
#> # A labelled, complex, multiplex, undirected network of 60 terrorists and 153
#> association ties and 153 trust ties
#>
#> -- Nodes
#> # A tibble: 60 x 3
#>   name          hijacker target
#>   <chr>         <lgl>   <chr>
#> 1 Majed Moqed   TRUE    Pentagon
#> 2 Khalid Al Mihdhar TRUE    Pentagon
#> 3 Hani Hanjour  TRUE    Pentagon
#> 4 Nawaf Alhazmi TRUE    Pentagon
#> 5 Salem Alhazmi TRUE    Pentagon
#> 6 Ahmed Alnami  TRUE    Pennsylvania
#> # i 54 more rows
#>
#> -- Ties
#> # A tibble: 153 x 3
#>   from   to type
#>   <int> <int> <chr>
#> 1     1     3 association
#> 2     1     3 trust
#> 3     2     3 association
#> 4     2     3 trust
#> 5     2     4 association
#> 6     2     4 trust
#> # i 147 more rows
#>

```

References

Krebs, Valdis. 2002. "Mapping networks of terrorist cells". *Connections* 24(3): 43-52.

irps_blogs

*One-mode directed network of links between US political blogs
(Adamic and Glance 2005)*

Description

This network consists of the blogosphere around the time of the 2004 US presidential election until February 2005. The 2004 election was the first in which blogging played a significant role. Ties were constructed from a crawl of the front page of each blog.

Political leaning is indicated as "Liberal" (or left leaning) or "Conservative" (or right leaning), sourced from blog directories. Some blogs were labelled manually, based on incoming and outgoing links and posts.

Usage

```
data(irps_blogs)
```

Format

```
#> -- # US political blogosphere circa 2004 -----
#> # A labelled, complex, directed network of 1490 blogs and 19090 link arcs
#>
#> -- Nodes
#> # A tibble: 1,490 x 3
#>   name                               Leaning Source
#>   <chr>                               <chr>   <chr>
#> 1 100monkeystyping.com               Liberal Blogarama
#> 2 12thharmonic.com/wordpress         Liberal BlogCatalog
#> 3 40ozblog.blogspot.com              Liberal Blogarama,BlogCatalog
#> 4 4lina.tblog.com                    Liberal Blogarama
#> 5 750volts.blogspot.com              Liberal Blogarama
#> 6 95theses.blogspot.com             Liberal Blogarama
#> # i 1,484 more rows
#>
#> -- Ties
#> # A tibble: 19,090 x 2
#>   from to
#>   <int> <int>
#> 1   267 1394
#> 2   267  483
#> 3   267 1051
#> 4   904 1479
#> 5   904  919
#> 6   904 1045
#> # i 19,084 more rows
#>
```

References

Adamic, Lada, and Natalie Glance. 2005. "The political blogosphere and the 2004 US Election: Divided they blog". *LinkKDD '05: Proceedings of the 3rd international workshop on Link discovery*, 36-43. doi:10.1145/1134271.1134277

Description

This network consists of books about US politics sold by Amazon.com. Ties represent books that are often purchased together, as revealed by Amazon's 'customers who bought this book also bought these other books' section on those books' pages on the website.

Information about the book's leaning "Liberal", "Neutral", or "Conservative" were added separately by Mark Newman based on the abstracts, descriptions, and reviews posted on Amazon.

These data should be cited as V. Krebs, unpublished, <http://www.orgnet.com/>.

Usage

```
data(irps_books)
```

Format

```
#> -- # Co-purchased US political books -----
#> # A labelled, undirected network of 105 books and 441 co-purchasing ties
#>
#> -- Nodes
#> # A tibble: 105 x 2
#>   name                                Leaning
#>   <chr>                                <chr>
#> 1 1000 Years for Revenge               Neutral
#> 2 Bush vs. the Beltway                 Conservative
#> 3 Charlie Wilson's War                 Conservative
#> 4 Losing Bin Laden                     Conservative
#> 5 Sleeping With the Devil              Neutral
#> 6 The Man Who Warned America           Conservative
#> # i 99 more rows
#>
#> -- Ties
#> # A tibble: 441 x 2
#>   from to
#>   <int> <int>
#> 1     1     2
#> 2     1     3
#> 3     1     4
#> 4     2     4
#> 5     1     5
#> 6     3     5
#> # i 435 more rows
#>
```

Author(s)

Valdis Krebs, Mark Newman

irps_nuclear	<i>Two-mode dynamic discourse network of Germany's nuclear energy phase-out (Haunss and Hollway 2023)</i>
--------------	---

Description

Following the 11 March 2011 Fukushima nuclear disaster in Japan, there was a vigorous public debate in Germany about the future of nuclear energy. This network captures the discourse established by 337 actors, including individual politicians, experts, parties, and the media, and their claims about nuclear energy and German nuclear energy policy. These claims were with respect to 54 concepts coded, and could be supportive or critical, and could also be repeated.

Usage

```
data(irps_nuclear)
```

Format

```
#> -- # German nuclear discourse network -----
#> # A dynamic, labelled, two-mode network of 337 speakers and 54 concepts and
#> 1164 claim ties from 2011-03-11 to 2011-06-30
#>
#> -- Nodes
#> # A tibble: 391 x 10
#>   name          type present politician govt coalition office org party power
#>   <chr>         <lgl> <lgl> <lgl>    <lgl> <lgl>    <lgl> <chr> <chr> <int>
#> 1 VFEW          FALSE TRUE  FALSE  FALSE NA      FALSE VFEW <NA>    0
#> 2 Angela Merk~ FALSE TRUE   TRUE   TRUE TRUE    TRUE  CDU  31      2
#> 3 Sunday Times FALSE TRUE  FALSE  FALSE NA      FALSE Sund~ <NA>    0
#> 4 SPD           FALSE TRUE   TRUE   FALSE FALSE  FALSE  SPD  32      1
#> 5 Norbert Röt~ FALSE TRUE   TRUE   TRUE TRUE    TRUE  CDU  31      1
#> 6 Torsten Kra~ FALSE TRUE  FALSE  FALSE NA      FALSE  Die ~ <NA>    0
#> # i 385 more rows
#>
#> -- Ties
#> # A tibble: 1,164 x 5
#>   from to time increment default
#>   <int> <int> <date>    <int> <lgl>
#> 1     1     338 2011-03-11     -1 FALSE
#> 2     2     339 2011-03-12      1 TRUE
#> 3     3     340 2011-03-13     -1 FALSE
#> 4     4     341 2011-03-13      1 TRUE
#> 5     2     342 2011-03-13     -1 TRUE
#> 6     5     343 2011-03-13      1 TRUE
#> # i 1,158 more rows
#>
```

References

Hauß Sebastian, James Hollway. 2023. "Multimodal mechanisms of political discourse dynamics and the case of Germany's nuclear energy phase-out". *Network Science*, 11(2):205-223. doi:10.1017/nws.2022.31

 irps_revere

Two-mode network of Paul Revere's (Fischer 1995)

Description

This network is of Paul Revere and 253 of his contemporary's overlapping memberships in seven colonial organisations. The data has been collected by Kieran Healy from the appendix to David Hackett Fischer's "Paul Revere's Ride". It highlights Paul Revere's centrality in this network, and thus his ability to mobilise the towns he rode through on horseback north from Boston on the night of April 18, 1775. This is in contrast to William Dawes, who set out the same night, but south. Despite both men coming from similar class and backgrounds, and riding through towns with similar demography and political leanings, only Paul Revere was able to mobilise those he encountered, and his social network was thought key to this.

Usage

```
data(irps_revere)
```

Format

```
#> # A labelled, two-mode network of 261 nodes and 319 ties
#>
#> -- Nodes
#> # A tibble: 261 x 2
#>   type name
#>   <lg1> <chr>
#> 1 FALSE Adams.John
#> 2 FALSE Adams.Samuel
#> 3 FALSE Allen.Dr
#> 4 FALSE Appleton.Nathaniel
#> 5 FALSE Ash.Gilbert
#> 6 FALSE Austin.Benjamin
#> # i 255 more rows
#>
#> -- Ties
#> # A tibble: 319 x 2
#>   from to
#>   <int> <int>
#> 1     1  257
#> 2     1  258
#> 3     2  257
#> 4     2  258
```

```
#> 5      2    260
#> 6      2    261
#> # i 313 more rows
#>
```

References

- Fischer, David Hackett. 1995. "Paul Revere's Ride". Oxford: Oxford University Press.
- Han, Shin-Kap. 2009. "The Other Ride of Paul Revere: The Brokerage Role in the Making of the American Revolution". *Mobilization: An International Quarterly*, 14(2): 143-162. doi:10.17813/maiq.14.2.g360870167085210
- Healy, Kieran. 2013. "Using Metadata to find Paul Revere".

irps_usgeo	<i>One-mode undirected network of US state contiguity (Meghanathan 2017)</i>
------------	--

Description

This network is of contiguity between US states. States that share a border are connected by a tie in the network. The data is a network of 107 ties among 50 US states (nodes). States are named by their two-letter ISO-3166 code. This data includes also the names of the capitol cities of each state, which are listed in the node attribute 'capitol'.

Usage

```
data(irps_usgeo)
```

Format

```
#> -- # US State Contiguity -----
#> # A labelled, undirected network of 50 states and 107 contiguity ties
#>
#> -- Nodes
#> # A tibble: 50 x 3
#>   name capitol      population
#>   <chr> <chr>          <int>
#> 1 AK    Juneau             NA
#> 2 AL    Montgomery        4780127
#> 3 AR    Little Rock       2915958
#> 4 AZ    Phoenix           6392307
#> 5 CA    Sacramento        37252895
#> 6 CO    Denver            5029324
#> # i 44 more rows
#>
#> -- Ties
#> # A tibble: 107 x 2
```

```
#>   from   to
#>   <int> <int>
#> 1     2    9
#> 2     2   10
#> 3     2   25
#> 4     2   42
#> 5     3   18
#> 6     3   24
#> # i 101 more rows
#>
```

References

Meghanathan, Natarajan. 2017. "Complex network analysis of the contiguous United States graph." *Computer and Information Science*, 10(1): 54-76. doi:10.5539/cis.v10n1p54

irps_wwi	<i>One-mode signed network of relationships between European major powers (Antal et al. 2006)</i>
----------	---

Description

This network records the evolution of the major relationship changes between the protagonists of World War I (WWI) from 1872 to 1907. It is incomplete both in terms of (eventual) parties to the war as well as some other relations, but gives a good overview of the main alliances and enmities.

The data series begins with the Three Emperors' League (1872, revived in 1881) between Germany, Austria-Hungary, and Russia. The Triple Alliance in 1882 joined Germany, Austria-Hungary, and Italy into a bloc that lasted until WWI. A bilateral alliance between Germany and Russia lapsed in 1890, and a French-Russian alliance developed between 1891-1894. The Entente Cordiale thawed and then fostered relations between Great Britain and France in 1904, and a British-Russian agreement in 1907 bound Great Britain, France, and Russia into the Triple Entente.

Usage

```
data(irps_wwi)
```

Format

```
#> -- # World War I Protagonists -----
#> # A dynamic, labelled, signed, undirected network of 6 European major powers
#> and 20 relationship ties from 1872 to 1918
#>
#> -- Nodes
#> # A tibble: 6 x 1
#>   name
#>   <chr>
#> 1 GBR
```

```

#> 2 FRA
#> 3 RUS
#> 4 AUH
#> 5 DEU
#> 6 ITA
#>
#> -- Ties
#> # A tibble: 20 x 5
#>   from to sign begin end
#>   <int> <int> <dbl> <dbl> <dbl>
#> 1     1     2    -1  1872  1904
#> 2     1     3    -1  1872  1907
#> 3     1     4    -1  1872  1918
#> 4     2     3    -1  1872  1890
#> 5     2     4    -1  1872  1918
#> 6     2     5    -1  1872  1918
#> # i 14 more rows
#>

```

References

Antal, Tibor, Pavel Krapivsky, and Sidney Redner. 2006. "Social balance on networks: The dynamics of friendship and enmity". *Physica D* 224: 130-136. doi:10.1016/j.physd.2006.09.028

ison_adolescents

One-mode subset of the adolescent society network (Coleman 1961)

Description

One-mode subset of Coleman's adolescent society network (Coleman 1961), as used in Feld's (1991) "Why your friends have more friends than you do". Coleman collected data on friendships among students in 12 U.S. high schools. Feld explored a subset of 8 girls from one of these schools, "Marketville", and gave them fictitious names, which are retained here.

Usage

```
data(ison_adolescents)
```

Format

```

#> -- # The Adolescent Society -----
#> # A labelled, undirected network of 8 adolescents and 10 friendships ties
#>
#> -- Nodes
#> # A tibble: 8 x 1
#>   name
#>   <chr>

```

```

#> 1 Betty
#> 2 Sue
#> 3 Alice
#> 4 Jane
#> 5 Dale
#> 6 Pam
#> # i 2 more rows
#>
#> -- Ties
#> # A tibble: 10 x 2
#>   from to
#>   <int> <int>
#> 1     1     2
#> 2     2     3
#> 3     3     4
#> 4     2     5
#> 5     3     5
#> 6     4     5
#> # i 4 more rows
#>

```

References

Coleman, James S. 1961. *The Adolescent Society*. New York: Free Press.

Feld, Scott. 1991. "Why your friends have more friends than you do" *American Journal of Sociology* 96(6): 1464-1477. doi:10.1086/229693.

ison_algebra	<i>Multiplex graph object of friends, social, and task ties (McFarland 2001)</i>
--------------	--

Description

Multiplex graph object of friends, social, and task ties between 16 anonymous students in an honors algebra class (M182). Each type of tie is weighted: the `friends` ties are weighted 2 = best friends, 1 = friend, and 0 is not a friend; `social` consists of social interactions per hour; and `tasks` consists of task interactions per hour.

Usage

```
data(ison_algebra)
```

Format

```

#> -- # M182 Algebra Class -----
#> # A multiplex, weighted, directed network of 16 nodes and 62 friends, 129
#> social, and 88 tasks ties

```

```

#>
#> -- Ties
#> # A tibble: 279 x 4
#>   from to type weight
#>   <int> <int> <chr> <dbl>
#> 1     1     5 social  1.2
#> 2     1     5 tasks  0.3
#> 3     1     8 social  0.15
#> 4     1     9 social  2.85
#> 5     1     9 tasks  0.3
#> 6     1    10 social  6.45
#> # i 273 more rows
#>

```

Source

See also `data(studentnets.M182, package = "NetData")`

Larger comprehensive data set publicly available, contact Daniel A. McFarland for details.

References

McFarland, Daniel A. (2001) "Student Resistance." *American Journal of Sociology* 107(3): 612-78.
[doi:10.1086/338779](https://doi.org/10.1086/338779).

ison_brandes

One-mode and two-mode centrality demonstration networks

Description

This network should solely be used for demonstration purposes as it does not describe a real network. To convert into the two-mode version, assign `ison_brandes %>% rename(type = twomode_type)`.

Usage

```
data(ison_brandes)
```

Format

```

#> # A undirected network of 11 nodes and 12 ties
#>
#> -- Nodes
#> # A tibble: 11 x 1
#>   twomode_type
#>   <lgl>
#> 1 FALSE
#> 2 FALSE
#> 3 TRUE

```

```

#> 4 FALSE
#> 5 TRUE
#> 6 TRUE
#> # i 5 more rows
#>
#> -- Ties
#> # A tibble: 12 x 2
#>   from to
#>   <int> <int>
#> 1     1     3
#> 2     2     3
#> 3     3     4
#> 4     4     5
#> 5     4     6
#> 6     5     7
#> # i 6 more rows
#>

```

ison_dolphins

One-mode, undirected network of frequent associations in a dolphin pod (Lusseau et al. 2003)

Description

These data contain the frequent associations between the 62 dolphins of a pod of dolphins living off Doubtful Sound, New Zealand. Additional information can be found in the literature cited below.

Usage

```
data(ison_dolphins)
```

Format

```

#> -- # Doubtful Sound dolphins -----
#> # A labelled, undirected network of 62 dolphins and 159 frequent association
#> ties
#>
#> -- Nodes
#> # A tibble: 62 x 1
#>   name
#>   <chr>
#> 1 Beak
#> 2 Beescratch
#> 3 Bumper
#> 4 CCL
#> 5 Cross
#> 6 DN16

```

```
#> # i 56 more rows
#>
#> -- Ties
#> # A tibble: 159 x 2
#>   from to
#>   <int> <int>
#> 1     4     9
#> 2     6    10
#> 3     7    10
#> 4     1    11
#> 5     3    11
#> 6     6    14
#> # i 153 more rows
#>
```

References

- Lusseau, David, K. Schneider, O. J. Boisseau, P. Haase, E. Sloaten, and S. M. Dawson. 2003. "The bottlenose dolphin community of Doubtful Sound features a large proportion of long-lasting associations", *Behavioral Ecology and Sociobiology* 54, 396-405.
- Lusseau, David. 2003. "The emergent properties of a dolphin social network", *Proc. R. Soc. London B* 270(S): S186-S188. doi:10.1098/rsbl.2003.0057
- Lusseau, David. 2007. "Evidence for social role in a dolphin social network". *Evolutionary Ecology* 21: 357–366. doi:10.1007/s1068200691050

ison_emotions	<i>One-mode, weighted network of emotional transitions (Trampe et al. 2015)</i>
---------------	---

Description

Emotions are highly interconnected, and one emotion often follows another. This network describes the transitions between 18 different emotions as experienced in everyday life. The data is collected from 11,000 participants who completed daily questionnaires on the emotions they felt at a given moment. While Trampe et al. (2015) created and analysed an undirected network in their paper, the directed network constructed by Will Hipson is shared here.

Usage

```
data(ison_emotions)
```

Format

```
#> -- # Emotional transitions -----
#> # A labelled, complex, weighted, directed network of 18 emotions and 315
#> transition arcs
#>
```

```

#> -- Nodes
#> # A tibble: 18 x 1
#>   name
#>   <chr>
#> 1 Alertness
#> 2 Amusement
#> 3 Anger
#> 4 Anxiety
#> 5 Awe
#> 6 Disdain
#> # i 12 more rows
#>
#> -- Ties
#> # A tibble: 315 x 3
#>   from   to weight
#>   <int> <int> <int>
#> 1     1     1   6191
#> 2     1     2     97
#> 3     1     3    214
#> 4     1     4   4784
#> 5     1     5     14
#> 6     1     6     82
#> # i 309 more rows
#>

```

References

- Trampe, Debra, Jordi Quoidbach, and Maxime Taquet. 2015. "Emotions in everyday life". *PLOS ONE*. doi:10.1371/journal.pone.0145450
- Hipson, Will. 2019. <https://www.r-bloggers.com/2019/03/network-analysis-of-emotions/>

ison_hightech

One-mode multiplex, directed network of managers of a high-tech company (Krackhardt 1987)

Description

21 managers of a company of just over 100 employees manufactured high-tech equipment on the west coast of the United States. Three types of ties were collected:

- *friends*: managers' answers to the question "Who is your friend?"
- *advice*: managers' answers to the question "To whom do you go to for advice?"
- *reports*: "To whom do you report?" based on company reports

The data is anonymised, but four nodal attributes are included:

- *age*: the manager's age in years

- *tenure*: the manager's length of service
- *level*: the manager's level in the corporate hierarchy, where 3 = CEO, 2 = Vice President, and 1 = manager
- *dept*: one of four departments, B, C, D, E, with the CEO alone in A

Usage

```
data(ison_hightech)
```

Format

```
#> -- # High-tech company managers -----
#> # A multiplex, directed network of 21 managers and 190 advice, 102 friends, and
#> 20 reports ties
#>
#> -- Nodes
#> # A tibble: 21 x 4
#>   age tenure level dept
#>   <dbl> <dbl> <dbl> <chr>
#> 1    33     9     1 E
#> 2    42    20     2 E
#> 3    40    13     1 C
#> 4    33     8     1 E
#> 5    32     3     1 C
#> 6    59    28     1 B
#> # i 15 more rows
#>
#> -- Ties
#> # A tibble: 312 x 3
#>   from to type
#>   <int> <int> <chr>
#> 1     1     2 friends
#> 2     1     2 advice
#> 3     1     2 reports
#> 4     1     4 friends
#> 5     1     4 advice
#> 6     1     8 friends
#> # i 306 more rows
#>
```

References

Krackhardt, David. 1987. "Cognitive social structures". *Social Networks* 9: 104-134.

ison_judo_moves *One-mode judo moves network (Bastazini 2025)*

Description

Judo is a martial art with a long history and many different techniques. It involves a dynamic 'chess match' of throws, holds, locks, submission techniques, and other maneuvers. The techniques are often combined in sequences to create fluid and effective combinations to score points or achieve victory. As the author of this network describes, "While individual techniques (called waza) are foundational, the real artistry lies in how they are chained together – through renraku-waza (combination techniques) and renzoku-waza (continuous combination techniques)" This network describes the relationships between 33 individual judo moves, as recognised by the Kodokan (the official international governing body of judo), where an arc indicates that one move can be followed by another.

Usage

```
data(ison_judo_moves)
```

Format

```
#> -- # Judo attack combinations -----
#> # A labelled, complex, directed network of 33 attacks and 81 sequence arcs
#>
#> -- Nodes
#> # A tibble: 33 x 1
#>   name
#>   <chr>
#> 1 Seoi.nage
#> 2 Seoi.otoshi
#> 3 O.uchi.gari
#> 4 Ko.uchi.gari
#> 5 Ippon.seoi.nage
#> 6 Osoto.gari
#> # i 27 more rows
#>
#> -- Ties
#> # A tibble: 81 x 2
#>   from to
#>   <int> <int>
#> 1     1     2
#> 2     1     3
#> 3     1     4
#> 4     3     4
#> 5     3     6
#> 6     3     7
#> # i 75 more rows
#>
```

References

- Bastazini, Vinicius. 2025. "The Dynamics of the "Gentle Way": Exploring Judo Attack Combinations as Networks in R", <https://geekcologist.wordpress.com/2025/05/27/the-dynamics-of-the-gentle-way-exploring-judo-attack-combinations-as-networks-in-r/>
- Kashiwazaki, Katsuhiko, and Hidetoshi Nakanishi. 1995. *Attacking Judo: A Guide to Combinations and Counters*. Ippon Books.
- Kawaishi, Mikinosuke. 1963. *Standing judo: The combinations and counter-attacks*. Budoworks.
- van Haesendonck, F.M. 1968. *Judo: Eyclopédie par l'Image*. Éditions Erasme: Anvers-Bruxelles.

ison_karateka

One-mode karateka network (Zachary 1977)

Description

The network was observed in a university Karate club in 1977. The network describes association patterns among 34 members and maps out allegiance patterns between members and either Mr. Hi, the instructor, or the John A. the club president after an argument about hiking the price for lessons. The allegiance of each node is listed in the obc argument which takes the value 1 if the individual sided with Mr. Hi after the fight and 2 if the individual sided with John A.

Usage

```
data(ison_karateka)
```

Format

```
#> -- # Zachary's karate club network -----
#> # A labelled, weighted, undirected network of 34 club members and 78
#> association ties
#>
#> -- Nodes
#> # A tibble: 34 x 2
#>   name allegiance
#>   <chr>         <dbl>
#> 1 Mr Hi           1
#> 2 2                1
#> 3 3                1
#> 4 4                1
#> 5 5                1
#> 6 6                1
#> # i 28 more rows
#>
#> -- Ties
#> # A tibble: 78 x 3
#>   from   to weight
#>   <int> <int> <dbl>
```

```
#> 1      1      2      4
#> 2      1      3      5
#> 3      2      3      6
#> 4      1      4      3
#> 5      2      4      3
#> 6      3      4      3
#> # i 72 more rows
#>
```

References

Zachary, Wayne W. 1977. "An Information Flow Model for Conflict and Fission in Small Groups." *Journal of Anthropological Research* 33(4):452–73. doi:10.1086/jar.33.4.3629752.

ison_koenigsberg

One-mode Seven Bridges of Koenigsberg network (Euler 1741)

Description

The Seven Bridges of Koenigsberg is a notable historical problem in mathematics and laid the foundations of graph theory. The city of Koenigsberg in Prussia (now Kaliningrad, Russia) was set on both sides of the Pregel River, and included two large islands which were connected to each other and the mainland by seven bridges. A weekend diversion for inhabitants was to find a walk through the city that would cross each bridge once and only once. The islands could not be reached by any route other than the bridges, and every bridge must have been crossed completely every time (one could not walk half way onto the bridge and then turn around and later cross the other half from the other side). In 1735, Leonard Euler proved that the problem has no solution.

Usage

```
data(ison_koenigsberg)
```

Format

```
#> -- # Seven Bridges of Koenigsberg network -----
#> # A labelled, undirected network of 4 landmasses and 7 bridge ties
#>
#> -- Nodes
#> # A tibble: 4 x 3
#>   name      lat  lon
#>   <chr>    <dbl> <dbl>
#> 1 Altstadt  54.7  20.5
#> 2 Kneiphof  54.7  20.5
#> 3 Lomse    54.7  20.5
#> 4 Vorstadt  54.7  20.5
#>
#> -- Ties
```

```
#> # A tibble: 7 x 3
#>   from to name
#>   <int> <int> <chr>
#> 1     1     2 Kraemer Bruecke
#> 2     1     2 Schmiedebruecke
#> 3     1     3 Holzbruecke
#> 4     2     3 Honigbruecke
#> 5     2     4 Gruene Bruecke
#> 6     2     4 Koettelbruecke
#> # i 1 more row
#>
```

Source

```
{igraphdata}
```

References

Euler, Leonard. 1741. “Solutio problematis ad geometriam situs pertinentis.” *Commentarii academiae scientiarum Petropolitanae*.

ison_laterals

Two-mode projection examples (Hollway 2021)

Description

These networks are for demonstration purposes and do not describe any real world network. All examples contain named nodes. The networks are gathered together as a list and can be retrieved simply by plucking the desired network.

Usage

```
data(ison_laterals)
```

Format

```
#> $ison_bb
#> # A labelled, two-mode network of 10 nodes and 12 ties
#>
#> -- Nodes
#> # A tibble: 10 x 2
#>   name type
#>   <chr> <lgl>
#> 1 A     FALSE
#> 2 B     FALSE
#> 3 C     FALSE
#> 4 D     FALSE
#> 5 U     TRUE
```

```
#> 6 V TRUE
#> # i 4 more rows
#>
#> -- Ties
#> # A tibble: 12 x 2
#>   from to
#>   <int> <int>
#> 1     1     5
#> 2     1     6
#> 3     2     5
#> 4     2     7
#> 5     2     8
#> 6     2     9
#> # i 6 more rows
#>
#>
#> $ison_bm
#> # A labelled, two-mode network of 8 nodes and 9 ties
#>
#> -- Nodes
#> # A tibble: 8 x 2
#>   name type
#>   <chr> <lgl>
#> 1 A FALSE
#> 2 B FALSE
#> 3 C FALSE
#> 4 D FALSE
#> 5 U TRUE
#> 6 V TRUE
#> # i 2 more rows
#>
#> -- Ties
#> # A tibble: 9 x 2
#>   from to
#>   <int> <int>
#> 1     1     5
#> 2     1     6
#> 3     2     5
#> 4     2     7
#> 5     2     8
#> 6     3     6
#> # i 3 more rows
#>
#>
#> $ison_mb
#> # A labelled, two-mode network of 8 nodes and 9 ties
#>
#> -- Nodes
```

```
#> # A tibble: 8 x 2
#>   name type
#>   <chr> <lgl>
#> 1 A     FALSE
#> 2 B     FALSE
#> 3 C     FALSE
#> 4 D     FALSE
#> 5 M     TRUE
#> 6 X     TRUE
#> # i 2 more rows
#>
#> -- Ties
#> # A tibble: 9 x 2
#>   from to
#>   <int> <int>
#> 1     1     5
#> 2     2     5
#> 3     2     6
#> 4     2     7
#> 5     3     5
#> 6     3     6
#> # i 3 more rows
#>
#>
#> $ison_mm
#> # A labelled, two-mode network of 6 nodes and 6 ties
#>
#> -- Nodes
#> # A tibble: 6 x 2
#>   name type
#>   <chr> <lgl>
#> 1 A     FALSE
#> 2 B     FALSE
#> 3 C     FALSE
#> 4 D     FALSE
#> 5 M     TRUE
#> 6 N     TRUE
#>
#> -- Ties
#> # A tibble: 6 x 2
#>   from to
#>   <int> <int>
#> 1     1     5
#> 2     2     5
#> 3     2     6
#> 4     3     5
#> 5     3     6
#> 6     4     6
```

```
#>
```

```
ison_lawfirm          One-mode lawfirm (Lazega 2001)
```

Description

One-mode network dataset collected by Lazega (2001) on the relations between partners in a corporate law firm called SG&R in New England 1988-1991. This particular subset includes the 36 partners among the 71 attorneys of this firm. Nodal attributes include seniority, formal status, office in which they work, gender, lawschool they attended, their age, and how many years they had been at the firm.

Usage

```
data(ison_lawfirm)
```

Format

```
#> -- # Lazega's Lawyers -----
#> # A multiplex, directed network of 71 attorneys and 892 advice, 1104 cowork,
#> and 575 friends ties
#>
#> -- Nodes
#> # A tibble: 71 x 7
#>   status gender office  seniority  age practice  school
#>   <chr>  <chr> <chr>      <dbl> <dbl> <chr>    <chr>
#> 1 partner man    Boston      31    64 litigation Harvard/Yale
#> 2 partner man    Boston      32    62 corporate  Harvard/Yale
#> 3 partner man    Hartford    13    67 litigation Harvard/Yale
#> 4 partner man    Boston      31    59 corporate  Other
#> 5 partner man    Hartford    31    59 litigation UConn
#> 6 partner man    Hartford    29    55 litigation Harvard/Yale
#> # i 65 more rows
#>
#> -- Ties
#> # A tibble: 2,571 x 3
#>   from  to type
#>   <int> <int> <chr>
#> 1     1   2 friends
#> 2     1   2 advice
#> 3     1   4 friends
#> 4     1   8 friends
#> 5     1  17 friends
#> 6     1  17 advice
#> # i 2,565 more rows
#>
```

Details

The larger data from which this subset comes includes also individual performance measurements (hours worked, fees brought in) and attitudes concerning various management policy options (see also {sand}), their strong-coworker network, advice network, friendship network, and indirect control network.

Source

{networkdata}

References

Lazega, Emmanuel. 2001. *The Collegial Phenomenon: The Social Mechanisms of Cooperation Among Peers in a Corporate Law Partnership*. Oxford: Oxford University Press.

ison_monks

Multiplex network of three one-mode signed, weighted networks and a three-wave longitudinal network of monks (Sampson 1969)

Description

The data were collected for an ethnographic study of community structure in a New England monastery. Various sociometric data was collected of the novices attending the minor seminary of 'Cloisterville' preparing to join the monastic order.

- type = "like" records whom novices said they liked most at three time points/waves
- type = "esteem" records whom novices said they held in esteem (sign > 0) and disesteem (sign < 0)
- type = "praise" records whom novices said they praised (sign > 0) and blamed (sign < 0)
- type = "influence" records whom novices said were a positive influence (sign > 0) and negative influence (sign < 0)

All networks are weighted. Novices' first choices are weighted 3, the second 2, and third choices 1. Some subjects offered tied ranks for their top four choices.

In addition to node names, a 'groups' variable records the four groups that Sampson observed during his time there:

- The *Loyal Opposition* consists of novices who entered the monastery first and defended existing practices
- The *Young Turks* arrived later during a period of change and questioned practices in the monastery
- The *Interstitial* did not take sides in the debate
- The *Outcasts* were novices that were not accepted in the group

Information about senior monks was not included. While type = "like" is observed over three waves, the rest of the data was recorded retrospectively from the end of the study, after the network fragmented. The waves in which the novitiates were expelled (1), voluntarily departed (2 and 3), or remained (4) are given in the nodal attribute "left".

Usage

```
data(ison_monks)
```

Format

```
#> -- # Sampson's Monks -----
#> # A longitudinal, labelled, multiplex, signed, weighted, directed network of 18
#> nodes and 112 esteem, 103 influence, 168 like, and 80 praise ties over 3 waves
#>
#> -- Nodes
#> # A tibble: 18 x 3
#>   name      groups      left
#>   <chr>     <chr>     <dbl>
#> 1 Romuald   Interstitial 3
#> 2 Bonaventure Loyal      4
#> 3 Ambrose   Loyal      4
#> 4 Berthold  Loyal      4
#> 5 Peter     Loyal      3
#> 6 Louis     Loyal      4
#> # i 12 more rows
#>
#> -- Ties
#> # A tibble: 463 x 6
#>   from  to sign type weight wave
#>   <int> <int> <dbl> <chr> <dbl> <dbl>
#> 1     1     2     1 like     1     2
#> 2     1     2     1 like     1     3
#> 3     1     3     1 like     1     3
#> 4     1     5     1 like     3     1
#> 5     1     5     1 like     3     2
#> 6     1     5     1 like     3     3
#> # i 457 more rows
#>
```

References

Sampson, Samuel F. 1969. *Crisis in a cloister*. Unpublished doctoral dissertation, Cornell University.

Breiger R., Boorman S. and Arabie P. 1975. "An algorithm for clustering relational data with applications to social network analysis and comparison with multidimensional scaling". *Journal of Mathematical Psychology*, 12: 328-383.

Description

A directed, simple, named, weighted graph with 32 nodes and 440 edges. Nodes are academics and edges illustrate the communication patterns on an Electronic Information Exchange System among them. Node attributes include the number of citations (Citations) and the discipline of the researchers (Discipline). Edge weights illustrate the number of emails sent from one academic to another over the studied time period.

Usage

```
data(ison_networkers)
```

Format

```
#> -- # EIES Networkers -----
#> # A labelled, weighted, directed network of 32 nodes and 440 arcs
#>
#> -- Nodes
#> # A tibble: 32 x 3
#>   name          Discipline Citations
#>   <chr>         <chr>      <dbl>
#> 1 Lin Freeman   Sociology    19
#> 2 Doug White    Anthropology  3
#> 3 Ev Rogers     Other       170
#> 4 Richard Alba  Sociology    23
#> 5 Phipps Arabie Other        16
#> 6 Carol Barner-Barry Other         6
#> # i 26 more rows
#>
#> -- Ties
#> # A tibble: 440 x 3
#>   from to weight
#>   <int> <int> <dbl>
#> 1     1     2  488
#> 2     1     3   28
#> 3     1     4   65
#> 4     1     5   20
#> 5     1     6   65
#> 6     1     7   45
#> # i 434 more rows
#>
```

Source

networkdata package

References

Freeman, Sue C. and Linton C. Freeman. 1979. *The networkers network: A study of the impact of a new communications medium on sociometric structure*. Social Science Research Reports No 46.

Irvine CA, University of California.

Wasserman Stanley and Katherine Faust. 1994. *Social Network Analysis: Methods and Applications*. Cambridge University Press, Cambridge.

ison_physicians *Four multiplex one-mode physician diffusion data (Coleman, Katz, and Menzel, 1966)*

Description

Ron Burt prepared this data from Coleman, Katz and Menzel's 1966 study on medical innovation. They had collected data from physicians in four towns in Illinois: Peoria, Bloomington, Quincy and Galesburg. These four networks are held as separate networks in a list.

Coleman, Katz and Menzel were concerned with the impact of network ties on the physicians' adoption of a new drug, tetracycline. Data on three types of ties were collected in response to three questions:

- advice: "When you need information or advice about questions of therapy where do you usually turn?"
- discussion: "And who are the three or four physicians with whom you most often find yourself discussing cases or therapy in the course of an ordinary week – last week for instance?"
- friendship: "Would you tell me the first names of your three friends whom you see most often socially?"

Additional questions and records of prescriptions provided additional information:

- recorded date of tetracycline adoption date
- years in practice (note that these are {messydates}-compatible dates)
- conferences attended (those that attended "Specialty" conferences presumably also attended "General" conferences)
- regular subscriptions to medical journals
- free_time spent associating with doctors
- discussions on medical matters when with other doctors socially
- memberships in clubs with other doctors
- number of top 3 friends that are doctors
- time practicing in current community
- patients load (ordinal)
- physical proximity to other physicians (in building/sharing office)
- medical specialty (GP/Internist/Pediatrician/Other)

Usage

`data(ison_physicians)`

Format

```

#> $Peoria
#> # A multiplex, directed network of 117 nodes and 242 advice, 154 discussion,
#> and 147 friendship ties
#>
#> -- Nodes
#> # A tibble: 117 x 12
#>   adoption specialty conferences journals practice community patients
#>   <dbl> <chr> <chr> <dbl> <chr> <chr> <chr>
#> 1     1 Pediatrician Specialty 9 1920..1929 20+yrs 101-150
#> 2     12 GP None 5 1945.. -1yr 76-100
#> 3     8 Internist General 7 1935..1939 10-20yrs 76-100
#> 4     9 GP General 6 1940..1944 5-10yrs 51-75
#> 5     9 GP General 4 1935..1939 10-20yrs 51-75
#> 6    10 Internist None 7 1930..1934 10-20yrs 101-150
#> # i 111 more rows
#> # i 5 more variables: doc_freetime <dbl>, doc_discuss <dbl>, doc_friends <dbl>,
#> # doc_club <dbl>, doc_proximity <chr>
#>
#> -- Ties
#> # A tibble: 543 x 3
#>   from to type
#>   <int> <int> <chr>
#> 1     1     8 friendship
#> 2     1    58 friendship
#> 3     1    87 advice
#> 4     1    90 advice
#> 5     1   110 advice
#> 6     1   112 friendship
#> # i 537 more rows
#>
#>
#> $Bloomington
#> # A multiplex, directed network of 50 nodes and 94 advice, 57 discussion, and
#> 60 friendship ties
#>
#> -- Nodes
#> # A tibble: 50 x 12
#>   adoption specialty conferences journals practice community patients
#>   <dbl> <chr> <chr> <dbl> <chr> <chr> <chr>
#> 1     98 Internist Specialty 8 1930..1934 10-20yrs 101-150
#> 2     1 GP General 3 1945.. 5-10yrs 76-100
#> 3     98 GP Specialty 4 1930..1934 10-20yrs 101-150
#> 4     7 Internist None 3 1945.. -1yr 26-50
#> 5     6 Internist General 9 1935..1939 5-10yrs 76-100
#> 6     1 GP Specialty 5 1935..1939 10-20yrs 101-150
#> # i 44 more rows
#> # i 5 more variables: doc_freetime <dbl>, doc_discuss <dbl>, doc_friends <dbl>,

```

```

#> # doc_club <dbl>, doc_proximity <chr>
#>
#> -- Ties
#> # A tibble: 211 x 3
#>   from to type
#>   <int> <int> <chr>
#> 1     1     3 friendship
#> 2     1    10 discussion
#> 3     1    24 advice
#> 4     1    44 advice
#> 5     2     4 advice
#> 6     2     6 advice
#> # i 205 more rows
#>
#>
#> $Quincy
#> # A multiplex, directed network of 44 nodes and 70 advice, 52 discussion, and
#> 52 friendship ties
#>
#> -- Nodes
#> # A tibble: 44 x 12
#>   adoption specialty conferences journals practice community patients
#>   <dbl> <chr> <chr> <dbl> <chr> <chr> <chr>
#> 1     2 Internist None 6 1935..1939 10-20yrs 151+
#> 2    18 GP General 3 1920..1929 20+yrs 151+
#> 3    18 Internist None 5 1945.. -1yr -25
#> 4     4 GP General 3 1930..1934 20+yrs 151+
#> 5    18 GP Specialty 4 1935..1939 10-20yrs 151+
#> 6     5 Internist General 5 ..1919 20+yrs 51-75
#> # i 38 more rows
#> # i 5 more variables: doc_freetime <dbl>, doc_discuss <dbl>, doc_friends <dbl>,
#> # doc_club <dbl>, doc_proximity <chr>
#>
#> -- Ties
#> # A tibble: 174 x 3
#>   from to type
#>   <int> <int> <chr>
#> 1     1     8 advice
#> 2     1     9 advice
#> 3     1    10 discussion
#> 4     1    13 friendship
#> 5     1    15 advice
#> 6     1    22 discussion
#> # i 168 more rows
#>
#>
#> $Galesburg
#> # A multiplex, directed network of 35 nodes and 74 advice, 46 discussion, and

```

```

#> 51 friendship ties
#>
#> -- Nodes
#> # A tibble: 35 x 12
#>   adoption specialty conferences journals practice  community patients
#>   <dbl> <chr>      <chr>          <dbl> <chr>      <chr>      <chr>
#> 1     18 GP      General          4 1935..1939 5-10yrs  101-150
#> 2     18 GP      None            4 1935..1939 -1yr     151+
#> 3      4 GP      General          6 1945..      2-5yrs  51-75
#> 4      5 GP      None            4 1935..1939 10-20yrs 101-150
#> 5      8 Internist General          6 1935..1939 5-10yrs  151+
#> 6      4 Internist Specialty          8 ..1919    20+yrs  76-100
#> # i 29 more rows
#> # i 5 more variables: doc_freetime <dbl>, doc_discuss <dbl>, doc_friends <dbl>,
#> #   doc_club <dbl>, doc_proximity <chr>
#>
#> -- Ties
#> # A tibble: 171 x 3
#>   from  to type
#>   <int> <int> <chr>
#> 1     1   5 advice
#> 2     1   6 advice
#> 3     1  20 discussion
#> 4     1  23 discussion
#> 5     1  30 friendship
#> 6     1  31 friendship
#> # i 165 more rows
#>

```

Source

```
{networkdata}
```

References

Coleman, James, Elihu Katz, and Herbert Menzel. 1966. *Medical innovation: A diffusion study*. Indianapolis: The Bobbs-Merrill Company.

ison_southern_women *Two-mode southern women (Davis, Gardner and Gardner 1941)*

Description

Two-mode network dataset collected by Davis, Gardner and Gardner (1941) about the pattern of a group of women's participation at informal social events in Old City during a 9 month period, as reported in the *Old City Herald* in 1936. By convention, the nodes are named by the women's first names and the code numbers of the events, but the women's surnames and titles (Miss, Mrs.) are

recorded here too. The events' dates are recorded in place of the Surname, and these dates are also offered as a tie attribute.

Usage

```
data(ison_southern_women)
```

Format

```
#> -- # Southern Women Data -----
#> # A labelled, two-mode network of 18 women and 14 social events and 89
#> participation ties
#>
#> -- Nodes
#> # A tibble: 32 x 4
#>   type name      Surname  Title
#>   <lg1> <chr>    <chr>    <chr>
#> 1 FALSE Evelyn   Jefferson Mrs
#> 2 FALSE Laura    Mandeville Miss
#> 3 FALSE Theresa  Anderson  Miss
#> 4 FALSE Brenda  Rogers    Miss
#> 5 FALSE Charlotte McDowd    Miss
#> 6 FALSE Frances  Anderson  Miss
#> # i 26 more rows
#>
#> -- Ties
#> # A tibble: 89 x 3
#>   from  to date
#>   <int> <int> <date>
#> 1    14    29 1936-02-23
#> 2    15    29 1936-02-23
#> 3    17    29 1936-02-23
#> 4    18    29 1936-02-23
#> 5     1    23 1936-02-25
#> 6     2    23 1936-02-25
#> # i 83 more rows
#>
```

References

Davis, Allison, Burleigh B. Gardner, and Mary R. Gardner. 1941. *Deep South*. Chicago: University of Chicago Press.

Description

These functions read information from CRAN or within an R package's working directory to create a networks of a package's dependencies:

- `read_cran()` creates a network of a package's dependencies on other packages available on CRAN. It looks for the `Depends`, `Imports` and `Suggests` fields in the package's `DESCRIPTION` file and creates a network where nodes are packages and ties are dependencies.
- `read_pkg()` creates a network of function dependencies from R scripts in a directory. It looks for function definitions and function calls within the scripts and creates a network where nodes are functions and edges are function calls. It can also include function calls to functions not defined within the scripts.

Usage

```
read_cran(pkg = "all")
```

```
read_pkg(dir = getwd())
```

Arguments

<code>pkg</code>	The name
<code>dir</code>	Character string or vector of character strings with the directory or directories to search for R scripts. If <code>NULL</code> (the default), the current working directory is used.

Details

Note that these functions are not as actively maintained as others in the package, so please let us know if any are not currently working for you or if there are missing import routines by [raising an issue on Github](#).

Value

A `tidygraph` object representing the network of package dependencies or function dependencies in a package.

Author(s)

Jakob Gepp

Source

<https://www.r-bloggers.com/2016/01/r-graph-objects-igraph-vs-network/>

https://github.com/STATWORX/helfRlein/blob/master/R/get_network.R

See Also

[as](#)

Other makes: [make_create](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_random](#), [make_read](#), [make_stochastic](#), [make_write](#)

Examples

```
# mnet <- read_cran()
# mnet <- to_ego(mnet, "manynet", max_dist = 2)
# mnet <- read_pkg()
```

make_create

Making networks with defined structures

Description

These functions create networks with particular structural properties.

- `create_empty()` creates an empty network without any ties.
- `create_filled()` creates a filled network with every possible tie realised.
- `create_ring()` creates a ring or chord network where each nodes' neighbours form a clique.
- `create_star()` creates a network with a maximally central node.
- `create_tree()` creates a network with successive branches.
- `create_lattice()` creates a network that forms a regular tiling.
- `create_components()` creates a network that clusters nodes into separate components.
- `create_core()` creates a network in which a certain proportion of 'core' nodes are densely tied to each other, and the rest peripheral, tied only to the core.
- `create_degree()` creates a network with a given (out/in)degree sequence, which can also be used to create k-regular networks.

These functions can create either one-mode or two-mode networks. To create a one-mode network, pass the main argument `n` a single integer, indicating the number of nodes in the network. To create a two-mode network, pass `n` a vector of *two* integers, where the first integer indicates the number of nodes in the first mode, and the second integer indicates the number of nodes in the second mode. As an alternative, an existing network can be provided to `n` and the number of modes, nodes, and directedness will be inferred.

Usage

```
create_empty(n, directed = FALSE)

create_filled(n, directed = FALSE)

create_ring(n, directed = FALSE, width = 1, ...)

create_star(n, directed = FALSE)

create_tree(n, directed = FALSE, width = 2)

create_lattice(n, directed = FALSE, width = 8)
```

```
create_components(n, directed = FALSE, membership = NULL)
```

```
create_degree(n, outdegree = NULL, indegree = NULL)
```

```
create_core(n, directed = FALSE, mark = NULL)
```

```
create_windmill(n)
```

```
create_cycle(n)
```

```
create_wheel(n)
```

Arguments

n	Given: <ul style="list-style-type: none"> • A single integer, e.g. $n = 10$, a one-mode network will be created. • A vector of two integers, e.g. $n = c(5, 10)$, a two-mode network will be created. • A manynet-compatible object, a network of the same dimensions will be created.
directed	Logical whether the graph should be directed. By default <code>directed = FALSE</code> . If the opposite direction is desired, use <code>to_redirected()</code> on the output of these functions.
width	Integer specifying the width of the ring, breadth of the branches, or maximum extent of the neighbourhood.
...	Additional arguments passed on to <code>igraph::make_ring()</code> .
membership	A vector of partition membership as integers. If left as <code>NULL</code> (the default), nodes in each mode will be assigned to two, equally sized partitions.
outdegree	Numeric scalar or vector indicating the desired outdegree distribution. By default <code>NULL</code> and is required. If <code>n</code> is an existing network object and the outdegree is not specified, then the outdegree distribution will be inferred from that of the network. Note that a scalar (single number) will result in a k -regular graph.
indegree	Numeric vector indicating the desired indegree distribution. By default <code>NULL</code> but not required unless a directed network is desired. If <code>n</code> is an existing directed network object and the indegree is not specified, then the indegree distribution will be inferred from that of the network.
mark	A logical vector the length of the nodes in the network. This can be created by, among other things, any <code>node_is_*</code> () function.

Value

By default a `tbl_graph` object is returned, but this can be coerced into other types of objects using `as_edgelist()`, `as_matrix()`, `as_tidygraph()`, or `as_network()`.

By default, all networks are created as undirected. This can be overruled with the argument `directed = TRUE`. This will return a directed network in which the arcs are out-facing or equivalent. This direction can be swapped using `to_redirected()`. In two-mode networks, the directed argument is ignored.

Lattice graphs

`create_lattice()` creates both two-dimensional grid and triangular lattices with as even dimensions as possible. When the width parameter is set to 4, nodes cannot have (in or out) degrees larger than 4. This creates regular square grid lattices where possible. Such a network is bipartite, that is partitionable into two types that are not adjacent to any of their own type. If the number of nodes is a prime number, it will only return a chain (a single dimensional lattice).

A width parameter of 8 creates a network where the maximum degree of any nodes is 8. This can create a triangular mesh lattice or a Queen's move lattice, depending on the dimensions. A width parameter of 12 creates a network where the maximum degree of any nodes is 12. Prime numbers of nodes will return a chain.

See Also

as

Other makes: [make_cran](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_random](#), [make_read](#), [make_stochastic](#), [make_write](#)

Examples

```
create_empty(10)
create_filled(10)
create_ring(8, width = 2)
create_star(12)
create_tree(c(7,8))
create_lattice(12, width = 4)
create_components(10, membership = c(1,1,1,2,2,2,3,3,3,3))
create_degree(10, outdegree = rep(1:5, 2))
create_core(6)
  create_windmill(6)
  create_cycle(6)
  create_wheel(6)
```

make_ego

Making ego networks through interviewing

Description

This function creates an ego network through interactive interview questions. It currently only supports a simplex, directed network of one or two modes. These directed networks can be reformatted as undirected using `to_undirected()`. Multiplex networks can be collected separately and then joined together afterwards.

The function supports the use of rosters or a maximum number of alters to collect. If a roster is provided it will offer ego all names. The function can also prompt ego to interpret each node's attributes, or about how ego considers their alters to be related.

Usage

```
create_ego(
  ego = NULL,
  max_alters = Inf,
  roster = NULL,
  interpreter = FALSE,
  interrelater = FALSE,
  twomode = FALSE
)
```

Arguments

ego	A character string. If desired, the name of ego can be declared as an argument. Otherwise the first prompt of the function will be to enter a name for ego.
max_alters	The maximum number of alters to collect. By default infinity, but many name generators will expect a maximum of e.g. 5 alters to be named.
roster	A vector of node names to offer as potential alters for ego.
interpreter	Logical. If TRUE, then it will ask for which attributes to collect and give prompts for each attribute for each node in the network. By default FALSE.
interrelater	Logical. If TRUE, then it will ask for the contacts from each of the alters perspectives too.
twomode	Logical. If TRUE, then it will assign ego to the first mode and all alters to a second mode.

See Also

Other makes: [make_cran](#), [make_create](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_random](#), [make_read](#), [make_stochastic](#), [make_write](#)

make_explicit

Making networks with explicit ties

Description

This function creates a network from a vector of explicitly named nodes and ties between them. `create_explicit()` largely wraps `igraph::graph_from_literal()`, but will also accept character input and not just a formula, and will never simplify the result.

Ties are indicated by -, and directed ties (arcs) require + at either or both ends. Ties are separated by commas, and isolates can be added as an additional, unlinked node after the comma within the formula. Sets of nodes can be linked to other sets of nodes through use of a semi-colon. See the example for a demonstration.

Usage

```
create_explicit(...)
```

Arguments

... Arguments passed on to {igraph}.

See Also

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_random](#), [make_read](#), [make_stochastic](#), [make_write](#)

Examples

```
create_explicit(A -+ B, B -+ C, A +++ C, D, E:F:G-+A, E:F+++G:H)
```

make_learning	<i>Making learning models on networks</i>
---------------	---

Description

These functions allow learning games to be played upon networks.

- `play_learning()` plays a learning model upon a network.
- `play_segregation()` plays a Schelling segregation model upon a network.

Usage

```
play_learning(.data, beliefs, closeness = Inf, steps, epsilon = 5e-04)
```

```
play_segregation(
  .data,
  attribute,
  heterophily = 0,
  who_moves = c("ordered", "random", "most_dissatisfied"),
  choice_function = c("satisficing", "optimising", "minimising"),
  steps
)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>beliefs</code>	A vector indicating the probabilities nodes put on some outcome being 'true'.
<code>closeness</code>	A threshold at which beliefs are too different to influence each other. By default Inf, i.e. there is no threshold.

steps	The number of steps forward in learning. By default the number of nodes in the network.
epsilon	The maximum difference in beliefs accepted for convergence to a consensus.
attribute	A string naming some nodal attribute in the network. Currently only tested for binary attributes.
heterophily	A score ranging between -1 and 1 as a threshold for how heterophilous nodes will accept their neighbours to be. A single proportion means this threshold is shared by all nodes, but it can also be a vector the same length of the nodes in the network for issuing different thresholds to different nodes. By default this is 0, meaning nodes will be dissatisfied if more than half of their neighbours differ on the given attribute.
who_moves	One of the following options: "ordered" (the default) checks each node in turn for whether they are dissatisfied and there is an available space that they can move to, "random" will check a node at random, and "most_dissatisfied" will check (one of) the most dissatisfied nodes first.
choice_function	One of the following options: "satisficing" (the default) will move the node to any coordinates that satisfy their heterophily threshold, "optimising" will move the node to coordinates that are most homophilous, and "minimising" distance will move the node to the next nearest unoccupied coordinates.

Learning models

The default is a Degroot learning model, but if closeness is defined as anything less than infinity, this becomes a Deffuant model. A Deffuant model is similar to a Degroot model, however nodes only learn from other nodes whose beliefs are not too dissimilar from their own.

References

- DeGroot, Morris H. 1974. "Reaching a consensus", *Journal of the American Statistical Association*, 69(345): 118–21. doi:[10.1080/01621459.1974.10480137](https://doi.org/10.1080/01621459.1974.10480137)
- Deffuant, Guillaume, David Neau, Frederic Amblard, and Gérard Weisbuch. 2000. "Mixing beliefs among interacting agents", *Advances in Complex Systems*, 3(1): 87-98. doi:[10.1142/S0219525900000078](https://doi.org/10.1142/S0219525900000078)
- Golub, Benjamin, and Matthew O. Jackson 2010. "Naive learning in social networks and the wisdom of crowds", *American Economic Journal*, 2(1): 112-49. doi:[10.1257/mic.2.1.112](https://doi.org/10.1257/mic.2.1.112)

See Also

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_explicit](#), [make_motifs](#), [make_play](#), [make_random](#), [make_read](#), [make_stochastic](#), [make_write](#)

Other models: [make_play](#)

Examples

```
play_learning(ison_networkers,
  rbinom(net_nodes(ison_networkers),1,prob = 0.25))
startValues <- rbinom(100,1,prob = 0.5)
```

```

startValues[sample(seq_len(100), round(100*0.2))] <- NA
latticeEg <- create_lattice(100)
latticeEg <- add_node_attribute(latticeEg, "startValues", startValues)
latticeEg
play_segregation(latticeEg, "startValues", 0.5)

```

make_mnet	<i>Multilevel, multiplex, multimodal, signed, dynamic or longitudinal changing networks</i>
-----------	---

Description

The 'mnet' class of network object is an additional class layered on top of the 'igraph' and 'tbl_graph' classes. Under the hood it is an 'igraph' object, which enables all the igraph functions to operate. It is also a 'tbl_graph' object, which enables it to be used with {ggraph}. However, 'mnet' objects offer prettier printing and a consistent structure that enables more complex forms of networks to be contained in a single object.

Usage

```

## S3 method for class 'mnet'
print(x, ..., n = 12)

print_all(x, ...)

describe_network(x)

describe_nodes(x)

describe_ties(x)

describe_changes(x)

```

Arguments

x	An object of class "mnet" or "tbl_graph".
...	Other arguments passed to or from other methods.
n	Number of observations to print across all network components, i.e. nodes, changes, and ties. By default 12.

Nodes

Nodes are held as vertices and vertex attributes in the 'igraph' object, but printed as a nodelist. Here the convention is for the first column of the nodelist to be called 'name' and records the labels of the nodes. Additional reserved columns include 'active' for changing networks and 'type' for multimodal networks.

Changes

Changes, that is a list of changes to the nodes in the network, are held internally as a graph attribute in the 'igraph' object, but printed as a changelist. Here the convention is for the 'wave' or 'time' column to appear first, followed by 'node' indicating to which node the change applies, 'var' for the variable to which the change applies, and 'value' for the new value to be applied.

Ties

Ties are held as edges and edge attributes in the 'igraph' object, but printed as an edgelist. Here the convention is for the first column of the edgelist to be called 'from' and the second column 'to', even if the network is not directed. Additional reserved columns include 'weight' for weighted networks, 'wave' for longitudinal networks, 'type' for multiplex networks, and 'sign' for signed networks.

Printing

When printed, 'mnet' objects will print to the console any information stored about the network's name, or its types of nodes or ties. It will also describe key features of the network, such as whether the network is multiplex, weighted, directed, etc.

It will then print tibbles for the nodes, changes, and ties in the network, as appropriate. That is, if there is no nodal data (e.g. it is an unlabelled network without any other nodal attributes), then this will be skipped. Similarly, if no nodal changes are logged, this information will be skipped too.

make_motifs

Making motifs

Description

create_motifs() is used to create a list of networks that represent the subgraphs or motifs corresponding to a certain number of nodes and direction. Note that currently only $n=2$ to $n=4$ is implemented, and the latter only for undirected networks.

Usage

```
create_motifs(n, directed = FALSE)
```

Arguments

n	Given: <ul style="list-style-type: none"> • A single integer, e.g. $n = 10$, a one-mode network will be created. • A vector of two integers, e.g. $n = c(5, 10)$, a two-mode network will be created. • A manynet-compatible object, a network of the same dimensions will be created.
directed	Logical whether the graph should be directed. By default <code>directed = FALSE</code> . If the opposite direction is desired, use <code>to_redirected()</code> on the output of these functions.

See Also

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_play](#), [make_random](#), [make_read](#), [make_stochastic](#), [make_write](#)

 make_play

Making diffusion models on networks

Description

These functions simulate diffusion or compartment models upon a network.

- `play_diffusion()` runs a single simulation of a compartment model, allowing the results to be visualised and examined.

These functions allow both a full range of compartment models, as well as simplex and complex diffusion to be simulated upon a network.

Usage

```
play_diffusion(
  .data,
  seeds = 1,
  contact = NULL,
  prevalence = 0,
  thresholds = 1,
  transmissibility = 1,
  latency = 0,
  recovery = 0,
  waning = 0,
  fatality = 0,
  immune = NULL,
  steps,
  old_version = FALSE
)
```

Arguments

- | | |
|--------------------|---|
| <code>.data</code> | An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package |
| <code>seeds</code> | A valid mark vector the length of the number of nodes in the network. |

contact	A matrix or network that replaces ".data" with some other explicit contact network, e.g. <code>create_components(.data, membership = node_in_structural(.data))</code> . Can be of arbitrary complexity, but must of the same dimensions as .data.
prevalence	The proportion that global prevalence contributes to diffusion. That is, if prevalence is 0.5, then the current number of infections is multiplied by 0.5 and added "prevalence" is 0 by default, i.e. there is no global mechanism. Note that this is endogenously defined and is updated at the outset of each step.
thresholds	A numeric vector indicating the thresholds each node has. By default 1. A single number means a generic threshold; for thresholds that vary among the population please use a vector the length of the number of nodes in the network. If 1 or larger, the threshold is interpreted as a simple count of the number of contacts/exposures sufficient for infection. If less than 1, the threshold is interpreted as complex, where the threshold concerns the proportion of contacts.
transmissibility	The transmission rate probability, β . By default 1, which means any node for which the threshold is met or exceeded will become infected. Anything lower means a correspondingly lower probability of adoption, even when the threshold is met or exceeded.
latency	The inverse probability those who have been exposed become infectious (infected), σ or κ . For example, if exposed individuals take, on average, four days to become infectious, then $\sigma = 0.75$ ($1/1-0.75 = 1/0.25 = 4$). By default 0, which means those exposed become immediately infectious (i.e. an SI model). Anything higher results in e.g. a SEI model.
recovery	The probability those who are infected recover, γ . For example, if infected individuals take, on average, four days to recover, then $\gamma = 0.25$. By default 0, which means there is no recovery (i.e. an SI model). Anything higher results in an SIR model.
waning	The probability those who are recovered become susceptible again, ξ . For example, if recovered individuals take, on average, four days to lose their immunity, then $\xi = 0.25$. By default 0, which means any recovered individuals retain lifelong immunity (i.e. an SIR model). Anything higher results in e.g. a SIRS model. $\xi = 1$ would mean there is no period of immunity, e.g. an SIS model.
fatality	The probability those who are infected are removed from the network, α . Note that fatality is distinct from a natural mortality rate. By default $\alpha = 0$, which means that there is no fatality. Where $\alpha > 0$, the nodal attribute 'active' will be added if it is not already present.
immune	A logical or numeric vector identifying nodes that begin the diffusion process as already recovered. This could be interpreted as those who are vaccinated or equivalent. Note however that a waning parameter will affect these nodes too. By default NULL, indicating that no nodes begin immune.
steps	The number of steps forward in the diffusion to play. By default the number of nodes in the network. If <code>steps = Inf</code> then the diffusion process will continue until there are no new infections or all nodes are infected.
old_version	This is included to maintain backward compatibility with the old version of this function, that would return a special object. The new version adds the diffusion event record as changes to the original network.

Simple and complex diffusion

By default, the function will simulate a simple diffusion process in which some infectious disease or idea diffuses from seeds through contacts at some constant rate (transmissibility).

These seeds can be specified by a vector index (the number of the position of each node in the network that should serve as a seed) or as a logical vector where TRUE is interpreted as already infected.

thresholds can be set such that adoption/infection requires more than one (the default) contact already being infected. This parameter also accepts a vector so that thresholds can vary.

Complex diffusion is where the thresholds are defined less than one. In this case, the thresholds are interpreted as proportional. That is, the threshold to adoption/infection is defined by the proportion of the node's contacts infected.

Nodes that cannot be infected can be indicated as immune with a logical vector or index, similar to how seeds are identified. Note that immune nodes are interpreted internally as Recovered (R) and are thus subject to waning (see below).

Compartment models

Compartment models are flexible models of diffusion or contagion, where nodes are compartmentalised into one of two or more categories.

The most basic model is the SI model. The SI model is the default in `play_diffusion()/play_diffusions()`, where nodes can only move from the Susceptible (S) category to the Infected (I) category. Whether nodes move from S to I depends on whether they are exposed to the infection, for instance through a contact, the transmissibility of the disease, and their thresholds to the disease.

Another common model is the SIR model. Here nodes move from S to I, as above, but additionally they can move from I to a Recovered (R) status. The probability that an infected node recovers at a timepoint is controlled by the recovery parameter.

The next most common models are the SIS and SIRS models. Here nodes move from S to I or additionally to R, as above, but additionally they can move from I or R back to a Susceptible (S) state. This probability is governed by the waning parameter. Where `recover > 0` and `waning = 1`, the Recovery (R) state will be skipped and the node will return immediately to the Susceptible (S) compartment.

Lastly, these functions also offer the possibility of specifying a latency period in which nodes have been infected but are not yet infectious. Where `latency > 0`, an additional Exposed (E) compartment is introduced that governs the probability that a node moves from this E compartment to infectiousness (I). This can be used in in SEI, SEIS, SEIR, and SEIRS models.

See Also

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_random](#), [make_read](#), [make_stochastic](#), [make_write](#)

Other models: [make_learning](#)

Other diffusion: [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [member_diffusion](#)

Examples

```
smeg <- generate_smallworld(15, 0.025)
```

make_random

Making unconditional and conditional random networks

Description

These functions are similar to the `create_*` functions, but include some element of randomisation. They are particularly useful for creating a distribution of networks for exploring or testing network properties.

- `generate_random()` generates a random network with ties appearing at some probability.
- `generate_configuration()` generates a random network consistent with a given degree distribution.
- `generate_man()` generates a random network conditional on the dyad census of Mutual, Asymmetric, and Null dyads, respectively.
- `generate_utilities()` generates a random utility matrix.

These functions can create either one-mode or two-mode networks. To create a one-mode network, pass the main argument `n` a single integer, indicating the number of nodes in the network. To create a two-mode network, pass `n` a vector of *two* integers, where the first integer indicates the number of nodes in the first mode, and the second integer indicates the number of nodes in the second mode. As an alternative, an existing network can be provided to `n` and the number of modes, nodes, and directedness will be inferred.

Usage

```
generate_random(n, p = 0.5, directed = FALSE, with_attr = TRUE)
```

```
generate_configuration(.data)
```

```
generate_man(n, man = NULL)
```

```
generate_utilities(n, steps = 1, volatility = 0, threshold = 0)
```

```
generate_permutation(.data, with_attr = TRUE)
```

Arguments

`n`

Given:

- A single integer, e.g. `n = 10`, a one-mode network will be created.
- A vector of two integers, e.g. `n = c(5, 10)`, a two-mode network will be created.
- A `manynet`-compatible object, a network of the same dimensions will be created.

p	Proportion of possible ties in the network that are realised or, if integer greater than 1, the number of ties in the network.
directed	Whether to generate network as directed. By default FALSE.
with_attr	Logical whether any attributes of the object should be retained. By default TRUE.
.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
man	Vector of Mutual, Asymmetric, and Null dyads, respectively. Can be specified as proportions, e.g. <code>c(0.5, 0.5, 0.5)</code> , or as a count, e.g. <code>c(10, 0, 20)</code> . Is inferred from n if it is an existing network object.
steps	Number of simulation steps to run. By default 1: a single, one-shot simulation. If more than 1, further iterations will update the utilities depending on the values of the volatility and threshold parameters.
volatility	How much change there is between steps. Only if volatility is more than 1 do further simulation steps make sense. This is passed on to <code>stats::rnorm</code> as the <code>sd</code> or standard deviation parameter.
threshold	This parameter can be used to mute or disregard stepwise changes in utility that are minor. The default 0 will recognise all changes in utility, but raising the threshold will mute any changes less than this threshold.

Value

By default a `tbl_graph` object is returned, but this can be coerced into other types of objects using `as_edgelist()`, `as_matrix()`, `as_tidygraph()`, or `as_network()`.

By default, all networks are created as undirected. This can be overruled with the argument `directed = TRUE`. This will return a directed network in which the arcs are out-facing or equivalent. This direction can be swapped using `to_redirected()`. In two-mode networks, the directed argument is ignored.

References

On random networks:

Erdos, Paul, and Alfred Renyi. 1959. "On Random Graphs I" *Publicationes Mathematicae*. 6: 290–297.

On configuration models:

Bollobas, Bela. 1980. "A Probabilistic Proof of an Asymptotic Formula for the Number of Labelled Regular Graphs". *European Journal of Combinatorics* 1: 311-316.

On dyad-census conditioned networks:

Holland, Paul W., and Samuel Leinhardt. 1976. "Local Structure in Social Networks." In D. Heise (Ed.), *Sociological Methodology*, pp 1-45. San Francisco: Jossey-Bass.

See Also

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_read](#), [make_stochastic](#), [make_write](#)

Examples

```
generate_random(12, 0.4)
# generate_random(c(6, 6), 0.4)
```

make_read

Making networks from external files

Description

Researchers regularly need to work with a variety of external data formats. The following functions enable importing from some common external file formats into objects that {manynet} and other graph/network packages in R can work with:

- `read_matrix()` imports adjacency matrices from Excel/csv files.
- `read_edgelist()` imports edgelists from Excel/csv files.
- `read_nodelist()` imports nodelists from Excel/csv files.
- `read_pajek()` imports Pajek (.net or .paj) files.
- `read_ucinet()` imports UCINET files from the header (##h).
- `read_dynetml()` imports DyNetML interchange format for rich social network data.
- `read_graphml()` imports GraphML files.
- `read_gml()` imports GML files.
- `read_gdf()` imports GDF files.

Usage

```
read_matrix(file = file.choose(), sv = c("comma", "semi-colon"), ...)
read_edgelist(file = file.choose(), sv = c("comma", "semi-colon"), ...)
read_nodelist(file = file.choose(), sv = c("comma", "semi-colon"), ...)
read_pajek(file = file.choose(), ties = NULL, ...)
read_ucinet(file = file.choose())
read_dynetml(file = file.choose())
read_graphml(file = file.choose())
read_gml(file = file.choose())
read_gdf(file = file.choose())
```

Arguments

file	A character string with the system path to the file to import. If left unspecified, an OS-specific file picker is opened to help users select it. Note that in <code>read_ucinet()</code> the file path should be to the header file (<code>##h</code>), if it exists and that it is currently not possible to import multiple networks from a single UCINET file. Please convert these one by one.
sv	Allows users to specify whether their csv file is "comma" (English) or "semi-colon" (European) separated.
...	Additional parameters passed to the read/write function.
ties	A character string indicating the ties/network, where the data contains several.

Details

Note that these functions are not as actively maintained as others in the package, so please let us know if any are not currently working for you or if there are missing import routines by [raising an issue on Github](#).

There are a number of repositories for network data that hold various datasets in different formats. See for example:

- [UCINET data](#)
- [networkdata](#)
- [GML datasets](#)
- UC Irvine Network Data Repository
- [SNAP Stanford Large Network Dataset Collection](#)

Please let us know if you identify any further repositories of social or political networks and we would be happy to add them here.

The `_ucinet` functions only work with relatively recent UCINET file formats, e.g. type 6406 files. To import earlier UCINET file types, you will need to update them first. To import multiple matrices packed into a single UCINET file, you will need to unpack them and convert them one by one.

Value

`read_edgelist()` and `read_nodelist()` will import into edgelist (tibble) format which can then be coerced or combined into different graph objects from there.

`read_pajek()` and `read_ucinet()` will import into a tidygraph format, since they already contain both edge and attribute data. `read_matrix()` will import into tidygraph format too. Note that all graphs can be easily coerced into other formats with `{manynet}`'s `as_` methods.

Source

`read_ucinet()` kindly supplied by Christian Steglich, constructed on 18 June 2015.

See Also

as

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_random](#), [make_stochastic](#), [make_write](#)

make_stochastic

Making networks with a stochastic element

Description

These functions are similar to the `create_*` functions, but include some element of randomisation. They are particularly useful for creating a distribution of networks for exploring or testing network properties.

- `generate_smallworld()` generates a small-world structure via ring rewiring at some probability.
- `generate_scalefree()` generates a scale-free structure via preferential attachment at some probability.
- `generate_fire()` generates a forest fire model.
- `generate_islands()` generates an islands model.
- `generate_citations()` generates a citations model.

These functions can create either one-mode or two-mode networks. To create a one-mode network, pass the main argument `n` a single integer, indicating the number of nodes in the network. To create a two-mode network, pass `n` a vector of *two* integers, where the first integer indicates the number of nodes in the first mode, and the second integer indicates the number of nodes in the second mode. As an alternative, an existing network can be provided to `n` and the number of modes, nodes, and directedness will be inferred.

Usage

```
generate_smallworld(n, p = 0.05, directed = FALSE, width = 2)

generate_scalefree(n, p = 1, directed = FALSE)

generate_fire(n, contacts = 1, their_out = 0, their_in = 1, directed = FALSE)

generate_islands(n, islands = 2, p = 0.5, bridges = 1, directed = FALSE)

generate_citations(
  n,
  ties = sample(1:4, 1),
  agebins = max(1, n/10),
  directed = FALSE
)
```

Arguments

n	Given: <ul style="list-style-type: none"> • A single integer, e.g. $n = 10$, a one-mode network will be created. • A vector of two integers, e.g. $n = c(5, 10)$, a two-mode network will be created. • A manynet-compatible object, a network of the same dimensions will be created.
p	Power of the preferential attachment, default is 1.
directed	Whether to generate network as directed. By default FALSE.
width	Integer specifying the width of the ring, breadth of the branches, or maximum extent of the neighbourhood.
contacts	Number of contacts or ambassadors chosen from among existing nodes in the network. By default 1. See <code>igraph::sample_forestfire()</code> .
their_out	Probability of tying to a contact's outgoing ties. By default 0.
their_in	Probability of tying to a contact's incoming ties. By default 1.
islands	Number of islands or communities to create. By default 2. See <code>igraph::sample_islands()</code> for more.
bridges	Number of bridges between islands/communities. By default 1.
ties	Number of ties to add per new node. By default a uniform random sample from 1 to 4 new ties.
agebins	Number of aging bins. By default either $\frac{n}{10}$ or 1, whichever is the larger. See <code>igraphr::sample_last_cit()</code> for more.

Value

By default a `tbl_graph` object is returned, but this can be coerced into other types of objects using `as_edgelist()`, `as_matrix()`, `as_tidygraph()`, or `as_network()`.

By default, all networks are created as undirected. This can be overruled with the argument `directed = TRUE`. This will return a directed network in which the arcs are out-facing or equivalent. This direction can be swapped using `to_redirected()`. In two-mode networks, the `directed` argument is ignored.

References**On small-world networks:**

Watts, Duncan J., and Steven H. Strogatz. 1998. "Collective Dynamics of 'Small-World' Networks." *Nature* 393(6684):440–42. doi:10.1038/30918.

On scale-free networks:

Barabasi, Albert-Laszlo, and Reka Albert. 1999. "Emergence of Scaling in Random Networks." *Science* 286(5439):509–12. doi:10.1126/science.286.5439.509.

On the forest-fire model:

Leskovec, Jure, Jon Kleinberg, and Christos Faloutsos. 2007. "Graph evolution: **Densification and shrinking diameters**". *ACM transactions on Knowledge Discovery from Data*, 1(1): 2-es.

See Also

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_random](#), [make_read](#), [make_write](#)

Examples

```
generate_smallworld(12, 0.025)
generate_smallworld(12, 0.25)
generate_scalefree(12, 0.25)
generate_scalefree(12, 1.25)
generate_fire(10)
generate_islands(10)
generate_citations(10)
```

make_write

Making networks to external files

Description

Researchers may want to save or work with networks outside R. The following functions offer ways to export to some common external file formats:

- `write_matrix()` exports an adjacency matrix to a .csv file.
- `write_edgelist()` exports an edgelist to a .csv file.
- `write_nodelist()` exports a nodelist to a .csv file.
- `write_pajek()` exports Pajek .net files.
- `write_ucinet()` exports a pair of UCINET files in V6404 file format (.##h, .##d).
- `write_graphml()` exports GraphML files.

Usage

```
write_matrix(.data, filename, ...)
```

```
write_edgelist(.data, filename, ...)
```

```
write_nodelist(.data, filename, ...)
```

```
write_pajek(.data, filename, ...)
```

```
write_ucinet(.data, filename, name)
```

```
write_graphml(.data, filename, ...)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none">• matrix (adjacency or incidence) from {base} R• edgelist, a data frame from {base} R or tibble from {tibble}• igraph, from the {igraph} package• network, from the {network} package• tbl_graph, from the {tidygraph} package
<code>filename</code>	Character string filename. If missing, the files will have the same name as the object and be saved to the working directory. An appropriate extension will be added if not included.
<code>...</code>	Additional parameters passed to the write function.
<code>name</code>	Character string to name the network internally, e.g. in UCINET. By default the name will be the same as the object.

Details

Note that these functions are not as actively maintained as others in the package, so please let us know if any are not currently working for you or if there are missing import routines by [raising an issue on Github](#).

Value

The `write_functions` export to different file formats, depending on the function.

A pair of UCINET files in V6404 file format (`.##h`, `.##d`)

Source

`write_ucinet()` kindly supplied by Christian Steglich, constructed on 18 June 2015.

See Also

[as](#)

Other makes: [make_cran](#), [make_create](#), [make_ego](#), [make_explicit](#), [make_learning](#), [make_motifs](#), [make_play](#), [make_random](#), [make_read](#), [make_stochastic](#)

Description

The `as_` functions in `{manynet}` coerce objects of any of the following common classes of social network objects in R into the declared class:

- `as_edgelist()` coerces the object into an edgelist, as data frames or tibbles.
- `as_matrix()` coerces the object into an adjacency (one-mode/unipartite) or incidence (two-mode/bipartite) matrix.
- `as_igraph()` coerces the object into an `{igraph}` graph object.
- `as_tidygraph()` coerces the object into a `{tidygraph}` `tbl_graph` object.
- `as_network()` coerces the object into a `{network}` network object.
- `as_siena()` coerces the (igraph/tidygraph) object into a SIENA dependent variable.
- `as_graphAM()` coerces the object into a graph adjacency matrix.
- `as_diffusion()` coerces a table of diffusion events into a `diff_model` object similar to the output of `play_diffusion()`.
- `as_diffnet()` coerces a `diff_model` object into a `{netdiffuseR}` `diffnet` object.

An effort is made for all of these coercion routines to be as lossless as possible, though some object classes are better at retaining certain kinds of information than others. Note also that there are some reserved column names in one or more object classes, which could otherwise lead to some unexpected results.

Usage

```
as_nodelist(.data)

as_changelist(.data)

as_edgelist(.data, twomode = FALSE)

as_matrix(.data, twomode = NULL)

as_igraph(.data, twomode = FALSE)

as_tidygraph(.data, twomode = FALSE)

as_network(.data, twomode = FALSE)

as_siena(.data, twomode = FALSE)

as_graphAM(.data, twomode = NULL)

as_diffusion(.data, twomode = FALSE, events)

as_diffnet(.data, twomode = FALSE)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>twomode</code>	Logical option used to override heuristics for distinguishing incidence (two-mode/bipartite) from adjacency (one-mode/unipartite) networks. By default FALSE.
<code>events</code>	A table (data frame or tibble) of diffusion events with columns <code>t</code> indicating the time (typically an integer) of the event, <code>nodes</code> indicating the number or name of the node involved in the event, and <code>event</code> , which can take on the values "I" for an infection event, "E" for an exposure event, or "R" for a recovery event.

Details

Edgelists are expected to be held in data.frame or tibble class objects. The first two columns of such an object are expected to be the senders and receivers of a tie, respectively, and are typically named "from" and "to" (even in the case of an undirected network). These columns can contain integers to identify nodes or character strings/factors if the network is labelled. If the sets of senders and receivers overlap, a one-mode network is inferred. If the sets contain no overlap, a two-mode network is inferred. If a third, numeric column is present, a weighted network will be created.

Matrices can be either adjacency (one-mode) or incidence (two-mode) matrices. Incidence matrices are typically inferred from unequal dimensions, but since in rare cases a matrix with equal dimensions may still be an incidence matrix, an additional argument `twomode` can be specified to override this heuristic.

This information is usually already embedded in `{igraph}`, `{tidygraph}`, and `{network}` objects.

Value

The currently implemented coercions or translations are:

	data.frame	diff_model	diffnet	igraph	list	matrix	network	network.goldfish	siena	tbl_graph
<code>as_diffnet</code>	0	1	0	0	0	0	0	0	0	0
<code>as_diffusion</code>	0	1	1	1	0	0	0	0	0	0
<code>as_edgelist</code>	1	0	0	1	0	1	1	1	1	1
<code>as_graphAM</code>	1	0	0	1	0	1	1	1	1	1
<code>as_igraph</code>	1	1	1	1	0	1	1	1	1	1
<code>as_matrix</code>	1	1	0	1	0	1	1	1	1	1
<code>as_network</code>	1	0	1	1	0	1	1	1	1	1
<code>as_siena</code>	0	0	0	1	0	0	0	0	0	0
<code>as_tidygraph</code>	1	1	1	1	1	1	1	1	1	1

`as_diffusion()` and `play_diffusion()` return a 'diff_model' object that contains two different tibbles (tables) – a table of diffusion events and a table of the number of nodes in each relevant

component (S, E, I, or R) – as well as a copy of the network upon which the diffusion ran. By default, a compact version of the component table is printed (to print all the changes at each time point, use `print(..., verbose = T)`). To retrieve the diffusion events table, use `summary(...)`.

See Also

Other modifications: [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```
test <- data.frame(from = c("A","B","B","C","C"), to = c("I","G","I","G","H"))
as_edgelist(test)
as_matrix(test)
as_igraph(test)
as_tidygraph(test)
as_network(test)
# How to create a diff_model object from (basic) observed data
events <- data.frame(time = c(0,1,1,2,3),
                    node = c(1,2,3,2,4),
                    var = "diffusion",
                    value = c("I","I","I","R","I"))
add_changes(create_filled(4), events)
```

manip_changes

Modifying changes to nodes over time

Description

These functions offer ways to modify data held about how nodes change over time. They include:

- `add_changes()` adds a table of changes to the nodes of a network.
- `mutate_changes()` can be used to update network changes.
- `filter_changes()` is used to subset network changes.
- `collect_changes()` is similar to `filter_changes()`, but collects the cumulative changes up to a time point.
- `apply_changes()` applies the changes collected up to a time point to a network, removing the changes.

An example of when this might be useful is to track change in the composition of a network (when nodes are present or absent over time), though the function can flexibly accommodate changes in other nodal attributes.

Usage

```

add_changes(.data, changes)

delete_changes(.data)

mutate_changes(.data, ...)

filter_changes(.data, ..., .by = NULL)

select_changes(.data, ..., .by = NULL)

collect_changes(.data, time)

apply_changes(.data, time)

```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>changes</code>	A data frame of changes. Ideally this will be in the form of "wave", "node", "var", and "value", but there are internal routines from some otherwise common formats. A data frame of composition change can be just two columns.
<code>...</code>	Additional arguments.
<code>.by</code>	An attribute name to join objects by. By default, NULL.
<code>time</code>	A time point or wave at which to present the network.

See Also

[to_time\(\)](#)

Examples

```

add_changes(ison_algebra,
            data.frame(wave = 2, node = 1, var = "active", value = FALSE))
filter_changes(fict_starwars, node == "Anakin")
select_changes(fict_starwars, node)
collect_changes(fict_starwars, time = 3)
collect_changes(fict_starwars, time = 3)

```

manip_correlation *Node correlation*

Description

This function performs a Pearson pairwise correlation on a given matrix or network data. It includes a switch: whereas for a two-mode network it will perform a regular correlation, including all rows, for an undirected network it will perform a correlation on a matrix with the diagonals removed, for a reciprocated network it will include the difference between reciprocated ties, and for complex networks it will include also the difference between the self ties in each pairwise calculation. This function runs in $O(mn^2)$ complexity.

Usage

```
to_correlation(.data, method = NULL)
```

```
to_cosine(.data)
```

Arguments

.data	<p>An object of a manynet-consistent class:</p> <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
method	<p>One of the following: "all" includes all information, "diag" excludes the diagonal (self-ties), "recip" excludes the diagonal but compares pairs' reciprocal ties, and "complex" compares pairs' reciprocal ties and their self ties. By default the appropriate method is chosen based on the network format.</p>

See Also

Other modifications: [manip_as](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Description

These functions reformat many-net-consistent data.

- `to_unnamed()` reformats labelled network data to unlabelled network data.
- `to_unweighted()` reformats weighted network data to unweighted network data, with all tie weights removed.
- `to_unsigned()` reformats signed network data to unsigned network data keeping just the "positive" or "negative" ties.
- `to_simplex()` reformats complex network data, containing loops, to simplex network data, without any loops.
- `to_uniplex()` reformats multiplex network data to a single type of tie.

If the format condition is not met, for example `to_undirected()` is used on a network that is already undirected, the network data is returned unaltered. No warning is given so that these functions can be used to ensure conformance.

Unlike the `as_*`() group of functions, these functions always return the same class as they are given, only transforming these objects' properties.

Usage

```
to_unnamed(.data)
```

```
to_unweighted(.data, threshold = 1)
```

```
to_unsigned(.data, keep = c("positive", "negative"))
```

```
to_simplex(.data)
```

```
to_uniplex(.data, tie)
```

Arguments

<code>.data</code>	An object of a many-net-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>threshold</code>	For a matrix, the threshold to binarise/dichotomise at.
<code>keep</code>	In the case of a signed network, whether to retain the "positive" or "negative" ties.
<code>tie</code>	Character string naming a tie attribute to retain from a graph.

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	data.frame	igraph	matrix	network	tbl_graph
to_simplex	1	1	1	1	1
to_undirected	1	1	1	1	1
to_uniplex	1	1	1	1	1
to_unnamed	1	1	1	1	1
to_unsigned	1	1	1	1	1
to_unweighted	1	1	1	1	1

Value

All `to_` functions return an object of the same class as that provided. So passing it an `igraph` object will return an `igraph` object and passing it a `network` object will return a `network` object, with certain modifications as outlined for each function.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```
as_tidygraph(create_filled(5)) %>%
  mutate_ties(type = sample(c("friend", "enemy"), 10, replace = TRUE)) %>%
  to_uniplex("friend")
```

manip_direction	<i>Modifying networks by formatting their directionality</i>
-----------------	--

Description

These functions reformat many-net-consistent data.

- `to_directed()` reformats undirected network data to a directed network.
- `to_undirected()` reformats directed network data to an undirected network, so that any pair of nodes with at least one directed edge will be connected by an undirected edge in the new network. This is equivalent to the "collapse" mode in `{igraph}`.
- `to_redirected()` formats directed network data by flipping/transposing any existing direction such that senders become receivers and receivers become senders. This essentially has no effect on undirected networks or reciprocated ties.
- `to_reciprocated()` reformats directed network data such that every directed tie is reciprocated.

- `to_acyclic()` reformats network data to an acyclic graph.

If the format condition is not met, for example `to_undirected()` is used on a network that is already undirected, the network data is returned unaltered. No warning is given so that these functions can be used to ensure conformance.

Unlike the `as_*`() group of functions, these functions always return the same class as they are given, only transforming these objects' properties.

Usage

```
to_directed(.data)

to_undirected(.data)

to_redirected(.data)

to_reciprocated(.data)

to_acyclic(.data)
```

Arguments

`.data` An object of a `manynet`-consistent class:

- `matrix` (adjacency or incidence) from `{base} R`
- `edgelist`, a data frame from `{base} R` or tibble from `{tibble}`
- `igraph`, from the `{igraph}` package
- `network`, from the `{network}` package
- `tbl_graph`, from the `{tidygraph}` package

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	<code>data.frame</code>	<code>igraph</code>	<code>matrix</code>	<code>network</code>	<code>tbl_graph</code>
<code>to_undirected</code>	1	1	1	1	1

Value

All `to_*` functions return an object of the same class as that provided. So passing it an `igraph` object will return an `igraph` object and passing it a `network` object will return a `network` object, with certain modifications as outlined for each function.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

`manip_from`*Joining lists of networks, graphs, and matrices*

Description

These functions offer tools for joining lists of many-net-consistent objects (matrices, igraph, tidygraph, or network objects) into a single object.

- `from_subgraphs()` modifies a list of subgraphs into a single tidygraph.
- `from_egos()` modifies a list of ego networks into a whole tidygraph
- `from_waves()` modifies a list of network waves into a longitudinal tidygraph.
- `from_slices()` modifies a list of time slices of a network into a dynamic tidygraph.
- `from_ties()` modifies a list of different ties into a multiplex tidygraph

Usage

```
from_subgraphs(netlist)
```

```
from_egos(netlist)
```

```
from_waves(netlist)
```

```
from_slices(netlist, remove.duplicates = FALSE)
```

```
from_ties(netlist, netnames)
```

Arguments

`netlist` A list of network, igraph, tidygraph, matrix, or edgelist objects.

`remove.duplicates`

Should duplicates be removed? By default FALSE. If TRUE, duplicated edges are removed.

`netnames`

A character vector of names for the different network objects, if not already named within the list.

Value

A tidygraph object combining the list of network data.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```

ison_adolescents %>%
  mutate(unicorn = sample(c("yes", "no"), 8, replace = TRUE)) %>%
  to_subgraphs(attribute = "unicorn") %>%
  from_subgraphs()
ison_adolescents %>%
  to_egos() %>%
  from_egos()
ison_adolescents %>%
  mutate_ties(wave = sample(1:4, 10, replace = TRUE)) %>%
  to_waves(attribute = "wave") %>%
  from_waves()
ison_adolescents %>%
  mutate_ties(time = 1:10, increment = 1) %>%
  add_ties(c(1,2), list(time = 3, increment = -1)) %>%
  to_slices(slice = c(5,7)) %>%
  from_slices()

```

manip_info

Modifying network data

Description

These functions allow users to add and edit information about the network itself. This includes the name, year, and mode of collection of the network, as well as definitions of the nodes and ties in the network. Where available, this information is printed for tidygraph-class objects, and can be used for printing a grand table in the {grand} package.

Usage

```
add_info(.data, ...)
```

```
mutate_net(.data, ...)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>...</code>	Named attributes. The following are currently recognised: "name", "year", and "doi" of the network, "collection" or "mode" of the network ("survey", "interview", "sensor", "observation", "archival", or "simulation"), "nodes" (a vector of the names of the nodes) or "vertex1"/"vertex2", "ties" or "edge.pos"/"edge.neg" for defining the ties.

Examples

```
add_info(ison_algebra, name = "Algebra")
```

manip_levels

Modifying network levels

Description

These functions reformat the levels in many-net-consistent network data.

- `to_onemode()` reformats two-mode network data into one-mode network data by simply removing the nodeset 'type' information. Note that this is not the same as `to_mode1()` or `to_mode2()`.
- `to_twomode()` reformats one-mode network data into two-mode network data, using a mark to distinguish the two sets of nodes.
- `to_multilevel()` reformats two-mode network data into multimodal network data, which allows for more levels and ties within modes.

If the format condition is not met, for example `to_onemode()` is used on a network that is already one-mode, the network data is returned unaltered. No warning is given so that these functions can be used to ensure conformance.

Unlike the `as_*`() group of functions, these functions always return the same class as they are given, only transforming these objects' properties.

Usage

```
to_onemode(.data)
```

```
to_twomode(.data, mark)
```

```
to_multilevel(.data)
```

Arguments

- | | |
|--------------------|--|
| <code>.data</code> | An object of a many-net-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package |
| <code>mark</code> | A logical vector marking two types or modes. By default "type". |

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	igraph	matrix	network	tbl_graph
to_multilevel	1	1	0	1
to_onemode	1	1	0	1
to_twomode	1	0	1	1

Value

All to_ functions return an object of the same class as that provided. So passing it an igraph object will return an igraph object and passing it a network object will return a network object, with certain modifications as outlined for each function.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

manip_miss

Modifying missing tie data

Description

These functions offer tools for imputing missing tie data. Currently two options are available:

- `na_to_zero()` replaces any missing values with zeros, which are the modal value in sparse social networks.
- `na_to_mean()` replaces missing values with the average non-missing value.

Usage

```
na_to_zero(.data)
```

```
na_to_mean(.data)
```

Arguments

- `.data` An object of a manynet-consistent class:
- matrix (adjacency or incidence) from `{base}` R
 - edgelist, a data frame from `{base}` R or tibble from `{tibble}`
 - igraph, from the `{igraph}` package
 - network, from the `{network}` package
 - tbl_graph, from the `{tidygraph}` package

Value

A data object of the same class as the function was given.

References**On missing data:**

Krause, Robert, Mark Huisman, Christian Steglich, and Tom A.B. Snijders. 2020. "Missing data in cross-sectional networks: An extensive comparison of missing data treatment methods". *Social Networks*, 62: 99-112. doi:[10.1016/j.socnet.2020.02.004](https://doi.org/10.1016/j.socnet.2020.02.004)

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```
missTest <- ison_adolescents %>%
  add_tie_attribute("weight", c(1,NA,NA,1,1,1,NA,NA,1,1)) %>%
  as_matrix
missTest
na_to_zero(missTest)
na_to_mean(missTest)
```

manip_nodes

Modifying node data

Description

These functions allow users to add and delete nodes and their attributes:

- `add_nodes()` adds an additional number of nodes to network data.
- `delete_nodes()` deletes nodes from network data.
- `add_node_attribute()`, `mutate()`, or `mutate_nodes()` offer ways to add a vector of values to a network as a nodal attribute.
- `rename_nodes()` and `rename()` rename nodal attributes.
- `bind_node_attributes()` appends all nodal attributes from one network to another, and `join_nodes()` merges all nodal attributes from one network to another.
- `filter_nodes()` subsets nodes based on some nodal attribute-related logical statement.

Note that while `add_*`/`delete_*` functions operate similarly as comparable `{igraph}` functions, `mutate*`, `bind*`, etc work like `{tidyverse}` or `{dplyr}`-style functions.

Usage

```

add_nodes(.data, nodes, attribute = NULL)

delete_nodes(.data, nodes)

add_node_attribute(.data, attr_name, vector)

mutate(.data, ...)

mutate_nodes(.data, ...)

select(.data, ...)

select_nodes(.data, ...)

bind_node_attributes(.data, object2)

join_nodes(
  .data,
  object2,
  .by = NULL,
  join_type = c("full", "left", "right", "inner")
)

rename_nodes(.data, ...)

rename(.data, ...)

filter_nodes(.data, ..., .by = NULL)

```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>nodes</code>	The number of nodes to be added.
<code>attribute</code>	A named list to be added as tie or node attributes.
<code>attr_name</code>	Name of the new attribute in the resulting object.
<code>vector</code>	A vector of values for the new attribute.
<code>...</code>	Additional arguments.
<code>object2</code>	A second object to copy nodes or ties from.
<code>.by</code>	An attribute name to join objects by. By default, NULL.
<code>join_type</code>	A type of join to be used. Options are "full", "left", "right", "inner".

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	igraph	network	tbl_graph
add_nodes	1	1	1
delete_nodes	1	1	1

Value

A data object of the same class as the function was given.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```
other <- create_filled(4) %>% mutate(name = c("A", "B", "C", "D"))
add_nodes(other, 4, list(name = c("Matthew", "Mark", "Luke", "Tim")))
other <- create_filled(4) %>% mutate(name = c("A", "B", "C", "D"))
another <- create_filled(3) %>% mutate(name = c("E", "F", "G"))
join_nodes(another, other)
```

manip_paths

Modifying networks paths

Description

These functions return tidygraphs containing only special sets of ties:

- `to_matching()` returns only the matching ties in some network data.
- `to_mentoring()` returns only ties to nodes' closest mentors.
- `to_eulerian()` returns only the Eulerian path within some network data.
- `to_tree()` returns the spanning tree in some network data or, if the data is unconnected, a forest of spanning trees.
- `to_dominating()` returns the dominating tree of the network

Usage

```
to_matching(.data, mark = "type", capacities = NULL)

to_mentoring(.data, elites = 0.1)

to_eulerian(.data)

to_tree(.data)

to_dominating(.data, from, direction = c("out", "in"))
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>mark</code>	A logical vector marking two types or modes. By default "type".
<code>capacities</code>	An integer or vector of integers the same length as the nodes in the network that describes the maximum possible degree the node can have in the matched network.
<code>elites</code>	The proportion of nodes to be selected as mentors. By default this is set at 0.1. This means that the top 10% of nodes in terms of degree, or those equal to the highest rank degree in the network, whichever is the higher, will be used to select the mentors. Note that if nodes are equidistant from two mentors, they will choose one at random. If a node is without a path to a mentor, for example because they are an isolate, a tie to themselves (a loop) will be created instead. Note that this is a different default behaviour than that described in Valente and Davis (1999).
<code>from</code>	The index or name of the node from which the path should be traced.
<code>direction</code>	String, either "out" or "in".

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	data.frame	igraph	matrix	network	tbl_graph
to_eulerian	0	1	0	0	1
to_matching	1	1	1	1	1
to_mentoring	0	1	0	0	1

Value

All `to_` functions return an object of the same class as that provided. So passing it an `igraph` object will return an `igraph` object and passing it a `network` object will return a `network` object, with certain modifications as outlined for each function.

`to_matching()`

This function attempts to solve the stable matching problem, also known as the stable marriage problem, upon a given two-mode network (or other network with a binary mark).

In the basic version, `to_matching()` uses `igraph::max_bipartite_match()` to return a network in which each node is only tied to one of its previous ties. The number of these ties left is its *cardinality*, and the algorithm seeks to maximise this such that, where possible, each node will be associated with just one node in the other mode or some other mark. The algorithm used is the push-relabel algorithm with greedy initialization and a global relabelling after every $\frac{n}{2}$ steps, where n is the number of nodes in the network.

In the more general version, each node may have a larger capacity, or even different capacities. Here an implementation of the Gale-Shapley algorithm is used, in which an iterative process of proposal and acceptance is repeated until all are matched or have exhausted their lists of preferences. This is, however, computationally slower.

References**On matching:**

Gale, David, and Lloyd Stowell Shapley. 1962. "College admissions and the stability of marriage". *The American Mathematical Monthly*, 69(1): 9–14. doi:10.2307/2312726

Goldberg, Andrew V., and Robert E. Tarjan. 1986. "A new approach to the maximum flow problem". *Proceedings of the 18th Annual ACM Symposium on Theory of Computing*. 136-146. doi:10.1145/12130.12144

On mentoring:

Valente, Thomas, and Rebecca Davis. 1999. "Accelerating the Diffusion of Innovations Using Opinion Leaders", *Annals of the American Academy of Political and Social Science* 566: 56-67. doi:10.1177/000271629956600105

On Eulerian trails:

Euler, Leonard. 1736. "Solutio problematis ad geometriam situs pertinentis". *Comment. Academiae Sci. I. Petropolitanae* 8: 128–140.

Hierholzer, Carl. 1873. "Ueber die Möglichkeit, einen Linienzug ohne Wiederholung und ohne Unterbrechung zu umfahren". *Mathematische Annalen*, 6(1): 30–32. doi:10.1007/BF01442866

On minimum spanning trees:

Boruvka, Otakar. 1926. "O jistem problemu minimalnim". *Prace Mor. Prirodoved. Spol. V Brne III* 3: 37-58.

Kruskal, Joseph B. 1956. "On the shortest spanning subtree of a graph and the travelling salesman problem". *Proceedings of the American Mathematical Society* 7(1): 48-50. doi:10.1090/S0002-9939195600786867

Prim, R.C. 1957. "Shortest connection networks and some generalizations". *Bell System Technical Journal* 36(6):1389-1401. doi:10.1002/j.15387305.1957.tb01515.x

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```
to_matching(ison_southern_women)
to_eulerian(delete_nodes(ison_koenigsberg, "Lomse"))
```

manip_permutation	<i>Network permutation</i>
-------------------	----------------------------

Description

to_permuted() permutes the network using a Fisher-Yates shuffle on both the rows and columns (for a one-mode network) or on each of the rows and columns (for a two-mode network).

Usage

```
to_permuted(.data, with_attr = TRUE)
```

Arguments

.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
with_attr	Logical whether any attributes of the object should be retained. By default TRUE.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Description

These functions add some format to manynet-consistent data.

- `to_redirected()` reformats the direction of directed network data, flipping any existing direction.
- `to_reciprocated()` reformats directed network data such that every directed tie is reciprocated.
- `to_acyclic()` reformats network data to an acyclic graph.
- `to_named()` reformats unlabelled network data to labelled network data from a vector of names or random baby names.
- `to_signed()` reformats unsigned network data to signed network data with signs from a mark vector or at random.

If the format condition is not met, for example `to_undirected()` is used on a network that is already undirected, the network data is returned unaltered. No warning is given so that these functions can be used to ensure conformance.

Unlike the `as_*`() group of functions, these functions always return the same class as they are given, only transforming these objects' properties.

Usage

```
to_named(.data, names = NULL)
```

```
to_signed(.data, mark = NULL)
```

```
to_weighted(.data, measure = NULL)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>names</code>	Character vector of the node names. NULL by default.
<code>mark</code>	A mark (logical vector) the length of the ties in the network.
<code>measure</code>	A numeric vector (measure) that will be added as the tie weights to the network. If this is NULL, then the tie weights will be drawn from a Poisson distribution with $\lambda = 4$.

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	data.frame	igraph	matrix	network	tbl_graph
to_acyclic	1	1	1	1	1
to_directed	1	1	1	1	1
to_named	1	1	1	1	1
to_reciprocated	1	1	1	1	1
to_redirected	1	1	1	1	1
to_simplex	0	1	1	0	1

Value

All `to_` functions return an object of the same class as that provided. So passing it an `igraph` object will return an `igraph` object and passing it a `network` object will return a `network` object, with certain modifications as outlined for each function.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

manip_project	<i>Modifying networks projection</i>
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Description

These functions offer tools for projecting many-net-consistent data:

- `to_mode1()` projects a two-mode network to a one-mode network of the first node set's (e.g. rows) joint affiliations to nodes in the second node set (columns).
- `to_mode2()` projects a two-mode network to a one-mode network of the second node set's (e.g. columns) joint affiliations to nodes in the first node set (rows).
- `to_ties()` projects a network to one where the ties become nodes and incident nodes become their ties.

Usage

```
to_mode1(.data, similarity = c("count", "jaccard", "rand", "pearson", "yule"))
```

```
to_mode2(.data, similarity = c("count", "jaccard", "rand", "pearson", "yule"))
```

```
to_ties(.data)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>similarity</code>	Method for establishing ties, currently "count" (default), "jaccard", or "rand". <ul style="list-style-type: none"> • "count" calculates the number of coinciding ties, and can be interpreted as indicating the degree of opportunities between nodes. • "jaccard" uses this count as the numerator in a proportion, where the denominator consists of any cell where either node has a tie. It can be interpreted as opportunity weighted by participation. • "rand", or the Simple Matching Coefficient, is a proportion where the numerator consists of the count of cells where both nodes are present or both are absent, over all possible cells. It can be interpreted as the (weighted) degree of behavioral mirroring between two nodes. • "pearson" (Pearson's coefficient) and "yule" (Yule's Q) produce correlations for valued and binary data, respectively. Note that Yule's Q has a straightforward interpretation related to the odds ratio.

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	data.frame	igraph	matrix	network	tbl_graph
<code>to_mode1</code>	1	1	1	1	1
<code>to_mode2</code>	1	1	1	1	1
<code>to_ties</code>	1	1	1	1	1

Value

All `to_` functions return an object of the same class as that provided. So passing it an igraph object will return an igraph object and passing it a network object will return a network object, with certain modifications as outlined for each function.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_reformat](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```
to_mode1(ison_southern_women)
to_mode2(ison_southern_women)
to_ties(ison_adolescents)
```

manip_reformat	<i>Modifying network formats</i>
----------------	----------------------------------

Description

These functions reformat manynet-consistent data.

- `to_anti()` reformats network data into its complement, where only ties *not* present in the original network are included in the new network.

Unlike the `as_*`() group of functions, these functions always return the same class as they are given, only transforming these objects' properties.

Usage

```
to_anti(.data)
```

Arguments

- `.data` An object of a manynet-consistent class:
- matrix (adjacency or incidence) from {base} R
 - edgelist, a data frame from {base} R or tibble from {tibble}
 - igraph, from the {igraph} package
 - network, from the {network} package
 - tbl_graph, from the {tidygraph} package

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	data.frame	igraph	matrix	network	tbl_graph
to_acyclic	1	1	1	1	1
to_anti	1	1	1	1	1
to_reciprocated	1	1	1	1	1
to_redirected	1	1	1	1	1

Value

All `to_*` functions return an object of the same class as that provided. So passing it an igraph object will return an igraph object and passing it a network object will return a network object, with certain modifications as outlined for each function.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_scope](#), [manip_split](#), [manip_ties](#)

Examples

```
to_anti(ison_southern_women)
```

manip_scope

Modifying networks scope

Description

These functions offer tools for transforming manynet-consistent objects (matrices, igraph, tidygraph, or network objects). Transforming means that the returned object may have different dimensions than the original object.

- `to_ego()` scopes a network into the local neighbourhood of a given node.
- `to_giant()` scopes a network into one including only the main component and no smaller components or isolates.
- `to_no_isolates()` scopes a network into one excluding all nodes without ties.
- `to_no_missing()` scopes a network to one retaining only complete cases, i.e. nodes with no missing values.
- `to_subgraph()` scopes a network into a subgraph by filtering on some node-related logical statement.
- `to_blocks()` reduces a network to ties between a given partition membership vector.

Usage

```
to_no_missing(.data)
```

```
to_ego(.data, node, max_dist = 1, min_dist = 0, direction = c("out", "in"))
```

```
to_time(.data, time)
```

```
to_giant(.data)
```

```
to_no_isolates(.data)
```

```
to_subgraph(.data, ...)
```

```
to_blocks(.data, membership, FUN = mean)
```

Arguments

.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
node	Name or index of node.
max_dist	The maximum breadth of the neighbourhood. By default 1.
min_dist	The minimum breadth of the neighbourhood. By default 0. Increasing this to 1 excludes the ego, and 2 excludes ego's direct alters.
direction	String, either "out" or "in".
time	A time point or wave at which to present the network.
...	Arguments passed on to dplyr::filter
membership	A vector of partition memberships.
FUN	A function for summarising block content. By default mean. Other recommended options include median, sum, min or max.

Details

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	data.frame	igraph	list	matrix	network	tbl_graph
to_blocks	1	1	0	1	1	1
to_ego	0	1	0	0	0	1
to_giant	1	1	0	1	1	1
to_no_isolates	1	1	1	1	1	1
to_subgraph	1	1	0	1	1	1

Value

All to_ functions return an object of the same class as that provided. So passing it an igraph object will return an igraph object and passing it a network object will return a network object, with certain modifications as outlined for each function.

to_blocks()

Reduced graphs provide summary representations of network structures by collapsing groups of connected nodes into single nodes while preserving the topology of the original structures.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_split](#), [manip_ties](#)

Examples

```
ison_adolescents %>%
  mutate_ties(wave = sample(1995:1998, 10, replace = TRUE)) %>%
  to_waves(attribute = "wave") %>%
  to_no_isolates()
```

manip_split

*Splitting networks into lists***Description**

These functions offer tools for splitting manynet-consistent objects (matrices, igraph, tidygraph, or network objects) into lists of networks.

Not all functions have methods available for all object classes. Below are the currently implemented S3 methods:

	data.frame	diff_model	igraph	matrix	network	tbl_graph
to_components	1	0	1	1	1	1
to_egos	1	0	1	1	1	1
to_slices	0	0	1	0	0	1
to_subgraphs	0	0	1	0	1	1
to_waves	1	1	1	0	0	1

Usage

```
to_egos(.data, max_dist = 1, min_dist = 0, direction = c("out", "in"))
```

```
to_subgraphs(.data, attribute)
```

```
to_components(.data)
```

```
to_waves(.data, attribute = "wave", panels = NULL, cumulative = FALSE)
```

```
to_slices(.data, attribute = "time", slice = NULL)
```

Arguments

- `.data` An object of a manynet-consistent class:
- matrix (adjacency or incidence) from {base} R
 - edgelist, a data frame from {base} R or tibble from {tibble}
 - igraph, from the {igraph} package
 - network, from the {network} package
 - tbl_graph, from the {tidygraph} package
- `max_dist` The maximum breadth of the neighbourhood. By default 1.

min_dist	The minimum breadth of the neighbourhood. By default 0. Increasing this to 1 excludes the ego, and 2 excludes ego's direct alters.
direction	String, either "out" or "in".
attribute	One or two attributes used to slice data.
panels	Would you like to select certain waves? NULL by default. That is, a list of networks for every available wave is returned. Users can also list specific waves they want to select.
cumulative	Whether to make wave ties cumulative. FALSE by default. That is, each wave is treated isolated.
slice	Character string or character list indicating the date(s) or integer(s) range used to slice data (e.g slice = c(1:2, 3:4)).

Value

The returned object will be a list of network objects.

Functions

- `to_egos()`: Returns a list of ego (or focal) networks.
- `to_subgraphs()`: Returns a list of subgraphs on some given node attribute.
- `to_components()`: Returns a list of the components in a network.
- `to_waves()`: Returns a network with some discrete observations over time into a list of those observations.
- `to_slices()`: Returns a list of a network with some continuous time variable at some time slice(s).

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_ties](#)

Examples

```

to_egos(ison_adolescents)
# graphs(to_egos(ison_adolescents,2))
ison_adolescents %>%
  mutate(unicorn = sample(c("yes", "no"), 8,
    replace = TRUE)) %>%
  to_subgraphs(attribute = "unicorn")
to_components(to_uniplex(fict_marvel, "relationship"))
ison_adolescents %>%
  mutate_ties(wave = sample(1995:1998, 10, replace = TRUE)) %>%
  to_waves(attribute = "wave")
ison_adolescents %>%
  mutate_ties(time = 1:10, increment = 1) %>%
  add_ties(c(1,2), list(time = 3, increment = -1)) %>%
  to_slices(slice = 7)

```

Description

These functions allow users to add and delete ties and their attributes:

- `add_ties()` adds additional ties to network data
- `delete_ties()` deletes ties from network data
- `add_tie_attribute()` and `mutate_ties()` offer ways to add a vector of values to a network as a tie attribute.
- `rename_ties()` renames tie attributes.
- `bind_ties()` appends the tie data from two networks and `join_ties()` merges ties from two networks, adding a tie attribute identifying the newly added ties.
- `filter_ties()` subsets ties based on some tie attribute-related logical statement.

Note that while `add_*`/`delete_*` functions operate similarly as comparable `{igraph}` functions, `mutate*`(), `bind*`(), etc work like `{tidyverse}` or `{dplyr}`-style functions.

Usage

```
add_ties(.data, ties, attribute = NULL)

delete_ties(.data, ties)

add_tie_attribute(.data, attr_name, vector)

mutate_ties(.data, ...)

rename_ties(.data, ...)

arrange_ties(.data, ...)

bind_ties(.data, ...)

join_ties(.data, object2, attr_name)

filter_ties(.data, ...)

select_ties(.data, ...)

summarise_ties(.data, ...)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>ties</code>	The number of ties to be added or an even list of ties.
<code>attribute</code>	A named list to be added as tie or node attributes.
<code>attr_name</code>	Name of the new attribute in the resulting object.
<code>vector</code>	A vector of values for the new attribute.
<code>...</code>	Additional arguments.
<code>object2</code>	A second object to copy nodes or ties from.

Value

A tidygraph (`tbl_graph`) data object.

See Also

Other modifications: [manip_as](#), [manip_correlation](#), [manip_deformat](#), [manip_direction](#), [manip_from](#), [manip_levels](#), [manip_miss](#), [manip_nodes](#), [manip_paths](#), [manip_permutation](#), [manip_preformat](#), [manip_project](#), [manip_reformat](#), [manip_scope](#), [manip_split](#)

Examples

```
other <- create_filled(4) %>% mutate(name = c("A", "B", "C", "D"))
mutate_ties(other, form = 1:6) %>% filter_ties(form < 4)
add_tie_attribute(other, "weight", c(1, 2, 2, 2, 1, 2))
ison_adolescents %>% add_ties(c("Betty", "Tina"))
delete_ties(ison_adolescents, 3)
delete_ties(ison_adolescents, "Alice|Sue")
```

 mark_core

Core-periphery clustering algorithms

Description

These functions identify nodes belonging to (some level of) the core of a network:

- `node_is_universal()` identifies whether nodes are adjacent to all other nodes in the network.
- `node_is_core()` identifies whether nodes belong to the core of the network, as opposed to the periphery.
- `node_in_core()` categorizes nodes into two or more core/periphery categories based on their coreness.

- `node_coreness()` returns a continuous measure of how closely each node resembles a typical core node.
- `node_kcoreness()` assigns nodes to their level of k-core.

Usage

```
node_is_universal(.data)
```

```
node_is_core(.data, method = c("degree", "eigenvector"))
```

```
node_kcoreness(.data)
```

```
node_coreness(.data)
```

```
node_in_core(.data, groups = 3, cluster_by = c("bins", "quantiles", "kmeans"))
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>method</code>	Which method to use to identify cores and periphery. By default this is "degree", which relies on the heuristic that high degree nodes are more likely to be in the core. An alternative is "eigenvector", which instead begins with high eigenvector nodes. Other methods, such as a genetic algorithm, CONCOR, and Rombach-Porter, can be added if there is interest.
<code>groups</code>	Number of categories to create. Must be at least 2 and at most the number of nodes in the network. Default is 3.
<code>cluster_by</code>	Method to use to create the categories. One of "bins" (equal-width bins), "quantiles" (quantile-based bins), or "kmeans" (k-means clustering). Default is "bins".

Universal/dominating node

A universal node is adjacent to all other nodes in the network. It is also sometimes called the dominating vertex because it represents a one-element dominating set. A network with a universal node is called a cone, and its universal node is called the apex of the cone. A classic example of a cone is a star graph, but friendship, wheel, and threshold graphs are also cones.

Core-periphery

This function is used to identify which nodes should belong to the core, and which to the periphery. It seeks to minimize the following quantity:

$$Z(S_1) = \sum_{(i < j) \in S_1} \mathbf{I}_{\{A_{ij}=0\}} + \sum_{(i < j) \notin S_1} \mathbf{I}_{\{A_{ij}=1\}}$$

where nodes $\{i, j, \dots, n\}$ are ordered in descending degree, A is the adjacency matrix, and the indicator function is 1 if the predicate is true or 0 otherwise. Note that minimising this quantity maximises density in the core block and minimises density in the periphery block; it ignores ties between these blocks.

k-coreness

k-coreness captures the maximal subgraphs in which each vertex has at least degree k , where k is also the order of the subgraph. As described in `igraph::coreness`, a node's coreness is k if it belongs to the k -core but not to the $(k+1)$ -core.

Core-periphery categories

This function categorizes nodes based on their coreness into a specified number of groups. The groups are labeled as "Core", "Semi-core", "Semi-periphery", and "Periphery" depending on the number of groups specified. The categorization can be done using different methods: equal-width bins, quantile-based bins, or k-means clustering.

References

On core-periphery partitioning:

Borgatti, Stephen P., & Everett, Martin G. 1999. "Models of core /periphery structures". *Social Networks*, 21, 375–395. doi:10.1016/S03788733(99)000192

Lip, Sean Z. W. 2011. "A Fast Algorithm for the Discrete Core/Periphery Bipartitioning Problem." doi:10.48550/arXiv.1102.5511

On k-coreness:

Seidman, Stephen B. 1983. "Network structure and minimum degree". *Social Networks*, 5(3), 269-287. doi:10.1016/03788733(83)90028X

Batagelj, Vladimir, and Matjaz Zaversnik. 2003. "An O(m) algorithm for cores decomposition of networks". *arXiv preprint cs/0310049*. doi:10.48550/arXiv.cs/0310049

On core-periphery categorization:

Wallerstein, Immanuel. 1974. "Dependence in an Interdependent World: The Limited Possibilities of Transformation Within the Capitalist World Economy." *African Studies Review*, 17(1), 1-26. doi:10.2307/523574

See Also

Other memberships: [member_brokerage](#), [member_cliques](#), [member_community_hier](#), [member_community_non](#), [member_components](#), [member_equivalence](#)

Examples

```
node_is_universal(create_star(11))
node_is_core(ison_adolescents)
#ison_adolescents %>%
# mutate(corep = node_is_core()) %>%
# graphr(node_color = "corep")
node_kcoreness(ison_adolescents)
```

```
node_coreness(ison_adolescents)
node_in_core(ison_adolescents)
```

mark_diff

Marking nodes based on diffusion properties

Description

These functions return logical vectors the length of the nodes in a network identifying which hold certain properties or positions in the network.

- `node_is_infected()` marks nodes that are infected by a particular time point.
- `node_is_exposed()` marks nodes that are exposed to a given (other) mark.
- `node_is_latent()` marks nodes that are latent at a particular time point.
- `node_is_recovered()` marks nodes that are recovered at a particular time point.

Usage

```
node_is_latent(.data, time = 0)

node_is_infected(.data, time = 0)

node_is_recovered(.data, time = 0)

node_is_exposed(.data, mark, time = 0)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>time</code>	A time step at which nodes are identified.
<code>mark</code>	vector denoting which nodes are infected

Exposed

`node_is_exposed()` is similar to `node_exposure()`, but returns a mark (TRUE/FALSE) vector indicating which nodes are currently exposed to the diffusion content. This diffusion content can be expressed in the 'mark' argument. If no 'mark' argument is provided, and '.data' is a `diff_model` object, then the function will return nodes exposure to the seed nodes in that diffusion.

See Also

Other marks: [mark_nodes](#), [mark_select](#), [mark_tie_select](#), [mark_ties](#), [mark_triangles](#)

Examples

```
# To mark nodes that are latent by a particular time point
node_is_latent(play_diffusion(create_tree(6), latency = 1), time = 1)
# To mark nodes that are infected by a particular time point
node_is_infected(play_diffusion(create_tree(6)), time = 1)
# To mark nodes that are recovered by a particular time point
node_is_recovered(play_diffusion(create_tree(6), recovery = 0.5), time = 3)
# To mark which nodes are currently exposed
(expos <- node_is_exposed(manynet::create_tree(14), mark = c(1,3)))
which(expos)
```

mark_features

Marking networks features

Description

These functions implement logical tests for various network features.

- `is_connected()` tests whether network is strongly connected, or weakly connected if undirected.
- `is_perfect_matching()` tests whether there is a matching for a network that covers every node in the network.
- `is_eulerian()` tests whether there is a Eulerian path for a network where that path passes through every tie exactly once.
- `is_acyclic()` tests whether network is a directed acyclic graph.
- `is_aperiodic()` tests whether network is aperiodic.

Usage

```
is_connected(.data)
```

```
is_perfect_matching(.data, mark = "type")
```

```
is_eulerian(.data)
```

```
is_acyclic(.data)
```

```
is_aperiodic(.data, max_path_length = 4)
```

Arguments

.data	An object of a {manynet}-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
mark	A logical vector marking two types or modes. By default "type".
max_path_length	Maximum path length considered. If negative, paths of all lengths are considered. By default 4, to avoid potentially very long computation times.

Value

TRUE if the condition is met, or FALSE otherwise.

is_connected

To test weak connection on a directed network, please see `to_undirected()`.

is_perfect_matching

For two-mode or bipartite networks, `to_matching()` is used to identify whether a perfect matching is possible. For one-mode networks, we use the Tutte theorem. Note that currently only subgraphs with cutpoints removed are tested, and not all possible subgraphs. This is to avoid computationally expensive combinatorial operations, but may come at the cost of some edge cases where a one-mode network cannot perfectly match as suggested.

Source

<https://stackoverflow.com/questions/55091438/r-igraph-find-all-cycles>

References**On perfect matching:**

Tutte, William T. 1950. "The factorization of locally finite graphs". *Canadian Journal of Mathematics*. 2: 44–49. doi:10.4153/cjm19500052

On aperiodicity:

Jarvis, J.P, and D.R. Shier. 1996. "Graph-theoretic analysis of finite Markov chains", in Shier, D.R., Wallenius, K.T. (eds) *Applied Mathematical Modeling: A Multidisciplinary Approach*. CRC Press.

See Also

Other marking: [mark_format](#), [mark_is](#)

Examples

```
is_connected(ison_southern_women)
is_perfect_matching(ison_southern_women)
is_eulerian(ison_brandes)
is_acyclic(ison_algebra)
is_aperiodic(ison_algebra)
```

mark_format

Marking networks formats

Description

These functions implement logical tests for various network properties. All `is_*`() functions return a logical scalar (TRUE or FALSE).

- `is_twomode()` marks networks TRUE if they contain two sets of nodes.
- `is_weighted()` marks networks TRUE if they contain tie weights.
- `is_directed()` marks networks TRUE if the ties specify which node is the sender and which the receiver.
- `is_labelled()` marks networks TRUE if there is a 'names' attribute for the nodes.
- `is_attributed()` marks networks TRUE if there are other nodal attributes than 'names' or 'type'.
- `is_signed()` marks networks TRUE if the ties can be either positive or negative.
- `is_complex()` marks networks TRUE if any ties are loops, with the sender and receiver being the same node.
- `is_multiplex()` marks networks TRUE if it contains multiple types of ties, such that there can be multiple ties between the same sender and receiver.
- `is_uniplex()` marks networks TRUE if it is neither complex nor multiplex.

Usage

```
is_twomode(.data)
is_weighted(.data)
is_directed(.data)
is_labelled(.data)
is_signed(.data)
is_complex(.data)
is_multiplex(.data)
```

```
is_uniplex(.data)
```

```
is_attributed(.data)
```

Arguments

`.data` An object of a manynet-consistent class:

- matrix (adjacency or incidence) from `{base}` R
- edgelist, a data frame from `{base}` R or tibble from `{tibble}`
- igraph, from the `{igraph}` package
- network, from the `{network}` package
- tbl_graph, from the `{tidygraph}` package

See Also

Other marking: [mark_features](#), [mark_is](#)

Examples

```
is_twomode(create_filled(c(2,2)))
is_weighted(create_tree(3))
is_directed(create_tree(2))
is_directed(create_tree(2, directed = TRUE))
is_labelled(create_empty(3))
is_signed(create_lattice(3))
is_complex(create_lattice(4))
is_multiplex(create_filled(c(3,3)))
is_uniplex(create_star(3))
is_attributed(ison_algebra)
```

mark_is

Marking networks classes

Description

These functions implement logical tests for networks' classes.

- `is_manynet()` marks a network TRUE if it is compatible with `{manynet}` functions.
- `is_edgelist()` marks a network TRUE if it is an edgelist.
- `is_graph()` marks a network TRUE if it contains graph-level information.
- `is_list()` marks a network TRUE if it is a (non-igraph) list of networks, for example a set of ego networks or a dynamic or longitudinal set of networks.
- `is_longitudinal()` marks a network TRUE if it contains longitudinal, panel data.
- `is_dynamic()` marks a network TRUE if it contains dynamic, time-stamped data.
- `is_changing()` marks a network TRUE if it contains changes to nodal attributes.

All `is_*`() functions return a logical scalar (TRUE or FALSE).

Usage

```
is_manynet(.data)
is_graph(.data)
is_edgelist(.data)
is_list(.data)
is_longitudinal(.data)
is_dynamic(.data)
is_changing(.data)
```

Arguments

`.data` An object of a manynet-consistent class:

- matrix (adjacency or incidence) from {base} R
- edgelist, a data frame from {base} R or tibble from {tibble}
- igraph, from the {igraph} package
- network, from the {network} package
- tbl_graph, from the {tidygraph} package

Value

TRUE if the condition is met, or FALSE otherwise.

See Also

Other marking: [mark_features](#), [mark_format](#)

Examples

```
is_manynet(create_filled(2))
is_graph(create_star(2))
is_edgelist(matrix(c(2,2), 1, 2))
is_edgelist(as_edgelist(matrix(c(2,2), 1, 2)))
is_longitudinal(create_tree(5, 3))
is_dynamic(create_tree(3))
is_changing(fict_starwars)
```

`mark_nodes`*Marking nodes based on structural properties*

Description

These functions return logical vectors the length of the nodes in a network identifying which hold certain properties or positions in the network.

- `node_is_isolate()` marks nodes that are isolates, with neither incoming nor outgoing ties.
- `node_is_independent()` marks nodes that are members of the largest independent set, aka largest internally stable set.
- `node_is_cutpoint()` marks nodes that cut or act as articulation points in a network, increasing the number of connected components when removed.
- `node_is_core()` marks nodes that are members of the network's core.
- `node_is_fold()` marks nodes that are in a structural fold between two or more triangles that are only connected by that node.
- `node_is_mentor()` marks a proportion of high indegree nodes as 'mentors' (see details).

Usage

```
node_is_isolate(.data)
node_is_pendant(.data)
node_is_independent(.data)
node_is_cutpoint(.data)
node_is_fold(.data)
node_is_mentor(.data, elites = 0.1)
node_is_neighbor(.data, node)
```

Arguments

`.data` An object of a manynet-consistent class:

- `matrix` (adjacency or incidence) from `{base}` R
- `edgelist`, a data frame from `{base}` R or tibble from `{tibble}`
- `igraph`, from the `{igraph}` package
- `network`, from the `{network}` package
- `tbl_graph`, from the `{tidygraph}` package

elites	<p>The proportion of nodes to be selected as mentors. By default this is set at 0.1. This means that the top 10% of nodes in terms of degree, or those equal to the highest rank degree in the network, whichever is the higher, will be used to select the mentors.</p> <p>Note that if nodes are equidistant from two mentors, they will choose one at random. If a node is without a path to a mentor, for example because they are an isolate, a tie to themselves (a loop) will be created instead. Note that this is a different default behaviour than that described in Valente and Davis (1999).</p>
node	Name or index of node.

References

On independent sets:

Tsukiyama, Shuji, Mikio Ide, Hiromu Ariyoshi, and Isao Shirawaka. 1977. "A new algorithm for generating all the maximal independent sets". *SIAM Journal on Computing*, 6(3):505–517. doi:10.1137/0206036

On articulation or cut-points:

Tarjan, Robert E. and Uzi Vishkin. 1985. "An Efficient Parallel Biconnectivity Algorithm", *SIAM Journal on Computing* 14(4): 862-874. doi:10.1137/0214061

On structural folds:

Vedres, Balazs, and David Stark. 2010. "Structural folds: Generative disruption in overlapping groups", *American Journal of Sociology* 115(4): 1150-1190. doi:10.1086/649497

On mentoring:

Valente, Thomas, and Rebecca Davis. 1999. "Accelerating the Diffusion of Innovations Using Opinion Leaders", *Annals of the American Academy of Political and Social Science* 566: 56-67.

See Also

Other marks: [mark_diff](#), [mark_select](#), [mark_tie_select](#), [mark_ties](#), [mark_triangles](#)

Examples

```
node_is_isolate(ison_brandes)
node_is_independent(ison_adolescents)
node_is_cutpoint(ison_brandes)
node_is_fold(create_explicit(A-B, B-C, A-C, C-D, C-E, D-E))
```

mark_select

*Marking nodes for selection based on measures***Description**

These functions return logical vectors the length of the nodes in a network identifying which hold certain properties or positions in the network.

- `node_is_random()` marks one or more nodes at random.
- `node_is_max()` and `node_is_min()` are more generally useful for converting the results from some node measure into a mark-class object. They can be particularly useful for highlighting which node or nodes are key because they minimise or, more often, maximise some measure.

Usage

```
node_is_random(.data, size = 1)
```

```
node_is_max(node_measure, ranks = 1)
```

```
node_is_min(node_measure, ranks = 1)
```

```
node_is_mean(node_measure, ranks = 1)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>size</code>	The number of nodes to select (as TRUE).
<code>node_measure</code>	An object created by a <code>node_</code> measure.
<code>ranks</code>	The number of ranks of max or min to return. For example, <code>ranks = 3</code> will return TRUE for nodes with scores equal to any of the top (or, for <code>node_is_min()</code> , bottom) three scores. By default, <code>ranks = 1</code> .

See Also

Other marks: [mark_diff](#), [mark_nodes](#), [mark_tie_select](#), [mark_ties](#), [mark_triangles](#)

Examples

```
node_is_random(ison_brandes, 2)
#node_is_max(migraph:::node_degree(ison_brandes))
#node_is_min(migraph:::node_degree(ison_brandes))
#node_is_mean(node_degree(ison_brandes))
```

`mark_ties`*Marking ties based on structural properties*

Description

These functions return logical vectors the length of the ties in a network identifying which hold certain properties or positions in the network.

- `tie_is_multiple()` marks ties that are multiples.
- `tie_is_loop()` marks ties that are loops.
- `tie_is_reciprocated()` marks ties that are mutual/reciprocated.
- `tie_is_feedback()` marks ties that are feedback arcs causing the network to not be acyclic.
- `tie_is_bridge()` marks ties that cut or act as articulation points in a network.
- `tie_is_path()` marks ties on a path from one node to another.

They are most useful in highlighting parts of the network that are particularly well- or poorly-connected.

Usage

```
tie_is_multiple(.data)
```

```
tie_is_loop(.data)
```

```
tie_is_reciprocated(.data)
```

```
tie_is_feedback(.data)
```

```
tie_is_bridge(.data)
```

```
tie_is_path(.data, from, to, all_paths = FALSE)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none">• matrix (adjacency or incidence) from {base} R• edgelist, a data frame from {base} R or tibble from {tibble}• igraph, from the {igraph} package• network, from the {network} package• tbl_graph, from the {tidygraph} package
<code>from</code>	The index or name of the node from which the path should be traced.
<code>to</code>	The index or name of the node to which the path should be traced.
<code>all_paths</code>	Whether to return a list of paths or sample just one. By default FALSE, sampling just a single path.

See Also

Other marks: [mark_diff](#), [mark_nodes](#), [mark_select](#), [mark_tie_select](#), [mark_triangles](#)

Examples

```
tie_is_multiple(fict_marvel)
tie_is_loop(fict_marvel)
tie_is_reciprocated(ison_algebra)
tie_is_feedback(ison_algebra)
tie_is_bridge(ison_brandes)
ison_adolescents %>%
  mutate_ties(route = tie_is_path(from = "Jane", to = 7))
  #graphr(edge_colour = "route")
```

 mark_tie_select

Marking ties for selection based on measures

Description

These functions return logical vectors the length of the ties in a network:

- `tie_is_random()` marks one or more ties at random.
- `tie_is_max()` and `tie_is_min()` are more useful for converting the results from some tie measure into a mark-class object. They can be particularly useful for highlighting which tie or ties are key because they minimise or, more often, maximise some measure.

Usage

```
tie_is_random(.data, size = 1)
```

```
tie_is_max(tie_measure)
```

```
tie_is_min(tie_measure)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>size</code>	The number of nodes to select (as TRUE).
<code>tie_measure</code>	An object created by a <code>tie_</code> measure.

See Also

Other marks: [mark_diff](#), [mark_nodes](#), [mark_select](#), [mark_ties](#), [mark_triangles](#)

Examples

```
# tie_is_max(migraph::tie_betweenness(ison_brandes))
#tie_is_min(migraph::tie_betweenness(ison_brandes))
```

mark_triangles

Marking ties based on structural properties

Description

These functions return logical vectors the length of the ties in a network identifying which hold certain properties or positions in the network.

- `tie_is_triangular()` marks ties that are in triangles.
- `tie_is_cyclical()` marks ties that are in cycles.
- `tie_is_transitive()` marks ties that complete transitive closure.
- `tie_is_triplet()` marks ties that are in a transitive triplet.
- `tie_is_simmelian()` marks ties that are both in a triangle and fully reciprocated.

They are most useful in highlighting parts of the network that are cohesively connected.

Usage

```
tie_is_triangular(.data)
```

```
tie_is_transitive(.data)
```

```
tie_is_triplet(.data)
```

```
tie_is_cyclical(.data)
```

```
tie_is_simmelian(.data)
```

```
tie_is_forbidden(.data)
```

```
tie_is_imbalanced(.data)
```

Arguments

`.data`

An object of a manynet-consistent class:

- matrix (adjacency or incidence) from `{base}` R
- edgelist, a data frame from `{base}` R or tibble from `{tibble}`
- `igraph`, from the `{igraph}` package
- `network`, from the `{network}` package
- `tbl_graph`, from the `{tidygraph}` package

See Also

Other marks: [mark_diff](#), [mark_nodes](#), [mark_select](#), [mark_tie_select](#), [mark_ties](#)

Examples

```
ison_monks %>% to_uniplex("like") %>%
  mutate_ties(tri = tie_is_triangular())
  #graphr(edge_color = "tri")
ison_adolescents %>% to_directed() %>%
  mutate_ties(trans = tie_is_transitive())
  #graphr(edge_color = "trans")
ison_adolescents %>% to_directed() %>%
  mutate_ties(trip = tie_is_triplet())
  #graphr(edge_color = "trip")
ison_adolescents %>% to_directed() %>%
  mutate_ties(cyc = tie_is_cyclical())
  #graphr(edge_color = "cyc")
ison_monks %>% to_uniplex("like") %>%
  mutate_ties(simmel = tie_is_simmelian())
  #graphr(edge_color = "simmel")
generate_random(8, directed = TRUE) %>%
  mutate_ties(forbid = tie_is_forbidden())
  #graphr(edge_color = "forbid")
tie_is_imbalanced(to_uniplex(fict_marvel, "relationship"))
```

measure_attributes_nodes

Describing attributes of nodes in a network

Description

These functions extract certain attributes from network data:

- `node_attribute()` returns an attribute's values for the nodes in a network.
- `node_names()` returns the names of the nodes in a network.
- `node_is_mode()` returns the mode of the nodes in a network.

These functions are also often used as helpers within other functions. `node_*` always return vectors the same length as the number of nodes in the network.

Usage

```
node_attribute(.data, attribute)
```

```
node_names(.data)
```

```
node_is_mode(.data)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>attribute</code>	Character string naming an attribute in the object.

See Also

Other measures: [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_info](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
node_attribute(fict_lotr, "Race")
node_names(ison_southern_women)
node_is_mode(ison_southern_women)
```

measure_attributes_ties

Describing attributes of ties in a network

Description

These functions extract certain attributes from network data:

- `tie_attribute()` returns an attribute's values for the ties in a network.
- `tie_weights()` returns the weights of the ties in a network.
- `tie_signs()` returns the signs of the ties in a network.
- `tie_is_twomode()` returns whether each tie in a network is a cross-mode tie.

These functions are also often used as helpers within other functions. `tie_*` always return vectors the same length as the number of ties in the network, respectively.

Usage

```
tie_attribute(.data, attribute)
```

```
tie_weights(.data)
```

```
tie_signs(.data)
```

```
tie_is_twomode(.data)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>attribute</code>	Character string naming an attribute in the object.

See Also

Other measures: [measure_attributes_nodes](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_info](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
tie_attribute(ison_algebra, "task_tie")
tie_weights(to_model(ison_southern_women))
tie_signs(to_uniplex(fict_marvel, "relationship"))
tie_is_twomode(fict_actually)
```

measure_central_between

Measures of betweenness-like centrality and centralisation

Description

These functions calculate common betweenness-related centrality measures for one- and two-mode networks:

- `node_betweenness()` measures the betweenness centralities of nodes in a network.
- `node_induced()` measures the induced betweenness centralities of nodes in a network.
- `node_flow()` measures the flow betweenness centralities of nodes in a network, which uses an electrical current model for information spreading in contrast to the shortest paths model used by normal betweenness centrality.
- `node_stress()` measures the stress centrality of nodes in a network.
- `tie_betweenness()` measures the number of shortest paths going through a tie.
- `net_betweenness()` measures the betweenness centralization for a network.

All measures attempt to use as much information as they are offered, including whether the networks are directed, weighted, or multimodal. If this would produce unintended results, first transform the salient properties using e.g. [to_undirected\(\)](#) functions. All centrality and centralization measures return normalized measures by default, including for two-mode networks.

Usage

```

node_betweenness(.data, normalized = TRUE, cutoff = NULL)

node_induced(.data, normalized = TRUE, cutoff = NULL)

node_flow(.data, normalized = TRUE)

node_stress(.data, normalized = TRUE)

tie_betweenness(.data, normalized = TRUE)

net_betweenness(.data, normalized = TRUE, direction = c("all", "out", "in"))

```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>normalized</code>	Logical scalar, whether the centrality scores are normalized. Different denominators are used depending on whether the object is one-mode or two-mode, the type of centrality, and other arguments.
<code>cutoff</code>	The maximum path length to consider when calculating betweenness. If negative or NULL (the default), there's no limit to the path lengths considered.
<code>direction</code>	Character string, "out" bases the measure on outgoing ties, "in" on incoming ties, and "all" on either/the sum of the two. For two-mode networks, "all" uses as numerator the sum of differences between the maximum centrality score for the mode against all other centrality scores in the network, whereas "in" uses as numerator the sum of differences between the maximum centrality score for the mode against only the centrality scores of the other nodes in that mode.

Value

A numeric vector giving the betweenness centrality measure of each node.

Betweenness centrality

Betweenness centrality is based on the number of shortest paths between other nodes that a node lies upon:

$$C_B(i) = \sum_{j,k:j \neq k, j \neq i, k \neq i} \frac{g_{jik}}{g_{jk}}$$

Induced centrality

Induced centrality or vitality centrality concerns the change in total betweenness centrality between networks with and without a given node:

$$C_I(i) = C_B(G) - C_B(G - i)$$

Flow betweenness centrality

Flow betweenness centrality concerns the total maximum flow, f , between other nodes j, k in a network G that a given node mediates:

$$C_F(i) = \sum_{j,k:j \neq k, j \neq i, k \neq i} f(j, k, G) - f(j, k, G - i)$$

When normalized (by default) this sum of differences is divided by the sum of flows $f(i, j, G)$.

Stress centrality

Stress centrality is the number of all shortest paths or geodesics, g , between other nodes that a given node mediates:

$$C_S(i) = \sum_{j,k:j \neq k, j \neq i, k \neq i} g_{jik}$$

High stress nodes lie on a large number of shortest paths between other nodes, and thus associated with bridging or spanning boundaries.

References**On betweenness centrality:**

Freeman, Linton. 1977. "A set of measures of centrality based on betweenness". *Sociometry*, 40(1): 35–41. doi:10.2307/3033543

On induced centrality:

Everett, Martin and Steve Borgatti. 2010. "Induced, endogenous and exogenous centrality" *Social Networks*, 32: 339-344. doi:10.1016/j.socnet.2010.06.004

On flow centrality:

Freeman, Lin, Stephen Borgatti, and Douglas White. 1991. "Centrality in Valued Graphs: A Measure of Betweenness Based on Network Flow". *Social Networks*, 13(2), 141-154.

Koschutzki, D., K.A. Lehmann, L. Peeters, S. Richter, D. Tenfelde-Podehl, and O. Zlotowski. 2005. "Centrality Indices". In U. Brandes and T. Erlebach (eds.), *Network Analysis: Methodological Foundations*. Berlin: Springer.

On stress centrality:

Shimbel, A. 1953. "Structural Parameters of Communication Networks". *Bulletin of Mathematical Biophysics*, 15:501-507. doi:10.1007/BF02476438

See Also

Other centrality: [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#)

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_info](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
node_betweenness(ison_southern_women)
node_induced(ison_adolescents)
(tb <- tie_betweenness(ison_adolescents))
ison_adolescents %>% mutate_ties(weight = tb)
net_betweenness(ison_southern_women, direction = "in")
```

measure_central_close *Measures of closeness-like centrality and centralisation*

Description

These functions calculate common closeness-related centrality measures that rely on path-length for one- and two-mode networks:

- `node_closeness()` measures the closeness centrality of nodes in a network.
- `node_reach()` measures nodes' reach centrality, or how many nodes they can reach within k steps.
- `node_harmonic()` measures nodes' harmonic centrality or valued centrality, which is thought to behave better than reach centrality for disconnected networks.
- `node_information()` measures nodes' information centrality or current-flow closeness centrality.
- `node_eccentricity()` measures nodes' eccentricity or maximum distance from another node in the network.
- `node_distance()` measures nodes' geodesic distance from or to a given node.
- `tie_closeness()` measures the closeness of each tie to other ties in the network.
- `net_closeness()` measures a network's closeness centralization.
- `net_reach()` measures a network's reach centralization.
- `net_harmonic()` measures a network's harmonic centralization.

All measures attempt to use as much information as they are offered, including whether the networks are directed, weighted, or multimodal. If this would produce unintended results, first transform the salient properties using e.g. [to_undirected\(\)](#) functions. All centrality and centralization measures return normalized measures by default, including for two-mode networks.

Usage

```

node_closeness(.data, normalized = TRUE, direction = "out", cutoff = NULL)

node_harmonic(.data, normalized = TRUE, cutoff = -1)

node_reach(.data, normalized = TRUE, cutoff = 2)

node_information(.data, normalized = TRUE)

node_eccentricity(.data, normalized = TRUE)

node_distance(.data, from, to, normalized = TRUE)

node_vitality(.data, normalized = TRUE)

node_randomwalk(.data, normalized = TRUE)

tie_closeness(.data, normalized = TRUE)

net_closeness(.data, normalized = TRUE, direction = c("all", "out", "in"))

net_reach(.data, normalized = TRUE, cutoff = 2)

net_harmonic(.data, normalized = TRUE, cutoff = 2)

```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>normalized</code>	Logical scalar, whether the centrality scores are normalized. Different denominators are used depending on whether the object is one-mode or two-mode, the type of centrality, and other arguments.
<code>direction</code>	Character string, "out" bases the measure on outgoing ties, "in" on incoming ties, and "all" on either/the sum of the two. For two-mode networks, "all" uses as numerator the sum of differences between the maximum centrality score for the mode against all other centrality scores in the network, whereas "in" uses as numerator the sum of differences between the maximum centrality score for the mode against only the centrality scores of the other nodes in that mode.
<code>cutoff</code>	Maximum path length to use during calculations.
<code>from, to</code>	Index or name of a node to calculate distances from or to.

Closeness centrality

Closeness centrality, status centrality, or barycenter centrality is defined as the reciprocal of the farness or distance, d , from a node to all other nodes in the network:

$$C_C(i) = \frac{1}{\sum_j d(i, j)}$$

When (more commonly) normalised, the numerator is instead $N - 1$.

Harmonic centrality

Harmonic centrality or valued centrality reverses the sum and reciprocal operations compared to closeness centrality:

$$C_H(i) = \sum_{i, i \neq j} \frac{1}{d(i, j)}$$

where $\frac{1}{d(i, j)} = 0$ where there is no path between i and j . Normalization is by $N - 1$. Since the harmonic mean performs better than the arithmetic mean on unconnected networks, i.e. networks with infinite distances, harmonic centrality is to be preferred in these cases.

Reach centrality

In some cases, longer path lengths are irrelevant and 'closeness' should be defined as how many others are in a local neighbourhood. How many steps out this neighbourhood should be defined as is given by the 'cutoff' parameter. This is usually termed k or m in equations, which is why this is sometimes called (m - or) k -step reach centrality:

$$C_R(i) = \sum_j d(i, j) \leq k$$

The maximum reach score is $N - 1$, achieved when the node can reach all other nodes in the network in k steps or less, but the normalised version, $\frac{C_R}{N-1}$, is more common. Note that if $k = 1$ (i.e. cutoff = 1), then this returns the node's degree. At higher cutoff reach centrality returns the size of the node's component.

Information centrality

Information centrality, also known as current-flow centrality, is a hybrid measure relating to both path-length and walk-based measures. The information centrality of a node is the harmonic average of the "bandwidth" or inverse path-length for all paths originating from the node.

As described in the {sna} package, information centrality works on an undirected but potentially weighted network excluding isolates (which take scores of zero). It is defined as:

$$C_I = \frac{1}{T + \frac{\sum T - 2 \sum C_1}{|N|}}$$

where $C = B^{-1}$ with B is a pseudo-adjacency matrix replacing the diagonal of $1 - A$ with $1 + k$, and T is the trace of C and S_R an arbitrary row sum (all rows in C have the same sum).

Nodes with higher information centrality have a large number of short paths to many others in the network, and are thus considered to have greater control of the flow of information.

Eccentricity centrality

Eccentricity centrality, graph centrality, or the Koenig number, is the (if normalized, inverse of) the distance to the furthest node:

$$C_E(i) = \frac{1}{\max_{j \in N} d(i, j)}$$

where the distance from i to j is ∞ if unconnected. As such it is only well defined for connected networks.

Closeness vitality centrality

The closeness vitality of a node is the change in the sum of all distances in a network, also known as the Wiener Index, when that node is removed. Note that the closeness vitality may be negative infinity if removing that node would disconnect the network. Formally:

$$C_V(i) = \sum_{j,k} d(j, k) - \sum_{j,k} d(j, k, G \setminus i)$$

where $d(j, k, G \setminus i)$ is the distance between nodes j and k in the network with node i removed.

Random walk closeness centrality

Random walk closeness centrality is based on the average length of random walks starting at all other nodes to reach a given node. It is defined as the inverse of the average hitting time to a node. This means that higher values are given to nodes that can be reached more quickly on average by random walks starting at other nodes. Formally:

$$C_{RW}(i) = \frac{1}{\frac{1}{N-1} \sum_{j \neq i} H_{ji}}$$

where H_{ji} is the hitting time from node j to node i .

References

On closeness centrality:

Bavelas, Alex. 1950. "Communication Patterns in Task-Oriented Groups". *The Journal of the Acoustical Society of America*, 22(6): 725–730. doi:10.1121/1.1906679

Harary, Frank. 1959. "Status and Contrastatus". *Sociometry*, 22(1): 23–43. doi:10.2307/2785610

On harmonic centrality:

Marchiori, Massimo, and Vito Latora. 2000. "Harmony in the small-world". *Physica A* 285: 539-546. doi:10.1016/S03784371(00)003113

Dekker, Anthony. 2005. "Conceptual distance in social network analysis". *Journal of Social Structure* 6(3).

On reach centrality:

Borgatti, Stephen P., Martin G. Everett, and J.C. Johnson. 2013. *Analyzing social networks*. London: SAGE Publications Limited.

On information centrality:

Stephenson, Karen, and Marvin Zelen. 1989. "Rethinking centrality: Methods and examples". *Social Networks* 11(1):1-37. doi:10.1016/03788733(89)900166

Brandes, Ulrik, and Daniel Fleischer. 2005. "Centrality Measures Based on Current Flow". *Proc. 22nd Symp. Theoretical Aspects of Computer Science LNCS 3404*: 533-544. doi:10.1007/9783-540318569_44

On eccentricity centrality:

Hage, Per, and Frank Harary. 1995. "Eccentricity and centrality in networks". *Social Networks*, 17(1): 57-63. doi:10.1016/03788733(94)002489

On closeness vitality centrality:

Koschuetzki, Dirk, Katharina Lehmann, Leon Peeters, Stefan Richter, Dagmar Tenfelde-Podehl, and Oliver Zlotowski. 2005. "Centrality Indices", in Brandes, Ulrik, and Thomas Erlebach (eds.). *Network Analysis: Methodological Foundations*. Springer: Berlin, pp. 16-61.

On random walk closeness centrality:

Noh, J.D. and R. Rieger. 2004. "Random Walks on Complex Networks". *Physical Review Letters*, 92(11): 118701. doi:10.1103/PhysRevLett.92.118701

See Also

Other centrality: [measure_central_between](#), [measure_central_degree](#), [measure_central_eigen](#)

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_info](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
node_closeness(ison_southern_women)
node_reach(ison_adolescents)
(ec <- tie_closeness(ison_adolescents))
ison_adolescents %>% mutate_ties(weight = ec)
net_closeness(ison_southern_women, direction = "in")
```

measure_central_degree

Measures of degree-like centrality and centralisation

Description

These functions calculate common degree-related centrality measures for one- and two-mode networks:

- `node_degree()` measures the degree centrality of nodes in an unweighted network, or weighted degree/strength of nodes in a weighted network; there are several related shortcut functions:

- node_deg() returns the unnormalised results.
- node_indegree() returns the direction = 'in' results.
- node_outdegree() returns the direction = 'out' results.
- node_multidegree() measures the ratio between types of ties in a multiplex network.
- node_posneg() measures the PN (positive-negative) centrality of a signed network.
- node_leverage() measures the leverage centrality of nodes in a network.
- tie_degree() measures the degree centrality of ties in a network
- net_degree() measures a network's degree centralization; there are several related shortcut functions:
 - net_indegree() returns the direction = 'out' results.
 - net_outdegree() returns the direction = 'out' results.

All measures attempt to use as much information as they are offered, including whether the networks are directed, weighted, or multimodal. If this would produce unintended results, first transform the salient properties using e.g. `to_undirected()` functions. All centrality and centralization measures return normalized measures by default, including for two-mode networks.

Usage

```
node_degree(
  .data,
  normalized = TRUE,
  alpha = 1,
  direction = c("all", "out", "in")
)

node_deg(.data, alpha = 0, direction = c("all", "out", "in"))

node_outdegree(.data, normalized = TRUE, alpha = 0)

node_indegree(.data, normalized = TRUE, alpha = 0)

node_multidegree(.data, tie1, tie2)

node_posneg(.data)

node_leverage(.data)

tie_degree(.data, normalized = TRUE)

net_degree(.data, normalized = TRUE, direction = c("all", "out", "in"))

net_outdegree(.data, normalized = TRUE)

net_indegree(.data, normalized = TRUE)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>normalized</code>	Logical scalar, whether the centrality scores are normalized. Different denominators are used depending on whether the object is one-mode or two-mode, the type of centrality, and other arguments.
<code>alpha</code>	Numeric scalar, the positive tuning parameter introduced in Opsahl et al (2010) for trading off between degree and strength centrality measures. By default, $\alpha = 0$, which ignores tie weights and the measure is solely based upon degree (the number of ties). $\alpha = 1$ ignores the number of ties and provides the sum of the tie weights as strength centrality. Values between 0 and 1 reflect different trade-offs in the relative contributions of degree and strength to the final outcome, with 0.5 as the middle ground. Values above 1 penalise for the number of ties. Of two nodes with the same sum of tie weights, the node with fewer ties will obtain the higher score. This argument is ignored except in the case of a weighted network.
<code>direction</code>	Character string, "out" bases the measure on outgoing ties, "in" on incoming ties, and "all" on either/the sum of the two. For two-mode networks, "all" uses as numerator the sum of differences between the maximum centrality score for the mode against all other centrality scores in the network, whereas "in" uses as numerator the sum of differences between the maximum centrality score for the mode against only the centrality scores of the other nodes in that mode.
<code>tie1</code>	Character string indicating the first uniplex network.
<code>tie2</code>	Character string indicating the second uniplex network.

Value

A single centralization score if the object was one-mode, and two centralization scores if the object was two-mode.

Depending on how and what kind of an object is passed to the function, the function will return a tidygraph object where the nodes have been updated

Degree centrality

The degree of a node is the number of connections it has. It is also sometimes called the valency of a node, $d(v)$. The maximum degree in a network is often denoted $\Delta(G)$ and the minimum degree in a network $\delta(G)$. The total degree of a network is the sum of all degrees, $\sum_v d(v)$. The degree sequence is the set of all nodes' degrees, ordered from largest to smallest. Directed networks discriminate between outdegree (degree of outgoing ties) and indegree (degree of incoming ties).

Leverage centrality

Leverage centrality concerns the degree of a node compared with that of its neighbours, J :

$$C_L(i) = \frac{1}{d(i)} \sum_{j \in J(i)} \frac{d(i) - d(j)}{d(i) + d(j)}$$

References

On multimodal centrality:

Faust, Katherine. 1997. "Centrality in affiliation networks." *Social Networks* 19(2): 157-191. doi:10.1016/S03788733(96)003000

Borgatti, Stephen P., and Martin G. Everett. 1997. "Network analysis of 2-mode data." *Social Networks* 19(3): 243-270. doi:10.1016/S03788733(96)003012

Borgatti, Stephen P., and Daniel S. Halgin. 2011. "Analyzing affiliation networks." In *The SAGE Handbook of Social Network Analysis*, edited by John Scott and Peter J. Carrington, 417–33. London, UK: Sage. doi:10.4135/9781446294413.n28

On strength centrality:

Opsahl, Tore, Filip Agneessens, and John Skvoretz. 2010. "Node centrality in weighted networks: Generalizing degree and shortest paths." *Social Networks* 32, 245-251. doi:10.1016/j.socnet.2010.03.006

On signed centrality:

Everett, Martin G., and Stephen P. Borgatti. 2014. "Networks Containing Negative Ties." *Social Networks* 38:111–20. doi:10.1016/j.socnet.2014.03.005

On leverage centrality:

Joyce, Karen E., Paul J. Laurienti, Jonathan H. Burdette, and Satoru Hayasaka. 2010. "A New Measure of Centrality for Brain Networks". *PLoS ONE* 5(8): e12200. doi:10.1371/journal.pone.0012200

See Also

`to_undirected()` for removing edge directions and `to_unweighted()` for removing weights from a graph.

Other centrality: `measure_central_between`, `measure_central_close`, `measure_central_eigen`

Other measures: `measure_attributes_nodes`, `measure_attributes_ties`, `measure_central_between`, `measure_central_close`, `measure_central_eigen`, `measure_closure`, `measure_cohesion`, `measure_diffusion_infer`, `measure_diffusion_net`, `measure_diffusion_node`, `measure_features`, `measure_heterogeneity`, `measure_hierarchy`, `measure_holes`, `measure_periods`, `measure_properties`, `member_diffusion`

Examples

```
node_degree(ison_southern_women)
tie_degree(ison_adolescents)
net_degree(ison_southern_women, direction = "in")
```

measure_central_eigen *Measures of eigenvector-like centrality and centralisation*

Description

These functions calculate common eigenvector-related centrality measures, or walk-based eigenmeasures, for one- and two-mode networks:

- `node_eigenvector()` measures the eigenvector centrality of nodes in a network.
- `node_power()` measures the Bonacich, beta, or power centrality of nodes in a network.
- `node_alpha()` measures the alpha or Katz centrality of nodes in a network.
- `node_pagerank()` measures the pagerank centrality of nodes in a network.
- `node_hub()` measures how well nodes in a network serve as hubs pointing to many authorities.
- `node_authority()` measures how well nodes in a network serve as authorities from many hubs.
- `tie_eigenvector()` measures the eigenvector centrality of ties in a network.
- `net_eigenvector()` measures the eigenvector centralization for a network.

All measures attempt to use as much information as they are offered, including whether the networks are directed, weighted, or multimodal. If this would produce unintended results, first transform the salient properties using e.g. `to_undirected()` functions. All centrality and centralization measures return normalized measures by default, including for two-mode networks.

Usage

```
node_eigenvector(.data, normalized = TRUE, scale = TRUE)
```

```
node_power(.data, normalized = TRUE, scale = FALSE, exponent = 1)
```

```
node_alpha(.data, alpha = 0.85)
```

```
node_pagerank(.data)
```

```
node_authority(.data)
```

```
node_hub(.data)
```

```
node_subgraph(.data)
```

```
tie_eigenvector(.data, normalized = TRUE)
```

```
net_eigenvector(.data, normalized = TRUE)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>normalized</code>	Logical scalar, whether the centrality scores are normalized. Different denominators are used depending on whether the object is one-mode or two-mode, the type of centrality, and other arguments.
<code>scale</code>	Logical scalar, whether to rescale the vector so the maximum score is 1.
<code>exponent</code>	Decay rate or attenuation factor for the Bonacich power centrality score. Can be positive or negative.
<code>alpha</code>	A constant that trades off the importance of external influence against the importance of connection. When $\alpha = 0$, only the external influence matters. As α gets larger, only the connectivity matters and we reduce to eigenvector centrality. By default $\alpha = 0.85$.

Details

We use `{igraph}` routines behind the scenes here for consistency and because they are often faster. For example, `igraph::eigencentralty()` is approximately 25% faster than `sna::evcent()`.

Value

A numeric vector giving the eigenvector centrality measure of each node.

A numeric vector giving each node's power centrality measure.

Eigenvector centrality

Eigenvector centrality operates as a measure of a node's influence in a network. The idea is that being connected to well-connected others results in a higher score. Each node's eigenvector centrality can be defined as:

$$x_i = \frac{1}{\lambda} \sum_{j \in N} a_{i,j} x_j$$

where $a_{i,j} = 1$ if i is linked to j and 0 otherwise, and λ is a constant representing the principal eigenvalue. Rather than performing this iteration, most routines solve the eigenvector equation $Ax = \lambda x$. Note that since `{igraph}` v2.1.1, the values will always be rescaled so that the maximum is 1.

Power or beta (or Bonacich) centrality

Power centrality includes an exponent that weights contributions to a node's centrality based on how far away those other nodes are.

$$c_b(i) = \sum A(i,j)(\alpha = \beta c(j))$$

Where β is positive, this means being connected to central people increases centrality. Where β is negative, this means being connected to central people decreases centrality (and being connected to more peripheral actors increases centrality). When $\beta = 0$, this is the outdegree. α is calculated to make sure the root mean square equals the network size.

Alpha centrality

Alpha or Katz (or Katz-Bonacich) centrality operates better than eigenvector centrality for directed networks because eigenvector centrality will return 0s for all nodes not in the main strongly-connected component. Each node's alpha centrality can be defined as:

$$x_i = \frac{1}{\lambda} \sum_{j \in N} a_{i,j} x_j + e_i$$

where $a_{i,j} = 1$ if i is linked to j and 0 otherwise, λ is a constant representing the principal eigenvalue, and e_i is some external influence used to ensure that even nodes beyond the main strongly connected component begin with some basic influence. Note that many equations replace $\frac{1}{\lambda}$ with α , hence the name.

For example, if $\alpha = 0.5$, then each direct connection (or alter) would be worth $(0.5)^1 = 0.5$, each secondary connection (or tertius) would be worth $(0.5)^2 = 0.25$, each tertiary connection would be worth $(0.5)^3 = 0.125$, and so on.

Rather than performing this iteration though, most routines solve the equation $x = (I - \frac{1}{\lambda} A^T)^{-1} e$.

Subgraph centrality

Subgraph centrality measures the participation of a node in all subgraphs in the network, giving higher weight to smaller subgraphs. It is defined as:

$$C_S(i) = \sum_{k=0}^{\infty} \frac{(A^k)_{ii}}{k!}$$

where $(A^k)_{ii}$ is the i th diagonal element of the k th power of the adjacency matrix A , representing the number of closed walks of length k starting and ending at node i . Weighting by $\frac{1}{k!}$ ensures that shorter walks contribute more to the centrality score than longer walks.

Subgraph centrality is a good choice of measure when the focus is on local connectivity and clustering around a node, as it captures the extent to which a node is embedded in tightly-knit groups within the network. Note though that because of the way spectral decomposition is used to calculate this measure, this is not a good measure for very large graphs.

References

On eigenvector centrality:

Bonacich, Phillip. 1991. "Simultaneous Group and Individual Centralities." *Social Networks* 13(2):155–68. doi:10.1016/03788733(91)90018O

On power centrality:

Bonacich, Phillip. 1987. "Power and Centrality: A Family of Measures." *The American Journal of Sociology*, 92(5): 1170–82. doi:10.1086/228631.

On alpha centrality:

Katz, Leo 1953. "A new status index derived from sociometric analysis". *Psychometrika*. 18(1): 39–43.

Bonacich, P. and Lloyd, P. 2001. "Eigenvector-like measures of centrality for asymmetric relations" *Social Networks*. 23(3):191-201.

On pagerank centrality:

Brin, Sergey and Page, Larry. 1998. "The anatomy of a large-scale hypertextual web search engine". *Proceedings of the 7th World-Wide Web Conference*. Brisbane, Australia.

On hub and authority centrality:

Kleinberg, Jon. 1999. "Authoritative sources in a hyperlinked environment". *Journal of the ACM* 46(5): 604–632. doi:10.1145/324133.324140

On subgraph centrality:

Estrada, Ernesto and Rodríguez-Velázquez, Juan A. 2005. "Subgraph centrality in complex networks". *Physical Review E* 71(5): 056103. doi:10.1103/PhysRevE.71.056103

See Also

Other centrality: [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#)

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_info](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
node_eigenvector(ison_southern_women)
node_power(ison_southern_women, exponent = 0.5)
tie_eigenvector(ison_adolescents)
net_eigenvector(ison_southern_women)
```

measure_closure

Measures of network closure

Description

These functions offer methods for summarising the closure in configurations in one-, two-, and three-mode networks:

- `net_reciprocity()` measures reciprocity in a (usually directed) network.
- `node_reciprocity()` measures nodes' reciprocity.
- `net_transitivity()` measures transitivity in a network.
- `node_transitivity()` measures nodes' transitivity.
- `net_equivalency()` measures equivalence or reinforcement in a (usually two-mode) network.
- `net_congruency()` measures congruency across two two-mode networks.

Usage

```

net_reciprocity(.data, method = "default")

node_reciprocity(.data)

net_transitivity(.data)

node_transitivity(.data)

net_equivalency(.data)

node_equivalency(.data)

net_congruency(.data, object2)

```

Arguments

.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
method	For reciprocity, either default or ratio. See ?igraph::reciprocity
object2	Optionally, a second (two-mode) matrix, igraph, or tidygraph

Details

For one-mode networks, shallow wrappers of igraph versions exist via `net_reciprocity` and `net_transitivity`.

For two-mode networks, `net_equivalency` calculates the proportion of three-paths in the network that are closed by fourth tie to establish a "shared four-cycle" structure.

For three-mode networks, `net_congruency` calculates the proportion of three-paths spanning two two-mode networks that are closed by a fourth tie to establish a "congruent four-cycle" structure.

Equivalency

The `net_equivalency()` function calculates the Robins and Alexander (2004) clustering coefficient for two-mode networks. Note that for weighted two-mode networks, the result is divided by the average tie weight.

References**On equivalency or four-cycles:**

Robins, Garry L, and Malcolm Alexander. 2004. Small worlds among interlocking directors: Network structure and distance in bipartite graphs. *Computational & Mathematical Organization Theory* 10(1): 69–94. doi:10.1023/B:CMOT.0000032580.12184.c0.

On congruency:

Knoke, David, Mario Diani, James Hollway, and Dimitris C Christopoulos. 2021. *Multimodal Political Networks*. Cambridge University Press. Cambridge University Press. doi:10.1017/9781108985000

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
net_reciprocity(ison_southern_women)
node_reciprocity(to_unweighted(ison_networkers))
net_transitivity(ison_adolescents)
node_transitivity(ison_adolescents)
net_equivalency(ison_southern_women)
node_equivalency(ison_southern_women)
```

measure_cohesion

Measures of network cohesion or connectedness

Description

These functions return values or vectors relating to how connected a network is and the number of nodes or edges to remove that would increase fragmentation.

- `net_density()` measures the ratio of ties to the number of possible ties.
- `net_components()` measures the number of (strong) components in the network.
- `net_cohesion()` measures the minimum number of nodes to remove from the network needed to increase the number of components.
- `net_adhesion()` measures the minimum number of ties to remove from the network needed to increase the number of components.
- `net_diameter()` measures the maximum path length in the network.
- `net_length()` measures the average path length in the network.
- `net_independence()` measures the independence number, or size of the largest independent set in the network.
- `net_strength()` measures the number of ties that would need to be removed from a network to increase its number of components.
- `net_toughness()` measures the number of nodes that would need to be removed from a network to increase its number of components.

Usage

```
net_density(.data)
net_components(.data)
net_cohesion(.data)
net_adhesion(.data)
net_diameter(.data)
net_length(.data)
net_independence(.data)
net_strength(.data)
net_toughness(.data)
```

Arguments

`.data` An object of a manynet-consistent class:

- matrix (adjacency or incidence) from {base} R
- edgelist, a data frame from {base} R or tibble from {tibble}
- igraph, from the {igraph} package
- network, from the {network} package
- tbl_graph, from the {tidygraph} package

Cohesion

To get the 'weak' components of a directed graph, please use `manynet::to_undirected()` first.

References**On cohesion:**

White, Douglas R and Frank Harary. 2001. "The Cohesiveness of Blocks In Social Networks: Node Connectivity and Conditional Density." *Sociological Methodology* 31(1): 305-59. doi:10.1111/00811750.00098

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```

net_density(ison_adolescents)
net_density(ison_southern_women)
  net_components(fict_thrones)
  net_components(to_undirected(fict_thrones))
net_cohesion(to_uniplex(fict_marvel, "relationship"))
net_cohesion(to_giant(to_uniplex(fict_marvel, "relationship")))
net_adhesion(to_uniplex(fict_marvel, "relationship"))
net_adhesion(to_giant(to_uniplex(fict_marvel, "relationship")))
net_diameter(to_uniplex(fict_marvel, "relationship"))
net_diameter(to_giant(to_uniplex(fict_marvel, "relationship")))
net_length(to_uniplex(fict_marvel, "relationship"))
net_length(to_giant(to_uniplex(fict_marvel, "relationship")))
net_independence(ison_adolescents)
net_strength(ison_adolescents)
net_toughness(ison_adolescents)

```

```
measure_diffusion_infection
```

Measures of network infection

Description

These functions allow measurement of various features of a diffusion process at the network level:

- `net_infection_complete()` measures the number of time steps until (the first instance of) complete infection. For diffusions that are not observed to complete, this function returns the value of `Inf` (infinity). This makes sure that at least ordinality is respected.
- `net_infection_total()` measures the proportion or total number of nodes that are infected/activated at some time by the end of the diffusion process. This includes nodes that subsequently recover. Where reinfection is possible, the proportion may be higher than 1.
- `net_infection_peak()` measures the number of time steps until the highest infection rate is observed.

Usage

```

net_infection_complete(.data)

net_infection_total(.data, normalized = TRUE)

net_infection_peak(.data)

```

Arguments

<code>.data</code>	Network data with nodal changes, as created by <code>play_diffusion()</code> , or a valid network diffusion model, as created by <code>as_diffusion()</code> .
<code>normalized</code>	Logical scalar, whether the centrality scores are normalized. Different denominators are used depending on whether the object is one-mode or two-mode, the type of centrality, and other arguments.

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Other diffusion: [make_play](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [member_diffusion](#)

Examples

```
smeg <- generate_smallworld(15, 0.025)
smeg_diff <- play_diffusion(smeg)
net_infection_complete(smeg_diff)
net_infection_total(smeg_diff)
net_infection_peak(smeg_diff)
```

measure_diffusion_net *Measures of network diffusion*

Description

These functions allow measurement of various features of a diffusion process at the network level:

- `net_transmissibility()` measures the average transmissibility observed in a diffusion simulation, or the number of new infections over the number of susceptible nodes.
- `net_recovery()` measures the average number of time steps nodes remain infected once they become infected.
- `net_reproduction()` measures the observed reproductive number in a diffusion simulation as the network's transmissibility over the network's average infection length.
- `net_immunity()` measures the proportion of nodes that would need to be protected through vaccination, isolation, or recovery for herd immunity to be reached.

Usage

```
net_transmissibility(.data)

net_recovery(.data, censor = TRUE)

net_reproduction(.data)

net_immunity(.data, normalized = TRUE)
```

Arguments

.data	Network data with nodal changes, as created by <code>play_diffusion()</code> , or a valid network diffusion model, as created by <code>as_diffusion()</code> .
censor	Where some nodes have not yet recovered by the end of the simulation, right censored values can be replaced by the number of steps. By default TRUE. Note that this will likely still underestimate recovery.
normalized	Logical scalar, whether the centrality scores are normalized. Different denominators are used depending on whether the object is one-mode or two-mode, the type of centrality, and other arguments.

Transmissibility

`net_transmissibility()` measures how many directly susceptible nodes each infected node will infect in each time period, on average. That is:

$$T = \frac{1}{n} \sum_{j=1}^n \frac{i_j}{s_j}$$

where i is the number of new infections in each time period, $j \in n$, and s is the number of nodes that could have been infected in that time period (note that $s \neq S$, or the number of nodes that are susceptible in the population). T can be interpreted as the proportion of susceptible nodes that are infected at each time period.

Recovery time

`net_recovery()` measures the average number of time steps that nodes in a network remain infected. Note that in a diffusion model without recovery, average infection length will be infinite. This will also be the case where there is right censoring. The longer nodes remain infected, the longer they can infect others.

Reproduction number

`net_reproduction()` measures a given diffusion's reproductive number. Here it is calculated as:

$$R = \min\left(\frac{T}{1/L}, \bar{k}\right)$$

where T is the observed transmissibility in a diffusion and L is the observed recovery length in a diffusion. Since L can be infinite where there is no recovery or there is right censoring, and since network structure places an upper limit on how many nodes each node may further infect (their degree), this function returns the minimum of R_0 and the network's average degree.

Interpretation of the reproduction number is oriented around $R = 1$. Where $R > 1$, the 'disease' will 'infect' more and more nodes in the network. Where $R < 1$, the 'disease' will not sustain itself and eventually die out. Where $R = 1$, the 'disease' will continue as endemic, if conditions allow.

Herd immunity

`net_immunity()` estimates the proportion of a network that need to be protected from infection for herd immunity to be achieved. This is known as the Herd Immunity Threshold or HIT:

$$1 - \frac{1}{R}$$

where R is the reproduction number from `net_reproduction()`. The HIT indicates the threshold at which the reduction of susceptible members of the network means that infections will no longer keep increasing. Note that there may still be more infections after this threshold has been reached, but there should be fewer and fewer. These excess infections are called the *overshoot*. This function does *not* take into account the structure of the network, instead using the average degree.

Interpretation is quite straightforward. A HIT or immunity score of 0.75 would mean that 75% of the nodes in the network would need to be vaccinated or otherwise protected to achieve herd immunity. To identify how many nodes this would be, multiply this proportion with the number of nodes in the network.

References

On epidemiological models:

Kermack, William O., and Anderson Gray McKendrick. 1927. "A contribution to the mathematical theory of epidemics". *Proc. R. Soc. London A* 115: 700-721. doi:10.1098/rspa.1927.0118

On the basic reproduction number:

Diekmann, Odo, Hans J.A.P. Heesterbeek, and Hans J.A.J. Metz. 1990. "On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations". *Journal of Mathematical Biology*, 28(4): 365–82. doi:10.1007/BF00178324

Kenah, Eben, and James M. Robins. 2007. "Second look at the spread of epidemics on networks". *Physical Review E*, 76(3 Pt 2): 036113. doi:10.1103/PhysRevE.76.036113

On herd immunity:

Garnett, G.P. 2005. "Role of herd immunity in determining the effect of vaccines against sexually transmitted disease". *The Journal of Infectious Diseases*, 191(1): S97-106. doi:10.1086/425271

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Other diffusion: [make_play](#), [measure_diffusion_infection](#), [measure_diffusion_node](#), [member_diffusion](#)

Examples

```
smeg <- generate_smallworld(15, 0.025)
smeg_diff <- play_diffusion(smeg, recovery = 0.2)
plot(smeg_diff)
# To calculate the average transmissibility for a given diffusion model
```

```

net_transmissibility(smeg_diff)
# To calculate the average infection length for a given diffusion model
net_recovery(smeg_diff)
# To calculate the reproduction number for a given diffusion model
net_reproduction(smeg_diff)
# Calculating the proportion required to achieve herd immunity
net_immunity(smeg_diff)
# To find the number of nodes to be vaccinated
net_immunity(smeg_diff, normalized = FALSE)

```

measure_diffusion_node

Measures of nodes in a diffusion

Description

These functions allow measurement of various features of a diffusion process:

- `node_adoption_time()`: Measures the number of time steps until nodes adopt/become infected
- `node_thresholds()`: Measures nodes' thresholds from the amount of exposure they had when they became infected
- `node_infection_length()`: Measures the average length nodes that become infected remain infected in a compartmental model with recovery
- `node_exposure()`: Measures how many exposures nodes have to a given mark

Usage

```
node_adoption_time(.data)
```

```
node_thresholds(.data, normalized = TRUE, lag = 1)
```

```
node_recovery(.data)
```

```
node_exposure(.data, mark, time = 0)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>normalized</code>	Logical scalar, whether the centrality scores are normalized. Different denominators are used depending on whether the object is one-mode or two-mode, the type of centrality, and other arguments.

lag	The number of time steps back upon which the thresholds are inferred.
mark	A valid 'node_mark' object or logical vector (TRUE/FALSE) of length equal to the number of nodes in the network.
time	A time point until which infections/adoptions should be identified. By default time = 0.

Adoption time

node_adoption_time() measures the time units it took until each node became infected. Note that an adoption time of 0 indicates that this was a seed node.

Thresholds

node_thresholds() infers nodes' thresholds based on how much exposure they had when they were infected. This inference is of course imperfect, especially where there is a sudden increase in exposure, but it can be used heuristically. In a threshold model, nodes activate when $\sum_{j:\text{active}} w_{ji} \geq \theta_i$, where w is some (potentially weighted) matrix, j are some already activated nodes, and θ is some pre-defined threshold value. Where a fractional threshold is used, the equation is $\frac{\sum_{j:\text{active}} w_{ji}}{\sum_j w_{ji}} \geq \theta_i$. That is, θ is now a proportion, and works regardless of whether w is weighted or not.

Recovery

node_recovery() measures the average length of time that nodes that become infected remain infected in a compartmental model with recovery. Infections that are not concluded by the end of the study period are calculated as infinite.

Exposure

node_exposure() calculates the number of infected/adopting nodes to which each susceptible node is exposed. It usually expects network data and an index or mark (TRUE/FALSE) vector of those nodes which are currently infected, but if a diff_model is supplied instead it will return nodes exposure at $t = 0$.

References

On diffusion measures:

Valente, Tom W. 1995. *Network models of the diffusion of innovations* (2nd ed.). Cresskill N.J.: Hampton Press.

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Other diffusion: [make_play](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [member_diffusion](#)

Examples

```
smeg <- generate_smallworld(15, 0.025)
smeg_diff <- play_diffusion(smeg, recovery = 0.2)
plot(smeg_diff)
# To measure when nodes adopted a diffusion/were infected
(times <- node_adoption_time(smeg_diff))
# To infer nodes' thresholds
node_thresholds(smeg_diff)
# To measure how long each node remains infected for
node_recovery(smeg_diff)
# To measure how much exposure nodes have to a given mark
node_exposure(smeg, mark = c(1,3))
node_exposure(smeg_diff)
```

measure_features

Measures of network topological features

Description

These functions measure certain topological features of networks:

- `net_core()` measures the correlation between a network and a core-periphery model with the same dimensions.
- `net_richclub()` measures the rich-club coefficient of a network.
- `net_factions()` measures the correlation between a network and a component model with the same dimensions. If no 'membership' vector is given for the data, `node_partition()` is used to partition nodes into two groups.
- `net_modularity()` measures the modularity of a network based on nodes' membership in defined clusters.
- `net_smallworld()` measures the small-world coefficient for one- or two-mode networks. Small-world networks can be highly clustered and yet have short path lengths.
- `net_scalefree()` measures the exponent of a fitted power-law distribution. An exponent between 2 and 3 usually indicates a power-law distribution.
- `net_balance()` measures the structural balance index on the proportion of balanced triangles, ranging between 0 if all triangles are imbalanced and 1 if all triangles are balanced.

These `net_*`() functions return a single numeric scalar or value.

Usage

```
net_core(
  .data,
  mark = NULL,
  method = c("correlation", "ident", "ndiff", "diff")
)
```

```

net_richclub(.data)

net_factions(.data, membership = NULL)

net_modularity(.data, membership = NULL, resolution = 1)

net_smallworld(.data, method = c("omega", "sigma", "SWI"), times = 100)

net_scalefree(.data)

net_balance(.data)

```

Arguments

- `.data` An object of a manynet-consistent class:
- matrix (adjacency or incidence) from `{base}` R
 - edgelist, a data frame from `{base}` R or tibble from `{tibble}`
 - igraph, from the `{igraph}` package
 - network, from the `{network}` package
 - tbl_graph, from the `{tidygraph}` package
- `mark` A logical vector the length of the nodes in the network. This can be created by, among other things, any `node_is_*`(`<>`) function.
- `method` There are three small-world measures implemented:
- "sigma" is the original equation from Watts and Strogatz (1998),

$$\frac{\frac{C}{C_r}}{\frac{L}{L_r}}$$

, where C and L are the observed clustering coefficient and path length, respectively, and C_r and L_r are the averages obtained from random networks of the same dimensions and density. A $\sigma > 1$ is considered to be small-world, but this measure is highly sensitive to network size.

- "omega" (the default) is an update from Telesford et al. (2011),

$$\frac{L_r}{L} - \frac{C}{C_l}$$

, where C_l is the clustering coefficient for a lattice graph with the same dimensions. ω ranges between 0 and 1, where 1 is as close to a small-world as possible.

- "SWI" is an alternative proposed by Neal (2017),

$$\frac{L - L_l}{L_r - L_l} \times \frac{C - C_r}{C_l - C_r}$$

, where L_l is the average path length for a lattice graph with the same dimensions. SWI also ranges between 0 and 1 with the same interpretation, but where there may not be a network for which $SWI = 1$.

membership	A vector of partition membership.
resolution	A proportion indicating the resolution scale. By default 1, which returns the original definition of modularity. The higher this parameter, the more smaller communities will be privileged. The lower this parameter, the fewer larger communities are likely to be found.
times	Integer of number of simulations.

Core-Periphery

`net_core()` calculates the Pearson correlation between the given network, where the nodes in the core are assigned by some given mark, and an ideal typical core-periphery network with the same number of nodes in the core and the periphery.

Modularity

Modularity measures the difference between the number of ties within each community from the number of ties expected within each community in a random graph with the same degrees, and ranges between -1 and +1. Modularity scores of +1 mean that ties only appear within communities, while -1 would mean that ties only appear between communities. A score of 0 would mean that ties are half within and half between communities, as one would expect in a random graph.

Modularity faces a difficult problem known as the resolution limit (Fortunato and Barthélemy 2007). This problem appears when optimising modularity, particularly with large networks or depending on the degree of interconnectedness, can miss small clusters that 'hide' inside larger clusters. In the extreme case, this can be where they are only connected to the rest of the network through a single tie. To help manage this problem, a `resolution` parameter is added. Please see the argument definition for more details.

Source

{`signnet`} by David Schoch

References

On core-periphery:

Borgatti, Stephen P., and Martin G. Everett. 2000. "Models of Core/Periphery Structures." *Social Networks* 21(4):375–95. doi:10.1016/S03788733(99)000192

On the rich-club coefficient:

Zhou, Shi, and Raul J. Mondragon. 2004. "The Rich-Club Phenomenon in the Internet Topology". *IEEE Communications Letters*, 8(3): 180-182. doi:10.1109/lcomm.2004.823426

On modularity:

Newman, Mark E.J. 2006. "Modularity and community structure in networks", *Proceedings of the National Academy of Sciences* 103(23): 8577-8696. doi:10.1073/pnas.0601602103

Murata, Tsuyoshi. 2010. "Modularity for Bipartite Networks". In: Memon, N., Xu, J., Hicks, D., Chen, H. (eds) *Data Mining for Social Network Data. Annals of Information Systems*, Vol 12. Springer, Boston, MA. doi:10.1007/9781441962874_7

On small-worldliness:

Watts, Duncan J., and Steven H. Strogatz. 1998. "Collective Dynamics of 'Small-World' Networks". *Nature* 393(6684):440–42. doi:10.1038/30918

Telesford QK, Joyce KE, Hayasaka S, Burdette JH, Laurienti PJ. 2011. "The ubiquity of small-world networks". *Brain Connectivity* 1(5): 367–75. doi:10.1089/brain.2011.0038

Neal, Zachary P. 2017. "How small is it? Comparing indices of small worldliness". *Network Science*. 5 (1): 30–44. doi:10.1017/nws.2017.5

On scale-free networks:

Barabasi, Albert-Laszlo, and Reka Albert. 1999. "Emergence of scaling in random networks", *Science*, 286(5439): 509-512. doi:10.1126/science.286.5439.509

Clauset, Aaron, Cosma Rohilla Shalizi, and Mark E.J. Newman. 2009. "Power-law distributions in empirical data", *SIAM Review*, 51(4): 661-703. doi:10.1137/070710111

Stumpf, Michael P.H., and Mason Porter. 2012. "Critical truths about power laws", *Science*, 335(6069): 665-666. doi:10.1126/science.1216142

Holme, Petter. 2019. "Rare and everywhere: Perspectives on scale-free networks", *Nature Communications*, 10(1): 1016. doi:10.1038/s41467019090388

On balance theory:

Heider, Fritz. 1946. "Attitudes and cognitive organization". *The Journal of Psychology*, 21: 107-112. doi:10.1080/00223980.1946.9917275

Cartwright, D., and Frank Harary. 1956. "Structural balance: A generalization of Heider's theory". *Psychological Review*, 63(5): 277-293. doi:10.1037/h0046049

See Also

`net_transitivity()` and `net_equivalency()` for how clustering is calculated

Other measures: `measure_attributes_nodes`, `measure_attributes_ties`, `measure_central_between`, `measure_central_close`, `measure_central_degree`, `measure_central_eigen`, `measure_closure`, `measure_cohesion`, `measure_diffusion_infection`, `measure_diffusion_net`, `measure_diffusion_node`, `measure_heterogeneity`, `measure_hierarchy`, `measure_holes`, `measure_periods`, `measure_properties`, `member_diffusion`

Examples

```
net_core(ison_adolescents)
net_core(ison_southern_women)
net_richclub(ison_adolescents)
  net_factions(ison_southern_women)
net_modularity(ison_adolescents,
  node_in_partition(ison_adolescents))
net_modularity(ison_southern_women,
  node_in_partition(ison_southern_women))
net_smallworld(ison_brandes)
net_smallworld(ison_southern_women)
net_scalefree(ison_adolescents)
net_scalefree(generate_scalefree(50, 1.5))
net_scalefree(create_lattice(100))
net_balance(to_uniplex(fict_marvel, "relationship"))
```

measure_heterogeneity *Measures of network diversity*

Description

These functions offer ways to measure the heterogeneity of an attribute across a network, within groups of a network, or the distribution of ties across this attribute:

- `net_richness()` measures the number of unique categories in a network attribute.
- `node_richness()` measures the number of unique categories of an attribute to which each node is connected.
- `net_diversity()` measures the heterogeneity of ties across a network.
- `node_diversity()` measures the heterogeneity of each node's local neighbourhood.
- `net_heterophily()` measures how embedded nodes in the network are within groups of nodes with the same attribute.
- `node_heterophily()` measures each node's embeddedness within groups of nodes with the same attribute.
- `net_assortativity()` measures the degree assortativity in a network.
- `net_spatial()` measures the spatial association/autocorrelation (global Moran's I) in a network.

Usage

```
net_richness(.data, attribute)
```

```
node_richness(.data, attribute)
```

```
net_diversity(  
  .data,  
  attribute,  
  method = c("blau", "teachman", "variation", "gini")  
)
```

```
node_diversity(  
  .data,  
  attribute,  
  method = c("blau", "teachman", "variation", "gini")  
)
```

```
net_heterophily(.data, attribute)
```

```
node_heterophily(.data, attribute)
```

```
net_homophily(.data, attribute, method = c("ie", "ei", "yule", "geary"))
```

```
node_homophily(.data, attribute, method = c("ie", "ei", "yule", "geary"))
net_assortativity(.data)
net_spatial(.data, attribute)
```

Arguments

.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
attribute	Name of a nodal attribute or membership vector to use as categories for the diversity measure.
method	Which method to use for net_diversity(). Either "blau" (Blau's index) or "teachman" (Teachman's index) for categorical attributes, or "variation" (coefficient of variation) or "gini" (Gini coefficient) for numeric attributes. Default is "blau". If an incompatible method is chosen for the attribute type, a suitable alternative will be used instead with a message.

Richness

Richness is a simple count of the number of different categories present for a given attribute.

Diversity

Blau's index (1977) uses a formula known also in other disciplines by other names (Gini-Simpson Index, Gini impurity, Gini's diversity index, Gibbs-Martin index, and probability of interspecific encounter (PIE)):

$$1 - \sum_{i=1}^k p_i^2$$

where p_i is the proportion of group members in i th category and k is the number of categories for an attribute of interest. This index can be interpreted as the probability that two members randomly selected from a group would be from different categories. This index finds its minimum value (0) when there is no variety, i.e. when all individuals are classified in the same category. The maximum value depends on the number of categories and whether nodes can be evenly distributed across categories.

Teachman's index (1980) is based on information theory and is calculated as:

$$-\sum_{i=1}^k p_i \log(p_i)$$

where p_i is the proportion of group members in i th category and k is the number of categories for an attribute of interest. This index finds its minimum value (0) when there is no variety, i.e. when

all individuals are classified in the same category. The maximum value depends on the number of categories and whether nodes can be evenly distributed across categories. It thus shares similar properties to Blau's index, but includes also a notion of richness that tends to give more weight to rare categories and thus tends to highlight imbalances more.

The coefficient of variation (CV) is a standardised measure of dispersion of a probability distribution or frequency distribution. It is defined as the ratio of the standard deviation σ to the mean μ :

$$CV = \frac{\sigma}{\mu}$$

It is often expressed as a percentage. The CV is useful because the standard deviation of data must always be understood in the context of the mean of the data. The CV is particularly useful when comparing the degree of variation from one data series to another, even if the means are drastically different from each other.

The Gini coefficient is a measure of statistical dispersion that is intended to represent the income or wealth distribution of a nation's residents, and is commonly used as a measure of inequality. It is defined as a ratio with values between 0 and 1, where 0 corresponds with perfect equality (everyone has the same income) and 1 corresponds with perfect inequality (one person has all the income, and everyone else has zero income). The Gini coefficient can be calculated from the Lorenz curve, which plots the proportion of the total income of the population that is cumulatively earned by the bottom $x\%$ of the population. The Gini coefficient is defined as the area between the line of equality and the Lorenz curve, divided by the total area under the line of equality.

Homophily

Given a partition of a network into a number of mutually exclusive groups then The E-I index is the number of ties between (or *external*) nodes grouped in some mutually exclusive categories minus the number of ties within (or *internal*) these groups divided by the total number of ties. This value can range from 1 to -1, where 1 indicates ties only between categories/groups and -1 ties only within categories/groups.

References

On richness:

Magurran, Anne E. 1988. *Ecological Diversity and Its Measurement*. Princeton: Princeton University Press. doi:10.1007/9789401573580

On diversity:

Blau, Peter M. 1977. *Inequality and heterogeneity*. New York: Free Press.

Teachman, Jay D. 1980. Analysis of population diversity: Measures of qualitative variation. *Sociological Methods & Research*, 8:341-362. doi:10.1177/004912418000800305

Page, Scott E. 2010. *Diversity and Complexity*. Princeton: Princeton University Press. doi:10.1515/9781400835140

On heterophily:

Krackhardt, David, and Robert N. Stern. 1988. Informal networks and organizational crises: an experimental simulation. *Social Psychology Quarterly* 51(2): 123-140. doi:10.2307/2786835

McPherson, Miller, Lynn Smith-Lovin, and James M. Cook. 2001. "Birds of a Feather: Homophily in Social Networks". *Annual Review of Sociology*, 27(1): 415-444. doi:10.1146/annurev.soc.27.1.415

On assortativity:

Newman, Mark E.J. 2002. "Assortative mixing in networks". *Physical Review Letters*, 89(20): 208701. doi:10.1103/physrevlett.89.208701

On spatial autocorrelation:

Moran, Patrick Alfred Pierce. 1950. "Notes on continuous stochastic phenomena". *Biometrika* 37(1): 17-23. doi:10.2307/2332142

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
net_richness(ison_networkers)
node_richness(ison_networkers, "Discipline")
marvel_friends <- to_unsigned(to_uniplex(fict_marvel, "relationship"), "positive")
net_diversity(marvel_friends, "Gender")
net_diversity(marvel_friends, "Appearances")
node_diversity(marvel_friends, "Gender")
node_diversity(marvel_friends, "Attractive")
net_heterophily(marvel_friends, "Gender")
net_heterophily(marvel_friends, "Attractive")
node_heterophily(marvel_friends, "Gender")
node_heterophily(marvel_friends, "Attractive")
net_homophily(marvel_friends, "Gender")
net_assortativity(ison_networkers)
net_spatial(ison_lawfirm, "age")
```

 measure_hierarchy

Graph theoretic dimensions of hierarchy

Description

These functions, together with `net_reciprocity()`, are used jointly to measure how hierarchical a network is:

- `net_connectedness()` measures the proportion of dyads in the network that are reachable to one another, or the degree to which network is a single component.
- `net_efficiency()` measures the Krackhardt efficiency score.
- `net_upperbound()` measures the Krackhardt (least) upper bound score.

Usage

```
net_by_hierarchy(.data)

net_connectedness(.data)

net_efficiency(.data)

net_upperbound(.data)
```

Arguments

`.data` An object of a manynet-consistent class:

- matrix (adjacency or incidence) from {base} R
- edgelist, a data frame from {base} R or tibble from {tibble}
- igraph, from the {igraph} package
- network, from the {network} package
- tbl_graph, from the {tidygraph} package

References

On hierarchy:

Krackhardt, David. 1994. Graph theoretical dimensions of informal organizations. In Carley and Prietula (eds) *Computational Organizational Theory*, Hillsdale, NJ: Lawrence Erlbaum Associates. Pp. 89-111.

Everett, Martin, and David Krackhardt. 2012. “A second look at Krackhardt’s graph theoretical dimensions of informal organizations.” *Social Networks*, 34: 159-163. doi:10.1016/j.socnet.2011.10.006

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_holes](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
net_connectedness(ison_networkers)
1 - net_reciprocity(ison_networkers)
net_efficiency(ison_networkers)
net_upperbound(ison_networkers)
```

Description

These function provide different measures of the degree to which nodes fill structural holes, as outlined in Burt (1992):

- `node_bridges()` measures the sum of bridges to which each node is adjacent.
- `node_redundancy()` measures the redundancy of each nodes' contacts.
- `node_effsize()` measures nodes' effective size.
- `node_efficiency()` measures nodes' efficiency.
- `node_constraint()` measures nodes' constraint scores for one-mode networks according to Burt (1992) and for two-mode networks according to Hollway et al (2020).
- `node_hierarchy()` measures nodes' exposure to hierarchy, where only one or two contacts are the source of closure.
- `node_neighbours_degree()` measures nodes' average nearest neighbors degree, or *knn*, a measure of the type of local environment a node finds itself in
- `tie_cohesion()` measures the ratio between common neighbors to ties' adjacent nodes and the total number of adjacent nodes, where high values indicate ties' embeddedness in dense local environments

Burt's theory holds that while those nodes embedded in dense clusters of close connections are likely exposed to the same or similar ideas and information, those who fill structural holes between two otherwise disconnected groups can gain some comparative advantage from that position.

Usage

```
node_bridges(.data)
```

```
node_redundancy(.data)
```

```
node_effsize(.data)
```

```
node_efficiency(.data)
```

```
node_constraint(.data)
```

```
node_hierarchy(.data)
```

```
node_neighbours_degree(.data)
```

```
tie_cohesion(.data)
```

Arguments

- `.data` An object of a manynet-consistent class:
- matrix (adjacency or incidence) from `{base}` R
 - edgelist, a data frame from `{base}` R or tibble from `{tibble}`
 - igraph, from the `{igraph}` package
 - network, from the `{network}` package
 - tbl_graph, from the `{tidygraph}` package

Details

A number of different ways of measuring these structural holes are available. Note that we use Borgatti's reformulation for unweighted networks in `node_redundancy()` and `node_effsize()`. Redundancy is thus $\frac{2t}{n}$, where t is the sum of ties and n the sum of nodes in each node's neighbourhood, and effective size is calculated as $n - \frac{2t}{n}$. Node efficiency is the node's effective size divided by its degree.

References

On structural holes:

Burt, Ronald S. 1992. *Structural Holes: The Social Structure of Competition*. Cambridge, MA: Harvard University Press.

Borgatti, Steven. 1997. "Structural Holes: Unpacking Burt's Redundancy Measures" *Connections* 20(1):35-38.

Burchard, Jake, and Benjamin Cornwell. 2018. "Structural Holes and Bridging in Two-Mode Networks." *Social Networks* 55:11–20. doi:10.1016/j.socnet.2018.04.001

Hollway, James, Jean-Frédéric Morin, and Joost Pauwelyn. 2020. "Structural conditions for novelty: The introduction of new environmental clauses to the trade regime complex." *International Environmental Agreements: Politics, Law and Economics* 20 (1): 61–83. doi:10.1007/s10784019-094645

On neighbours average degree:

Barrat, Alain, Marc Barthelemy, Romualdo Pastor-Satorras, and Alessandro Vespignani. 2004. "The architecture of complex weighted networks", *Proc. Natl. Acad. Sci.* 101: 3747.

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_periods](#), [measure_properties](#), [member_diffusion](#)

Examples

```
node_bridges(ison_adolescents)
node_bridges(ison_southern_women)
node_redundancy(ison_adolescents)
```

```

node_redundancy(ison_southern_women)
node_effsize(ison_adolescents)
node_effsize(ison_southern_women)
node_efficiency(ison_adolescents)
node_efficiency(ison_southern_women)
node_constraint(ison_southern_women)
node_hierarchy(ison_adolescents)
node_hierarchy(ison_southern_women)

```

measure_periods	<i>Measures of network change</i>
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Description

These functions measure certain topological features of networks:

- `net_waves()` measures the number of waves in longitudinal network data.
- `net_change()` measures the Hamming distance between two or more networks.
- `net_stability()` measures the Jaccard index of stability between two or more networks.
- `net_correlation()` measures the product-moment correlation between two networks.

These `net_*()` functions return a numeric vector the length of the number of networks minus one. E.g., the periods between waves.

Usage

```

net_waves(.data)

net_change(.data, object2)

net_stability(.data, object2)

net_correlation(.data, object2)

```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>object2</code>	A network object.

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_properties](#), [member_diffusion](#)

measure_properties *Describing network properties*

Description

These functions extract certain attributes from given network data:

- `net_name()` returns the name of the network, if it has one.
- `net_nodes()` returns the total number of nodes (of any mode) in a network.
- `net_ties()` returns the number of ties in a network.
- `net_dims()` returns the dimensions of a network in a vector as long as the number of modes in the network.
- `net_node_names()` returns a vector of the names of the nodes in a network, if they have been defined.
- `net_node_attributes()` returns a vector of nodal attributes in a network.
- `net_tie_names()` returns a vector of the names of the ties in a network, if they have been defined.
- `net_tie_attributes()` returns a vector of tie attributes in a network.

These functions are also often used as helpers within other functions.

Usage

```
net_name(.data, prefix = NULL)
```

```
net_nodes(.data)
```

```
net_ties(.data)
```

```
net_dims(.data)
```

```
net_node_names(.data)
```

```
net_node_attributes(.data)
```

```
net_tie_names(.data)
```

```
net_tie_attributes(.data)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>prefix</code>	An optional string to be added before the name of the network.

Value

`net_*`() functions always relate to the overall graph or network, usually returning a scalar. `net_dims()` returns an integer of the number of nodes in a one-mode network, or two integers representing the number of nodes in each nodeset in the case of a two-mode network. `net_*_attributes()` returns a string vector with the names of all node or tie attributes in the network.

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [member_diffusion](#)

Examples

```
net_name(ison_southern_women)
net_nodes(ison_southern_women)
net_ties(ison_southern_women)
net_dims(ison_southern_women)
net_dims(to_model(ison_southern_women))
net_node_names(ison_algebra)
net_node_attributes(fict_lotr)
net_tie_names(ison_algebra)
net_tie_attributes(ison_algebra)
```

member_brokerage	<i>Memberships of brokerage</i>
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Description

These functions include ways to take a census of the brokerage positions of nodes in a network:

- `node_in_brokerage()` returns nodes membership as a powerhouse, connector, linchpin, or sideline according to Hamilton et al. (2020).

Usage

```
node_in_brokering(.data, membership)
```

Arguments

`.data` An object of a manynet-consistent class:

- matrix (adjacency or incidence) from {base} R
- edgelist, a data frame from {base} R or tibble from {tibble}
- igraph, from the {igraph} package
- network, from the {network} package
- tbl_graph, from the {tidygraph} package

`membership` A vector of partition membership as integers.

See Also

Other memberships: [mark_core](#), [member_cliques](#), [member_community_hier](#), [member_community_non](#), [member_components](#), [member_equivalence](#)

member_cliques	<i>Clique partitioning algorithms</i>
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Description

These functions create a vector of nodes' memberships in cliques:

- `node_in_roulette()` assigns nodes to maximally diverse groups.

Usage

```
node_in_roulette(.data, num_groups, group_size, times = NULL)
```

Arguments

`.data` An object of a manynet-consistent class:

- matrix (adjacency or incidence) from {base} R
- edgelist, a data frame from {base} R or tibble from {tibble}
- igraph, from the {igraph} package
- network, from the {network} package
- tbl_graph, from the {tidygraph} package

`num_groups` An integer indicating the number of groups desired.

`group_size` An integer indicating the desired size of most of the groups. Note that if the number of nodes is not divisible into groups of equal size, there may be some larger or smaller groups.

times An integer of the number of search iterations the algorithm should complete. By default this is the number of nodes in the network multiplied by the number of groups. This heuristic may be insufficient for small networks and numbers of groups, and burdensome for large networks and numbers of groups, but can be overwritten. At every 10th iteration, a stronger perturbation of a number of successive changes, approximately the number of nodes divided by the number of groups, will take place irrespective of whether it improves the objective function.

Maximally diverse grouping problem

This well known computational problem is a NP-hard problem with a number of relevant applications, including the formation of groups of students that have encountered each other least or least recently. Essentially, the aim is to return a membership of nodes in cliques that minimises the sum of their previous (weighted) ties:

$$\sum_{g=1}^m \sum_{i=1}^{n-1} \sum_{j=i+1}^n x_{ij} y_{ig} y_{jg}$$

where $y_{ig} = 1$ if node i is in group g , and 0 otherwise.

x_{ij} is the existing network data. If this is an empty network, the function will just return cliques. To run this repeatedly, one can join a clique network of the membership result with the original network, using this as the network data for the next round.

A form of the Lai and Hao (2016) iterated maxima search (IMS) is used here. This performs well for small and moderately sized networks. It includes both weak and strong perturbations to an initial solution to ensure that a robust solution from the broader state space is identified. The user is referred to Lai and Hao (2016) and Lai et al (2021) for more details.

References

On the maximally diverse grouping problem:

Lai, Xiangjing, and Jin-Kao Hao. 2016. "Iterated Maxima Search for the Maximally Diverse Grouping Problem." *European Journal of Operational Research* 254(3):780–800. doi:10.1016/j.ejor.2016.05.018.

Lai, Xiangjing, Jin-Kao Hao, Zhang-Hua Fu, and Dong Yue. 2021. "Neighborhood Decomposition Based Variable Neighborhood Search and Tabu Search for Maximally Diverse Grouping." *European Journal of Operational Research* 289(3):1067–86. doi:10.1016/j.ejor.2020.07.048.

See Also

Other memberships: [mark_core](#), [member_brokerage](#), [member_community_hier](#), [member_community_non](#), [member_components](#), [member_equivalence](#)

member_community_hier *Hierarchical community partitioning algorithms*

Description

These functions offer algorithms for hierarchically clustering networks into communities. Since all of the following are hierarchical, their dendrograms can be plotted:

- `node_in_betweenness()` is a hierarchical, decomposition algorithm where edges are removed in decreasing order of the number of shortest paths passing through the edge.
- `node_in_greedy()` is a hierarchical, agglomerative algorithm, that tries to optimize modularity in a greedy manner.
- `node_in_eigen()` is a top-down, hierarchical algorithm.
- `node_in_walktrap()` is a hierarchical, agglomerative algorithm based on random walks.

The different algorithms offer various advantages in terms of computation time, availability on different types of networks, ability to maximise modularity, and their logic or domain of inspiration.

Usage

```
node_in_betweenness(.data)
```

```
node_in_greedy(.data)
```

```
node_in_eigen(.data)
```

```
node_in_walktrap(.data, times = 50)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base} R</code> • edgelist, a data frame from <code>{base} R</code> or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>times</code>	Integer indicating number of simulations/walks used. By default, <code>times=50</code> .

Edge-betweenness

This is motivated by the idea that edges connecting different groups are more likely to lie on multiple shortest paths when they are the only option to go from one group to another. This method yields good results but is very slow because of the computational complexity of edge-betweenness calculations and the betweenness scores have to be re-calculated after every edge removal. Networks of ~700 nodes and ~3500 ties are around the upper size limit that are feasible with this approach.

Fast-greedy

Initially, each node is assigned a separate community. Communities are then merged iteratively such that each merge yields the largest increase in the current value of modularity, until no further increases to the modularity are possible. The method is fast and recommended as a first approximation because it has no parameters to tune. However, it is known to suffer from a resolution limit.

Leading eigenvector

In each step, the network is bifurcated such that modularity increases most. The splits are determined according to the leading eigenvector of the modularity matrix. A stopping condition prevents tightly connected groups from being split further. Note that due to the eigenvector calculations involved, this algorithm will perform poorly on degenerate networks, but will likely obtain a higher modularity than fast-greedy (at some cost of speed).

Walktrap

The general idea is that random walks on a network are more likely to stay within the same community because few edges lead outside a community. By repeating random walks of 4 steps many times, information about the hierarchical merging of communities is collected.

References

On edge-betweenness community detection:

Newman, Mark, and Michelle Girvan. 2004. "Finding and evaluating community structure in networks." *Physical Review E* 69: 026113. doi:10.1103/PhysRevE.69.026113

On fast-greedy community detection:

Clauset, Aaron, Mark E.J. Newman, and Cristopher Moore. 2004. "Finding community structure in very large networks." *Physical Review E*, 70: 066111. doi:10.1103/PhysRevE.70.066111

On leading eigenvector community detection:

Newman, Mark E.J. 2006. "Finding community structure using the eigenvectors of matrices" *Physical Review E* 74:036104. doi:10.1103/PhysRevE.74.036104

On walktrap community detection:

Pons, Pascal, and Matthieu Latapy. 2005. "Computing communities in large networks using random walks". 1-20. doi:10.48550/arXiv.physics/0512106

See Also

Other memberships: [mark_core](#), [member_brokerage](#), [member_cliques](#), [member_community_non](#), [member_components](#), [member_equivalence](#)

Examples

```
node_in_betweenness(ison_adolescents)
node_in_greedy(ison_adolescents)
node_in_eigen(ison_adolescents)
node_in_walktrap(ison_adolescents)
```

member_community_non *Non-hierarchical community partitioning algorithms*

Description

These functions offer algorithms for partitioning networks into sets of communities:

- `node_in_community()` runs either optimal or, for larger networks, finds the algorithm that maximises modularity and returns that membership vector.
- `node_in_optimal()` is a problem-solving algorithm that seeks to maximise modularity over all possible partitions.
- `node_in_partition()` is a greedy, iterative, deterministic partitioning algorithm that results in two equally-sized communities.
- `node_in_infomap()` is an algorithm based on the information in random walks.
- `node_in_springlass()` is a greedy, iterative, probabilistic algorithm, based on analogy to model from statistical physics.
- `node_in_fluid()` is a propagation-based partitioning algorithm, based on analogy to model from fluid dynamics.
- `node_in_louvain()` is an agglomerative multilevel algorithm that seeks to maximise modularity over all possible partitions.
- `node_in_leiden()` is an agglomerative multilevel algorithm that seeks to maximise the Constant Potts Model over all possible partitions.

The different algorithms offer various advantages in terms of computation time, availability on different types of networks, ability to maximise modularity, and their logic or domain of inspiration.

Usage

```
node_in_community(.data)
```

```
node_in_optimal(.data)
```

```
node_in_partition(.data)
```

```
node_in_infomap(.data, times = 50)
```

```
node_in_springlass(.data, max_k = 200, resolution = 1)
```

```
node_in_fluid(.data)
```

```
node_in_louvain(.data, resolution = 1)
```

```
node_in_leiden(.data, resolution = 1)
```

Arguments

.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
times	Integer indicating number of simulations/walks used. By default, times=50.
max_k	Integer constant, the number of spins to use as an upper limit of communities to be found. Some sets can be empty at the end.
resolution	The Reichardt-Bornholdt “gamma” resolution parameter for modularity. By default 1, making existing and non-existing ties equally important. Smaller values make existing ties more important, and larger values make missing ties more important.

Community

This function runs through all available community detection algorithms for a given network type, finds the algorithm that returns the largest modularity score, and returns the corresponding membership partition. Where feasible (a small enough network), the optimal problem solving technique is used to ensure the maximal modularity partition.

Optimal

The general idea is to calculate the modularity of all possible partitions, and choose the community structure that maximises this modularity measure. Note that this is an NP-complete problem with exponential time complexity. The guidance in the igraph package is networks of <50-200 nodes is probably fine.

Infomap

Motivated by information theoretic principles, this algorithm tries to build a grouping that provides the shortest description length for a random walk, where the description length is measured by the expected number of bits per node required to encode the path.

Spin-glass

This is motivated by analogy to the Potts model in statistical physics. Each node can be in one of k "spin states", and ties (particle interactions) provide information about which pairs of nodes want similar or different spin states. The final community definitions are represented by the nodes' spin states after a number of updates. A different implementation than the default is used in the case of signed networks, such that nodes connected by negative ties will be more likely found in separate communities.

Fluid

The general idea is to observe how a discrete number of fluids interact, expand and contract, in a non-homogenous environment, i.e. the network structure. Unlike the `{igraph}` implementation that this function wraps, this function iterates over all possible numbers of communities and returns the membership associated with the highest modularity.

Louvain

The general idea is to take a hierarchical approach to optimising the modularity criterion. Nodes begin in their own communities and are re-assigned in a local, greedy way: each node is moved to the community where it achieves the highest contribution to modularity. When no further modularity-increasing reassignments are possible, the resulting communities are considered nodes (like a reduced graph), and the process continues.

Leiden

The general idea is to optimise the Constant Potts Model, which does not suffer from the resolution limit, instead of modularity. As outlined in the `{igraph}` package, the Constant Potts Model object function is:

$$\frac{1}{2m} \sum_{ij} (A_{ij} - \gamma n_i n_j) \delta(\sigma_i, \sigma_j)$$

where m is the total tie weight, A_{ij} is the tie weight between i and j , γ is the so-called resolution parameter, n_i is the node weight of node i , and $\delta(\sigma_i, \sigma_j) = 1$ if and only if i and j are in the same communities and 0 otherwise. Compared to the Louvain method, the Leiden algorithm additionally tries to avoid unconnected communities.

References

On optimal community detection:

Brandes, Ulrik, Daniel Delling, Marco Gaertler, Robert Gorke, Martin Hoefer, Zoran Nikoloski, Dorothea Wagner. 2008. "On Modularity Clustering", *IEEE Transactions on Knowledge and Data Engineering* 20(2):172-188.

On partitioning community detection:

Kernighan, Brian W., and Shen Lin. 1970. "An efficient heuristic procedure for partitioning graphs." *The Bell System Technical Journal* 49(2): 291-307. doi:10.1002/j.15387305.1970.tb01770.x

On infomap community detection:

Rosvall, M., and C. T. Bergstrom. 2008. "Maps of information flow reveal community structure in complex networks", *PNAS* 105:1118. doi:10.1073/pnas.0706851105

Rosvall, M., D. Axelsson, and C. T. Bergstrom. 2009. "The map equation", *Eur. Phys. J. Special Topics* 178: 13. doi:10.1140/epjst/e2010011791

On spinglass community detection:

Reichardt, Jorg, and Stefan Bornholdt. 2006. "Statistical Mechanics of Community Detection" *Physical Review E*, 74(1): 016110–14. doi:10.1073/pnas.0605965104

Traag, Vincent A., and Jeroen Bruggeman. 2009. "Community detection in networks with positive and negative links". *Physical Review E*, 80(3): 036115. doi:10.1103/PhysRevE.80.036115

On fluid community detection:

Parés Ferran, Dario Garcia Gasulla, Armand Vilalta, Jonatan Moreno, Eduard Ayguade, Jesus Labarta, Ulises Cortes, and Toyotaro Suzumura. 2018. "Fluid Communities: A Competitive, Scalable and Diverse Community Detection Algorithm". In: *Complex Networks & Their Applications VI* Springer, 689: 229. doi:10.1007/9783319721507_19

On Louvain community detection:

Blondel, Vincent, Jean-Loup Guillaume, Renaud Lambiotte, Etienne Lefebvre. 2008. "Fast unfolding of communities in large networks", *J. Stat. Mech.* P10008.

On Leiden community detection:

Traag, Vincent A., Ludo Waltman, and Nees Jan van Eck. 2019. "From Louvain to Leiden: guaranteeing well-connected communities", *Scientific Reports*, 9(1):5233. doi:10.1038/s41598-01941695z

See Also

Other memberships: [mark_core](#), [member_brokerage](#), [member_cliques](#), [member_community_hier](#), [member_components](#), [member_equivalence](#)

Examples

```
node_in_optimal(ison_adolescents)
node_in_partition(ison_adolescents)
node_in_partition(ison_southern_women)
node_in_infomap(ison_adolescents)
node_in_spinglass(ison_adolescents)
node_in_fluid(ison_adolescents)
node_in_louvain(ison_adolescents)
node_in_leiden(ison_adolescents)
```

member_components

Component partitioning algorithms

Description

These functions create a vector of nodes' memberships in components:

- `node_in_component()` assigns nodes' component membership using edge direction where available.
- `node_in_weak()` assigns nodes' component membership ignoring edge direction.
- `node_in_strong()` assigns nodes' component membership based on edge direction.

In graph theory, components, sometimes called connected components, are induced subgraphs from partitioning the nodes into disjoint sets. All nodes that are members of the same partition as i are reachable from i .

For directed networks, strongly connected components consist of subgraphs where there are paths in each direction between member nodes. Weakly connected components consist of subgraphs where there is a path in either direction between member nodes.

Usage

```
node_in_component(.data)
```

```
node_in_weak(.data)
```

```
node_in_strong(.data)
```

Arguments

- | | |
|-------|--|
| .data | <p>An object of a manynet-consistent class:</p> <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package |
|-------|--|

See Also

Other memberships: [mark_core](#), [member_brokerage](#), [member_cliques](#), [member_community_hier](#), [member_community_non](#), [member_equivalence](#)

Examples

```
ison_monks %>% to_uniplex("esteem") %>%
  mutate_nodes(comp = node_in_component())
```

member_diffusion	<i>Membership of nodes in a diffusion</i>
------------------	---

Description

node_in_adopter() classifies membership of nodes into diffusion categories by where on the distribution of adopters they fell. Valente (1995) defines five memberships:

- *Early adopter*: those with an adoption time less than the average adoption time minus one standard deviation of adoptions times
- *Early majority*: those with an adoption time between the average adoption time and the average adoption time minus one standard deviation of adoptions times

- *Late majority*: those with an adoption time between the average adoption time and the average adoption time plus one standard deviation of adoptions times
- *Laggard*: those with an adoption time greater than the average adoption time plus one standard deviation of adoptions times
- *Non-adopter*: those without an adoption time, i.e. never adopted

Usage

```
node_in_adopter(.data)
```

Arguments

`.data` An object of a manynet-consistent class:

- matrix (adjacency or incidence) from `{base}` R
- edgelist, a data frame from `{base}` R or tibble from `{tibble}`
- igraph, from the `{igraph}` package
- network, from the `{network}` package
- tbl_graph, from the `{tidygraph}` package

References

On adopter classes:

Valente, Tom W. 1995. *Network models of the diffusion of innovations* (2nd ed.). Cresskill N.J.: Hampton Press.

See Also

Other measures: [measure_attributes_nodes](#), [measure_attributes_ties](#), [measure_central_between](#), [measure_central_close](#), [measure_central_degree](#), [measure_central_eigen](#), [measure_closure](#), [measure_cohesion](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#), [measure_features](#), [measure_heterogeneity](#), [measure_hierarchy](#), [measure_holes](#), [measure_periods](#), [measure_properties](#)

Other diffusion: [make_play](#), [measure_diffusion_infection](#), [measure_diffusion_net](#), [measure_diffusion_node](#)

Examples

```
smeg <- generate_smallworld(15, 0.025)
smeg_diff <- play_diffusion(smeg, recovery = 0.2)
# To classify nodes by their position in the adoption curve
(adopts <- node_in_adopter(smeg_diff))
summary(adopts)
```

member_equivalence *Equivalence clustering algorithms*

Description

These functions combine an appropriate `node_by_*`() function together with methods for calculating the hierarchical clusters provided by a certain distance calculation.

- `node_in_equivalence()` assigns nodes membership based on their equivalence with respective to some census/class. The following functions call this function, together with an appropriate census.
 - `node_in_structural()` assigns nodes membership based on their having equivalent ties to the same other nodes.
 - `node_in_regular()` assigns nodes membership based on their having equivalent patterns of ties.
 - `node_in_automorphic()` assigns nodes membership based on their having equivalent distances to other nodes.

A `plot()` method exists for investigating the dendrogram of the hierarchical cluster and showing the returned cluster assignment.

Usage

```
node_in_equivalence(  
  .data,  
  census,  
  k = c("silhouette", "elbow", "strict"),  
  cluster = c("hierarchical", "concor", "cosine"),  
  distance = c("euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski"),  
  range = 8L  
)  
  
node_in_structural(  
  .data,  
  k = c("silhouette", "elbow", "strict"),  
  cluster = c("hierarchical", "concor", "cosine"),  
  distance = c("euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski"),  
  range = 8L  
)  
  
node_in_regular(  
  .data,  
  k = c("silhouette", "elbow", "strict"),  
  cluster = c("hierarchical", "concor", "cosine"),  
  distance = c("euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski"),  
  range = 8L  
)
```

```
node_in_automorphic(
  .data,
  k = c("silhouette", "elbow", "strict"),
  cluster = c("hierarchical", "concor", "cosine"),
  distance = c("euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski"),
  range = 8L
)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
<code>census</code>	A matrix returned by a <code>node_by_*</code> () function.
<code>k</code>	Typically a character string indicating which method should be used to select the number of clusters to return. By default "silhouette", other options include "elbow" and "strict". "strict" returns classes with members only when strictly equivalent. "silhouette" and "elbow" select classes based on the distance between clusters or between nodes within a cluster. Fewer, identifiable letters, e.g. "e" for elbow, is sufficient. Alternatively, if k is passed an integer, e.g. k = 3, then all selection routines are skipped in favour of this number of clusters.
<code>cluster</code>	Character string indicating whether clusters should be clustered hierarchically ("hierarchical") or through convergence of correlations ("concor"). Fewer, identifiable letters, e.g. "c" for CONCOR, is sufficient.
<code>distance</code>	Character string indicating which distance metric to pass on to <code>stats::dist</code> . By default "euclidean", but other options include "maximum", "manhattan", "canberra", "binary", and "minkowski". Fewer, identifiable letters, e.g. "e" for Euclidean, is sufficient.
<code>range</code>	Integer indicating the maximum number of (k) clusters to evaluate. Ignored when k = "strict" or a discrete number is given for k.

Source

<https://github.com/aslez/concoR>

See Also

Other memberships: [mark_core](#), [member_brokerage](#), [member_cliques](#), [member_community_hier](#), [member_community_non](#), [member_components](#)

Examples

```
(nse <- node_in_structural(ison_algebra))
(nre <- node_in_regular(ison_southern_women,
  cluster = "concor"))
if(require("sna", quietly = TRUE)){
  (nae <- node_in_automorphic(ison_southern_women,
    k = "elbow"))
}
```

 model_cluster

Methods for equivalence clustering

Description

These functions are used to cluster some census object:

- `cluster_hierarchical()` returns a hierarchical clustering object created by `stats::hclust()`.
- `cluster_concor()` returns a hierarchical clustering object created from a convergence of correlations procedure (CONCOR).
- `cluster_cosine()` returns a hierarchical clustering object created by `stats::hclust()` on cosine dissimilarities, rather than correlations, as created by `to_cosine()`.

These functions are not intended to be called directly, but are called within `node_in_equivalence()` and related functions. They are exported and listed here to provide more detailed documentation.

Usage

```
cluster_hierarchical(census, distance)
```

```
cluster_cosine(census, distance)
```

```
cluster_concor(.data, census)
```

Arguments

- | | |
|----------|---|
| census | A matrix returned by a <code>node_by_*</code> () function. |
| distance | Character string indicating which distance metric to pass on to <code>stats::dist</code> . By default "euclidean", but other options include "maximum", "manhattan", "canberra", "binary", and "minkowski". Fewer, identifiable letters, e.g. "e" for Euclidean, is sufficient. |
| .data | An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package |

CONCOR

First a matrix of Pearson correlation coefficients between each pair of nodes profiles in the given census is created. Then, again, we find the correlations of this square, symmetric matrix, and continue to do this iteratively until each entry is either 1 or -1. These values are used to split the data into two partitions, with members either holding the values 1 or -1. This procedure from census to convergence is then repeated within each block, allowing further partitions to be found. Unlike UCINET, partitions are continued until there are single members in each partition. Then a distance matrix is constructed from records of in which partition phase nodes were separated, and this is given to `stats::hclust()` so that dendrograms etc can be returned.

References

On CONCOR clustering:

Breiger, Ronald L., Scott A. Boorman, and Phipps Arabie. 1975. "An Algorithm for Clustering Relational Data with Applications to Social Network Analysis and Comparison with Multidimensional Scaling". *Journal of Mathematical Psychology*, 12: 328-83. doi:10.1016/0022-2496(75)900280.

model_kselect

Methods for selecting clusters

Description

These functions help select the number of clusters to return from `hc`, some hierarchical clustering object:

- `k_strict()` selects a number of clusters in which there is no distance between cluster members.
- `k_elbow()` selects a number of clusters in which there is a fair trade-off between parsimony and fit according to the elbow method.
- `k_silhouette()` selects a number of clusters that optimises the silhouette score.

These functions are generally not user-facing but used internally in e.g. the `*_equivalence()` functions.

Usage

```
k_strict(hc, .data)
```

```
k_elbow(hc, .data, census, range)
```

```
k_silhouette(hc, .data, range)
```

Arguments

hc	A hierarchical clustering object.
.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
census	A motif census object.
range	An integer indicating the maximum number of options to consider. The minimum of this and the number of nodes in the network is used.

References**On the elbow method:**

Thorndike, Robert L. 1953. "Who Belongs in the Family?". *Psychometrika*, 18(4): 267–76. doi:10.1007/BF02289263.

On the silhouette method:

Rousseeuw, Peter J. 1987. "Silhouettes: A Graphical Aid to the Interpretation and Validation of Cluster Analysis." *Journal of Computational and Applied Mathematics*, 20: 53–65. doi:10.1016/03770427(87)901257.

 motif_brokerage

Motifs of brokerage

Description

These functions include ways to take a census of the brokerage positions of nodes in a network:

- `node_by_brokerage()` returns the Gould-Fernandez brokerage roles played by nodes in a network.
- `net_by_brokerage()` returns the Gould-Fernandez brokerage roles in a network.
- `node_brokering_activity()` measures nodes' brokerage activity.
- `node_brokering_exclusivity()` measures nodes' brokerage exclusivity.

Usage

```
node_by_brokerage(.data, membership, standardized = FALSE)
```

```
net_by_brokerage(.data, membership, standardized = FALSE)
```

```
node_brokering_activity(.data, membership)
```

```
node_brokering_exclusivity(.data, membership)
```

Arguments

<code>.data</code>	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from <code>{base}</code> R • edgelist, a data frame from <code>{base}</code> R or tibble from <code>{tibble}</code> • igraph, from the <code>{igraph}</code> package • network, from the <code>{network}</code> package • tbl_graph, from the <code>{tidygraph}</code> package
<code>membership</code>	A vector of partition membership as integers.
<code>standardized</code>	Whether the score should be standardized into a z-score indicating how many standard deviations above or below the average the score lies.

References**On brokerage motifs:**

Gould, Roger V., and Roberto M. Fernandez. 1989. "Structures of Mediation: A Formal Approach to Brokerage in Transaction Networks." *Sociological Methodology*, 19: 89-126. doi:10.2307/270949

Jasny, Lorien, and Mark Lubell. 2015. "Two-Mode Brokerage in Policy Networks." *Social Networks* 41:36–47. doi:10.1016/j.socnet.2014.11.005

On brokerage activity and exclusivity:

Hamilton, Matthew, Jacob Hileman, and Orjan Bodin. 2020. "Evaluating heterogeneous brokerage: New conceptual and methodological approaches and their application to multi-level environmental governance networks" *Social Networks* 61: 1-10. doi:10.1016/j.socnet.2019.08.002

See Also

Other motifs: [motif_diffusion](#), [motif_net](#), [motif_node](#)

Examples

```
# node_by_brokerage(ison_networkers, "Discipline")
# net_by_brokerage(ison_networkers, "Discipline")
node_brokering_exclusivity(ison_networkers, "Discipline")
```

motif_diffusion

Motifs of diffusion

Description

- `net_by_hazard()` measures the hazard rate or instantaneous probability that nodes will adopt/become infected at that time.
- `node_by_exposure()` produces a motif matrix of nodes' exposure to infection/adoption by time step.

Usage

```
node_by_exposure(.data)
```

```
net_by_hazard(.data)
```

Arguments

- `.data` An object of a manynet-consistent class:
- matrix (adjacency or incidence) from `{base}` R
 - edgelist, a data frame from `{base}` R or tibble from `{tibble}`
 - igraph, from the `{igraph}` package
 - network, from the `{network}` package
 - tbl_graph, from the `{tidygraph}` package

Hazard rate

The hazard rate is the instantaneous probability of adoption/infection at each time point (Allison 1984). In survival analysis, hazard rate is formally defined as:

$$\lambda(t) = \lim_{h \rightarrow +0} \frac{F(t+h) - F(t)}{h} \frac{1}{1 - F(t)}$$

By approximating $h = 1$, we can rewrite the equation as

$$\lambda(t) = \frac{F(t+1) - F(t)}{1 - F(t)}$$

If we estimate $F(t)$, the probability of not having adopted the innovation in time t , from the proportion of adopters in that time, such that $F(t) \sim q_t/n$, we now have (ultimately for $t > 1$):

$$\lambda(t) = \frac{q_{t+1}/n - q_t/n}{1 - q_t/n} = \frac{q_{t+1} - q_t}{n - q_t} = \frac{q_t - q_{t-1}}{n - q_{t-1}}$$

where q_i is the number of adopters in time t , and n is the number of vertices in the graph.

The shape of the hazard rate indicates the pattern of new adopters over time. Rapid diffusion with convex cumulative adoption curves will have hazard functions that peak early and decay over time. Slow concave cumulative adoption curves will have hazard functions that are low early and rise over time. Smooth hazard curves indicate constant adoption whereas those that oscillate indicate variability in adoption behavior over time.

Source

```
{netdiffuseR}
```

References

On hazard rates:

- Allison, Paul D. 1984. *Event history analysis: Regression for longitudinal event data*. London: Sage Publications. doi:10.4135/9781412984195
- Wooldridge, Jeffrey M. 2010. *Econometric Analysis of Cross Section and Panel Data* (2nd ed.). Cambridge: MIT Press.

See Also

Other motifs: [motif_brokerage](#), [motif_net](#), [motif_node](#)

Examples

```
node_by_exposure(play_diffusion(create_tree(12)))
# To calculate the hazard rates at each time point
smeg <- generate_smallworld(15, 0.025)
net_by_hazard(play_diffusion(smeg, transmissibility = 0.3))
```

motif_net

Motifs at the network level

Description

These functions include ways to take a census of the graphlets in a network:

- `net_by_dyad()` returns a census of dyad motifs in a network.
- `net_by_triad()` returns a census of triad motifs in a network.
- `net_by_tetrad()` returns a census of tetrad motifs in a network.
- `net_by_mixed()` returns a census of triad motifs that span a one-mode and a two-mode network.

See also [graph classes](#).

Usage

```
net_by_dyad(.data)

net_by_triad(.data)

net_by_tetrad(.data)

net_by_mixed(.data, object2)
```

Arguments

.data	An object of a manynet-consistent class: <ul style="list-style-type: none"> • matrix (adjacency or incidence) from {base} R • edgelist, a data frame from {base} R or tibble from {tibble} • igraph, from the {igraph} package • network, from the {network} package • tbl_graph, from the {tidygraph} package
object2	A second, two-mode migraph-consistent object.

Tetrad census

The tetrad census counts the number of four-node configurations in the network. The function returns a matrix with a special naming convention:

- E4 (aka co-K4): This is an empty set of four nodes; no ties
- I4 (aka co-diamond): This is a set of four nodes with just one tie
- H4 (aka co-C4): This set of four nodes includes two non-adjacent ties
- L4 (aka co-paw): This set of four nodes includes two adjacent ties
- D4 (aka co-claw): This set of four nodes includes three adjacent ties, in the form of a triangle with one isolate
- U4 (aka P4, four-actor line): This set of four nodes includes three ties arranged in a line
- Y4 (aka claw): This set of four nodes includes three ties all adjacent to a single node
- P4 (aka paw, kite): This set of four nodes includes four ties arranged as a triangle with an extra tie hanging off of one of the nodes
- C4 (aka bifan): This is a symmetric box or 4-cycle or set of shared choices
- Z4 (aka diamond): This resembles C4 but with an extra tie cutting across the box
- X4 (aka K4): This resembles C4 but with two extra ties cutting across the box; a realisation of all possible ties

Graphs of these motifs can be shown using `plot(net_by_tetrad(ison_southern_women))`.

Source

Alejandro Espinosa 'netmem'

References**On the dyad census:**

Holland, Paul W., and Samuel Leinhardt. 1970. "A Method for Detecting Structure in Sociometric Data". *American Journal of Sociology*, 76: 492-513. doi:10.1016/B9780124424500.500286

Wasserman, Stanley, and Katherine Faust. 1994. "Social Network Analysis: Methods and Applications". Cambridge: Cambridge University Press.

On the triad census:

Davis, James A., and Samuel Leinhardt. 1967. "The Structure of Positive Interpersonal Relations in Small Groups." 55.

On the tetrad census:

Ortmann, Mark, and Ulrik Brandes. 2017. "Efficient Orbit-Aware Triad and Quad Census in Directed and Undirected Graphs." *Applied Network Science* 2(1):13. doi:10.1007/s41109017-00272.

McMillan, Cassie, and Diane Felmlee. 2020. "Beyond Dyads and Triads: A Comparison of Tetrads in Twenty Social Networks". *Social Psychology Quarterly* 83(4): 383-404. doi:10.1177/0190272520944151

On the mixed census:

Hollway, James, Alessandro Lomi, Francesca Pallotti, and Christoph Stadtfeld. 2017. "Multi-level Social Spaces: The Network Dynamics of Organizational Fields." *Network Science* 5(2): 187–212. doi:10.1017/nws.2017.8

See Also

Other motifs: [motif_brokerage](#), [motif_diffusion](#), [motif_node](#)

Examples

```
net_by_dyad(manynet::ison_algebra)
net_by_triad(manynet::ison_adolescents)
net_by_tetrad(ison_southern_women)
net_by_mixed(fict_marvel)
```

 motif_node

Motifs at the nodal level

Description

These functions include ways to take a census of the positions of nodes in a network:

- `node_by_tie()` returns a census of the ties in a network. For directed networks, out-ties and in-ties are bound together. For multiplex networks, the various types of ties are bound together.
- `node_by_triad()` returns a census of the triad configurations nodes are embedded in.
- `node_by_tetrad()` returns a census of nodes' positions in motifs of four nodes.
- `node_by_path()` returns the shortest path lengths of each node to every other node in the network.

Usage

```
node_by_tie(.data)

node_by_dyad(.data)

node_by_triad(.data)
```

```
node_by_tetrad(.data)
```

```
node_by_path(.data)
```

Arguments

- `.data` An object of a manynet-consistent class:
- matrix (adjacency or incidence) from `{base}` R
 - edgelist, a data frame from `{base}` R or tibble from `{tibble}`
 - igraph, from the `{igraph}` package
 - network, from the `{network}` package
 - tbl_graph, from the `{tidygraph}` package

Tetrad census

The nodal tetrad census counts the number of four-node configurations that each node is embedded in. The function returns a matrix with a special naming convention:

- E4 (aka co-K4): This is an empty set of four nodes; no ties
- I4 (aka co-diamond): This is a set of four nodes with just one tie
- H4 (aka co-C4): This set of four nodes includes two non-adjacent ties
- L4 (aka co-paw): This set of four nodes includes two adjacent ties
- D4 (aka co-claw): This set of four nodes includes three adjacent ties, in the form of a triangle with one isolate
- U4 (aka P4, four-actor line): This set of four nodes includes three ties arranged in a line
- Y4 (aka claw): This set of four nodes includes three ties all adjacent to a single node
- P4 (aka paw, kite): This set of four nodes includes four ties arranged as a triangle with an extra tie hanging off of one of the nodes
- C4 (aka bifan): This is a symmetric box or 4-cycle or set of shared choices
- Z4 (aka diamond): This resembles C4 but with an extra tie cutting across the box
- X4 (aka K4): This resembles C4 but with two extra ties cutting across the box; a realisation of all possible ties

Graphs of these motifs can be shown using `plot(node_by_tetrad(ison_southern_women))`.

References

On the dyad census:

Holland, Paul W., and Samuel Leinhardt. 1970. "A Method for Detecting Structure in Sociometric Data". *American Journal of Sociology*, 76: 492-513. doi:10.1016/B9780124424500.500286

On the triad census:

Davis, James A., and Samuel Leinhardt. 1967. "The Structure of Positive Interpersonal Relations in Small Groups." 55.

On the tetrad census:

Ortmann, Mark, and Ulrik Brandes. 2017. "Efficient Orbit-Aware Triad and Quad Census in Directed and Undirected Graphs." *Applied Network Science* 2(1):13. doi:10.1007/s41109017-00272.

McMillan, Cassie, and Diane Felmlee. 2020. "Beyond Dyads and Triads: A Comparison of Tetrads in Twenty Social Networks". *Social Psychology Quarterly* 83(4): 383-404. doi:10.1177/0190272520944151

On paths:

Dijkstra, Edsger W. 1959. "A note on two problems in connexion with graphs". *Numerische Mathematik* 1, 269-71. doi:10.1007/BF01386390.

Opsahl, Tore, Filip Agneessens, and John Skvoretz. 2010. "Node centrality in weighted networks: Generalizing degree and shortest paths". *Social Networks* 32(3): 245-51. doi:10.1016/j.socnet.2010.03.006.

See Also

Other motifs: [motif_brokerage](#), [motif_diffusion](#), [motif_net](#)

Examples

```
task_eg <- to_named(to_uniplex(ison_algebra, "tasks"))
(tie_cen <- node_by_tie(task_eg))
node_by_dyad(ison_networkers)
(triad_cen <- node_by_triad(task_eg))
node_by_tetrad(ison_southern_women)
node_by_path(ison_adolescents)
node_by_path(ison_southern_women)
```

tutorials

Open and extract code from tutorials

Description

These functions make it easy to use the tutorials in the {manynet} and {migraph} packages:

- `run_tute()` runs a {learnr} tutorial from either the {manynet} or {migraph} packages, wraps `learnr::run_tutorial()` with some convenience.
- `extract_tute()` extracts and opens just the solution code from a {manynet} or {migraph} tutorial, saving the .R script to the current working directory.

Usage

```
run_tute(tute)
```

```
extract_tute(tute)
```

Arguments

`tute` String, name of the tutorial (e.g. "tutorial2").

Index

- * **centrality**
 - measure_central_between, 110
 - measure_central_close, 113
 - measure_central_degree, 117
 - measure_central_eigen, 121
- * **datasets**
 - fict_actually, 5
 - fict_friends, 6
 - fict_greys, 7
 - fict_lotr, 8
 - fict_marvel, 9
 - fict_potter, 11
 - fict_starwars, 12
 - fict_thrones, 14
 - irps_911, 16
 - irps_blogs, 17
 - irps_books, 18
 - irps_nuclear, 20
 - irps_revere, 21
 - irps_usgeo, 22
 - irps_wwi, 23
 - ison_adolescents, 24
 - ison_algebra, 25
 - ison_brandes, 26
 - ison_dolphins, 27
 - ison_emotions, 28
 - ison_hightech, 29
 - ison_judo_moves, 31
 - ison_karateka, 32
 - ison_koenigsberg, 33
 - ison_laterals, 34
 - ison_lawfirm, 37
 - ison_monks, 38
 - ison_networkers, 39
 - ison_physicians, 41
 - ison_southern_women, 44
- * **diffusion**
 - make_play, 55
 - measure_diffusion_infection, 128
 - measure_diffusion_net, 129
 - measure_diffusion_node, 132
 - member_diffusion, 156
- * **makes**
 - make_cran, 45
 - make_create, 47
 - make_ego, 49
 - make_explicit, 50
 - make_learning, 51
 - make_motifs, 54
 - make_play, 55
 - make_random, 58
 - make_read, 60
 - make_stochastic, 62
 - make_write, 64
- * **marking**
 - mark_features, 97
 - mark_format, 99
 - mark_is, 100
- * **marks**
 - mark_diff, 96
 - mark_nodes, 102
 - mark_select, 104
 - mark_tie_select, 106
 - mark_ties, 105
 - mark_triangles, 107
- * **measures**
 - measure_attributes_nodes, 108
 - measure_attributes_ties, 109
 - measure_central_between, 110
 - measure_central_close, 113
 - measure_central_degree, 117
 - measure_central_eigen, 121
 - measure_closure, 124
 - measure_cohesion, 126
 - measure_diffusion_infection, 128
 - measure_diffusion_net, 129
 - measure_diffusion_node, 132
 - measure_features, 134

- measure_heterogeneity, 138
- measure_hierarchy, 141
- measure_holes, 143
- measure_periods, 145
- measure_properties, 146
- member_diffusion, 156
- * memberships**
 - mark_core, 93
 - member_brokerage, 147
 - member_cliques, 148
 - member_community_hier, 150
 - member_community_non, 152
 - member_components, 155
 - member_equivalence, 158
- * models**
 - make_learning, 51
 - make_play, 55
- * modifications**
 - manip_as, 65
 - manip_correlation, 70
 - manip_deformat, 71
 - manip_direction, 72
 - manip_from, 74
 - manip_levels, 76
 - manip_miss, 77
 - manip_nodes, 78
 - manip_paths, 80
 - manip_permutation, 83
 - manip_preformat, 84
 - manip_project, 85
 - manip_reformat, 87
 - manip_scope, 88
 - manip_split, 90
 - manip_ties, 92
- * motifs**
 - motif_brokerage, 162
 - motif_diffusion, 163
 - motif_net, 165
 - motif_node, 167
- add_changes (manip_changes), 68
- add_info (manip_info), 75
- add_node_attribute (manip_nodes), 78
- add_nodes (manip_nodes), 78
- add_tie_attribute (manip_ties), 92
- add_ties (manip_ties), 92
- apply_changes (manip_changes), 68
- arrange_ties (manip_ties), 92
- as, 46, 49, 62, 65
- as_changelist (manip_as), 65
- as_diffnet (manip_as), 65
- as_diffusion (manip_as), 65
- as_edgelist (manip_as), 65
- as_graphAM (manip_as), 65
- as_igraph (manip_as), 65
- as_matrix (manip_as), 65
- as_network (manip_as), 65
- as_nodelist (manip_as), 65
- as_siena (manip_as), 65
- as_tidygraph (manip_as), 65
- bind_node_attributes (manip_nodes), 78
- bind_ties (manip_ties), 92
- clear_glossary (glossary), 15
- cluster_concor (model_cluster), 160
- cluster_cosine (model_cluster), 160
- cluster_hierarchical (model_cluster), 160
- collect_changes (manip_changes), 68
- create_components (make_create), 47
- create_core (make_create), 47
- create_cycle (make_create), 47
- create_degree (make_create), 47
- create_ego (make_ego), 49
- create_empty (make_create), 47
- create_explicit (make_explicit), 50
- create_filled (make_create), 47
- create_lattice (make_create), 47
- create_motifs (make_motifs), 54
- create_ring (make_create), 47
- create_star (make_create), 47
- create_tree (make_create), 47
- create_wheel (make_create), 47
- create_windmill (make_create), 47
- data_overview, 4
- delete_changes (manip_changes), 68
- delete_nodes (manip_nodes), 78
- delete_ties (manip_ties), 92
- describe_changes (make_mnet), 53
- describe_network (make_mnet), 53
- describe_nodes (make_mnet), 53
- describe_ties (make_mnet), 53
- extract_tute (tutorials), 169
- fict_actually, 5

- fict_friends, 6
- fict_greys, 7
- fict_lotr, 8
- fict_marvel, 9
- fict_potter, 11
- fict_starwars, 12
- fict_thrones, 14
- filter_changes (manip_changes), 68
- filter_nodes (manip_nodes), 78
- filter_ties (manip_ties), 92
- from_egos (manip_from), 74
- from_slices (manip_from), 74
- from_subgraphs (manip_from), 74
- from_ties (manip_from), 74
- from_waves (manip_from), 74

- generate_citations (make_stochastic), 62
- generate_configuration (make_random), 58
- generate_fire (make_stochastic), 62
- generate_islands (make_stochastic), 62
- generate_man (make_random), 58
- generate_permutation (make_random), 58
- generate_random (make_random), 58
- generate_scalefree (make_stochastic), 62
- generate_smallworld (make_stochastic), 62
- generate_utilities (make_random), 58
- gloss (glossary), 15
- glossary, 15

- interface, 15
- irps_911, 16
- irps_blogs, 17
- irps_books, 18
- irps_nuclear, 20
- irps_revere, 21
- irps_usgeo, 22
- irps_wwi, 23
- is_acyclic (mark_features), 97
- is_aperiodic (mark_features), 97
- is_attributed (mark_format), 99
- is_changing (mark_is), 100
- is_complex (mark_format), 99
- is_connected (mark_features), 97
- is_directed (mark_format), 99
- is_dynamic (mark_is), 100
- is_edgelist (mark_is), 100
- is_eulerian (mark_features), 97
- is_graph (mark_is), 100
- is_labelled (mark_format), 99
- is_list (mark_is), 100
- is_longitudinal (mark_is), 100
- is_manynet (mark_is), 100
- is_multiplex (mark_format), 99
- is_perfect_matching (mark_features), 97
- is_signed (mark_format), 99
- is_twomode (mark_format), 99
- is_uniplex (mark_format), 99
- is_weighted (mark_format), 99
- ison_adolescents, 24
- ison_algebra, 25
- ison_brandes, 26
- ison_dolphins, 27
- ison_emotions, 28
- ison_hightech, 29
- ison_judo_moves, 31
- ison_karateka, 32
- ison_koenigsberg, 33
- ison_laterals, 34
- ison_lawfirm, 37
- ison_monks, 38
- ison_networkers, 39
- ison_physicians, 41
- ison_southern_women, 44

- join_nodes (manip_nodes), 78
- join_ties (manip_ties), 92

- k_elbow (model_kselect), 161
- k_silhouette (model_kselect), 161
- k_strict (model_kselect), 161

- make_cran, 45, 49–52, 55, 57, 60, 62, 64, 65
- make_create, 46, 47, 50–52, 55, 57, 60, 62, 64, 65
- make_ego, 46, 49, 49, 51, 52, 55, 57, 60, 62, 64, 65
- make_explicit, 46, 49, 50, 50, 52, 55, 57, 60, 62, 64, 65
- make_learning, 46, 49–51, 51, 55, 57, 60, 62, 64, 65
- make_mnet, 53
- make_motifs, 46, 49–52, 54, 57, 60, 62, 64, 65
- make_play, 46, 49–52, 55, 55, 60, 62, 64, 65, 129, 131, 133, 157
- make_random, 46, 49–52, 55, 57, 58, 62, 64, 65
- make_read, 46, 49–52, 55, 57, 60, 60, 64, 65

- make_stochastic*, 46, 49–52, 55, 57, 60, 62, 62, 65
make_write, 46, 49–52, 55, 57, 60, 62, 64, 64
manip_as, 65, 70, 72–74, 77, 78, 80, 83, 85, 86, 88, 89, 91, 93
manip_changes, 68
manip_correlation, 68, 70, 72–74, 77, 78, 80, 83, 85, 86, 88, 89, 91, 93
manip_deformat, 68, 70, 71, 73, 74, 77, 78, 80, 83, 85, 86, 88, 89, 91, 93
manip_direction, 68, 70, 72, 72, 74, 77, 78, 80, 83, 85, 86, 88, 89, 91, 93
manip_from, 68, 70, 72, 73, 74, 77, 78, 80, 83, 85, 86, 88, 89, 91, 93
manip_info, 75
manip_levels, 68, 70, 72–74, 76, 78, 80, 83, 85, 86, 88, 89, 91, 93
manip_miss, 68, 70, 72–74, 77, 77, 80, 83, 85, 86, 88, 89, 91, 93
manip_nodes, 68, 70, 72–74, 77, 78, 78, 83, 85, 86, 88, 89, 91, 93
manip_paths, 68, 70, 72–74, 77, 78, 80, 80, 83, 85, 86, 88, 89, 91, 93
manip_permutation, 68, 70, 72–74, 77, 78, 80, 83, 83, 85, 86, 88, 89, 91, 93
manip_preformat, 68, 70, 72–74, 77, 78, 80, 83, 84, 86, 88, 89, 91, 93
manip_project, 68, 70, 72–74, 77, 78, 80, 83, 85, 85, 88, 89, 91, 93
manip_reformat, 68, 70, 72–74, 77, 78, 80, 83, 85, 86, 87, 89, 91, 93
manip_scope, 68, 70, 72–74, 77, 78, 80, 83, 85, 86, 88, 88, 91, 93
manip_split, 68, 70, 72–74, 77, 78, 80, 83, 85, 86, 88, 89, 90, 93
manip_ties, 68, 70, 72–74, 77, 78, 80, 83, 85, 86, 88, 89, 91, 92
mark_core, 93, 148, 149, 151, 155, 156, 159
mark_diff, 96, 103, 104, 106–108
mark_features, 97, 100, 101
mark_format, 98, 99, 101
mark_is, 98, 100, 100
mark_nodes, 97, 102, 104, 106–108
mark_select, 97, 103, 104, 106–108
mark_tie_select, 97, 103, 104, 106, 106, 108
mark_ties, 97, 103, 104, 105, 107, 108
mark_triangles, 97, 103, 104, 106, 107, 107
measure_attributes_nodes, 108, 110, 113, 117, 120, 124, 126, 127, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_attributes_ties, 109, 109, 113, 117, 120, 124, 126, 127, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_central_between, 109, 110, 110, 117, 120, 124, 126, 127, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_central_close, 109, 110, 113, 113, 120, 124, 126, 127, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_central_degree, 109, 110, 113, 117, 117, 124, 126, 127, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_central_eigen, 109, 110, 113, 117, 120, 121, 126, 127, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_closure, 109, 110, 113, 117, 120, 124, 124, 127, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_cohesion, 109, 110, 113, 117, 120, 124, 126, 126, 129, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_diffusion_infection, 57, 109, 110, 113, 117, 120, 124, 126, 127, 128, 131, 133, 137, 141, 142, 144, 146, 147, 157
measure_diffusion_net, 57, 109, 110, 113, 117, 120, 124, 126, 127, 129, 129, 133, 137, 141, 142, 144, 146, 147, 157
measure_diffusion_node, 57, 109, 110, 113, 117, 120, 124, 126, 127, 129, 131, 132, 137, 141, 142, 144, 146, 147, 157
measure_features, 109, 110, 113, 117, 120, 124, 126, 127, 129, 131, 133, 134, 141, 142, 144, 146, 147, 157
measure_heterogeneity, 109, 110, 113, 117, 120, 124, 126, 127, 129, 131, 133, 137, 138, 142, 144, 146, 147, 157
measure_hierarchy, 109, 110, 113, 117, 120, 124, 126, 127, 129, 131, 133, 137, 141, 141, 144, 146, 147, 157

- measure_holes, [109](#), [110](#), [113](#), [117](#), [120](#), [124](#), [126](#), [127](#), [129](#), [131](#), [133](#), [137](#), [141](#), [142](#), [143](#), [146](#), [147](#), [157](#)
- measure_periods, [109](#), [110](#), [113](#), [117](#), [120](#), [124](#), [126](#), [127](#), [129](#), [131](#), [133](#), [137](#), [141](#), [142](#), [144](#), [145](#), [147](#), [157](#)
- measure_properties, [109](#), [110](#), [113](#), [117](#), [120](#), [124](#), [126](#), [127](#), [129](#), [131](#), [133](#), [137](#), [141](#), [142](#), [144](#), [146](#), [146](#), [157](#)
- member_brokerage, [95](#), [147](#), [149](#), [151](#), [155](#), [156](#), [159](#)
- member_cliques, [95](#), [148](#), [148](#), [151](#), [155](#), [156](#), [159](#)
- member_community_hier, [95](#), [148](#), [149](#), [150](#), [155](#), [156](#), [159](#)
- member_community_non, [95](#), [148](#), [149](#), [151](#), [152](#), [156](#), [159](#)
- member_components, [95](#), [148](#), [149](#), [151](#), [155](#), [155](#), [159](#)
- member_diffusion, [57](#), [109](#), [110](#), [113](#), [117](#), [120](#), [124](#), [126](#), [127](#), [129](#), [131](#), [133](#), [137](#), [141](#), [142](#), [144](#), [146](#), [147](#), [156](#)
- member_equivalence, [95](#), [148](#), [149](#), [151](#), [155](#), [156](#), [158](#)
- model_cluster, [160](#)
- model_kselect, [161](#)
- motif_brokerage, [162](#), [165](#), [167](#), [169](#)
- motif_diffusion, [163](#), [163](#), [167](#), [169](#)
- motif_net, [163](#), [165](#), [165](#), [169](#)
- motif_node, [163](#), [165](#), [167](#), [167](#)
- mutate (manip_nodes), [78](#)
- mutate_changes (manip_changes), [68](#)
- mutate_net (manip_info), [75](#)
- mutate_nodes (manip_nodes), [78](#)
- mutate_ties (manip_ties), [92](#)

- na_to_mean (manip_miss), [77](#)
- na_to_zero (manip_miss), [77](#)
- net_adhesion (measure_cohesion), [126](#)
- net_assortativity (measure_heterogeneity), [138](#)
- net_balance (measure_features), [134](#)
- net_betweenness (measure_central_between), [110](#)
- net_by_brokerage (motif_brokerage), [162](#)
- net_by_dyad (motif_net), [165](#)
- net_by_hazard (motif_diffusion), [163](#)
- net_by_hierarchy (measure_hierarchy), [141](#)
- net_by_mixed (motif_net), [165](#)
- net_by_tetrad (motif_net), [165](#)
- net_by_triad (motif_net), [165](#)
- net_change (measure_periods), [145](#)
- net_closeness (measure_central_close), [113](#)
- net_cohesion (measure_cohesion), [126](#)
- net_components (measure_cohesion), [126](#)
- net_congruency (measure_closure), [124](#)
- net_connectedness (measure_hierarchy), [141](#)
- net_core (measure_features), [134](#)
- net_correlation (measure_periods), [145](#)
- net_degree (measure_central_degree), [117](#)
- net_density (measure_cohesion), [126](#)
- net_diameter (measure_cohesion), [126](#)
- net_dims (measure_properties), [146](#)
- net_diversity (measure_heterogeneity), [138](#)
- net_efficiency (measure_hierarchy), [141](#)
- net_eigenvector (measure_central_eigen), [121](#)
- net_equivalency (measure_closure), [124](#)
- net_equivalency(), [137](#)
- net_factions (measure_features), [134](#)
- net_harmonic (measure_central_close), [113](#)
- net_heterophily (measure_heterogeneity), [138](#)
- net_homophily (measure_heterogeneity), [138](#)
- net_immunity (measure_diffusion_net), [129](#)
- net_indegree (measure_central_degree), [117](#)
- net_independence (measure_cohesion), [126](#)
- net_infection_complete (measure_diffusion_infection), [128](#)
- net_infection_peak (measure_diffusion_infection), [128](#)
- net_infection_total (measure_diffusion_infection), [128](#)
- net_length (measure_cohesion), [126](#)
- net_modularity (measure_features), [134](#)
- net_name (measure_properties), [146](#)

- net_node_attributes
 - (measure_properties), 146
- net_node_names (measure_properties), 146
- net_nodes (measure_properties), 146
- net_outdegree (measure_central_degree), 117
- net_reach (measure_central_close), 113
- net_reciprocity (measure_closure), 124
- net_recovery (measure_diffusion_net), 129
- net_reproduction
 - (measure_diffusion_net), 129
- net_richclub (measure_features), 134
- net_richness (measure_heterogeneity), 138
- net_scalefree (measure_features), 134
- net_smallworld (measure_features), 134
- net_spatial (measure_heterogeneity), 138
- net_stability (measure_periods), 145
- net_strength (measure_cohesion), 126
- net_tie_attributes
 - (measure_properties), 146
- net_tie_names (measure_properties), 146
- net_ties (measure_properties), 146
- net_toughness (measure_cohesion), 126
- net_transitivity (measure_closure), 124
- net_transitivity(), 137
- net_transmissibility
 - (measure_diffusion_net), 129
- net_upperbound (measure_hierarchy), 141
- net_waves (measure_periods), 145
- node_adoption_time
 - (measure_diffusion_node), 132
- node_alpha (measure_central_eigen), 121
- node_attribute
 - (measure_attributes_nodes), 108
- node_authority (measure_central_eigen), 121
- node_betweenness
 - (measure_central_between), 110
- node_bridges (measure_holes), 143
- node_brokering_activity
 - (motif_brokerage), 162
- node_brokering_exclusivity
 - (motif_brokerage), 162
- node_by_brokerage (motif_brokerage), 162
- node_by_dyad (motif_node), 167
- node_by_exposure (motif_diffusion), 163
- node_by_path (motif_node), 167
- node_by_tetrad (motif_node), 167
- node_by_tie (motif_node), 167
- node_by_triad (motif_node), 167
- node_closeness (measure_central_close), 113
- node_constraint (measure_holes), 143
- node_coreness (mark_core), 93
- node_deg (measure_central_degree), 117
- node_degree (measure_central_degree), 117
- node_distance (measure_central_close), 113
- node_diversity (measure_heterogeneity), 138
- node_eccentricity
 - (measure_central_close), 113
- node_efficiency (measure_holes), 143
- node_effsize (measure_holes), 143
- node_eigenvector
 - (measure_central_eigen), 121
- node_equivalency (measure_closure), 124
- node_exposure (measure_diffusion_node), 132
- node_flow (measure_central_between), 110
- node_harmonic (measure_central_close), 113
- node_heterophily
 - (measure_heterogeneity), 138
- node_hierarchy (measure_holes), 143
- node_homophily (measure_heterogeneity), 138
- node_hub (measure_central_eigen), 121
- node_in_adopter (member_diffusion), 156
- node_in_automorphic
 - (member_equivalence), 158
- node_in_betweenness
 - (member_community_hier), 150
- node_in_brokering (member_brokerage), 147
- node_in_community
 - (member_community_non), 152
- node_in_component (member_components), 155
- node_in_core (mark_core), 93
- node_in_eigen (member_community_hier), 150
- node_in_equivalence

- (member_equivalence), 158
- node_in_fluid (member_community_non), 152
- node_in_greedy (member_community_hier), 150
- node_in_infomap (member_community_non), 152
- node_in_leiden (member_community_non), 152
- node_in_louvain (member_community_non), 152
- node_in_optimal (member_community_non), 152
- node_in_partition (member_community_non), 152
- node_in_regular (member_equivalence), 158
- node_in_roulette (member_cliques), 148
- node_in_spinglass (member_community_non), 152
- node_in_strong (member_components), 155
- node_in_structural (member_equivalence), 158
- node_in_walktrap (member_community_hier), 150
- node_in_weak (member_components), 155
- node_indegree (measure_central_degree), 117
- node_induced (measure_central_between), 110
- node_information (measure_central_close), 113
- node_is_core (mark_core), 93
- node_is_cutpoint (mark_nodes), 102
- node_is_exposed (mark_diff), 96
- node_is_fold (mark_nodes), 102
- node_is_independent (mark_nodes), 102
- node_is_infected (mark_diff), 96
- node_is_isolate (mark_nodes), 102
- node_is_latent (mark_diff), 96
- node_is_max (mark_select), 104
- node_is_mean (mark_select), 104
- node_is_mentor (mark_nodes), 102
- node_is_min (mark_select), 104
- node_is_mode (measure_attributes_nodes), 108
- node_is_neighbor (mark_nodes), 102
- node_is_pendant (mark_nodes), 102
- node_is_random (mark_select), 104
- node_is_recovered (mark_diff), 96
- node_is_universal (mark_core), 93
- node_kcoreness (mark_core), 93
- node_leverage (measure_central_degree), 117
- node_multidegree (measure_central_degree), 117
- node_names (measure_attributes_nodes), 108
- node_neighbours_degree (measure_holes), 143
- node_outdegree (measure_central_degree), 117
- node_pagerank (measure_central_eigen), 121
- node_posneg (measure_central_degree), 117
- node_power (measure_central_eigen), 121
- node_randomwalk (measure_central_close), 113
- node_reach (measure_central_close), 113
- node_reciprocity (measure_closure), 124
- node_recovery (measure_diffusion_node), 132
- node_redundancy (measure_holes), 143
- node_richness (measure_heterogeneity), 138
- node_stress (measure_central_between), 110
- node_subgraph (measure_central_eigen), 121
- node_thresholds (measure_diffusion_node), 132
- node_transitivity (measure_closure), 124
- node_vitality (measure_central_close), 113
- play_diffusion (make_play), 55
- play_learning (make_learning), 51
- play_seggregation (make_learning), 51
- print_mnet (make_mnet), 53
- print_all (make_mnet), 53
- print_glossary (glossary), 15
- read_cran (make_cran), 45
- read_dynetml (make_read), 60
- read_edgelist (make_read), 60
- read_gdf (make_read), 60

- read_gml (make_read), 60
- read_graphml (make_read), 60
- read_matrix (make_read), 60
- read_nodelist (make_read), 60
- read_pajek (make_read), 60
- read_pkg (make_cran), 45
- read_ucinet (make_read), 60
- rename (manip_nodes), 78
- rename_nodes (manip_nodes), 78
- rename_ties (manip_ties), 92
- run_tute (tutorials), 169

- select (manip_nodes), 78
- select_changes (manip_changes), 68
- select_nodes (manip_nodes), 78
- select_ties (manip_ties), 92
- snet_abort (interface), 15
- snet_info (interface), 15
- snet_minor_info (interface), 15
- snet_progress_along (interface), 15
- snet_progress_nodes (interface), 15
- snet_progress_seq (interface), 15
- snet_progress_step (interface), 15
- snet_prompt (interface), 15
- snet_success (interface), 15
- snet_unavailable (interface), 15
- snet_warn (interface), 15
- summarise_ties (manip_ties), 92

- table_data (data_overview), 4
- tie_attribute
 - (measure_attributes_ties), 109
- tie_betweenness
 - (measure_central_between), 110
- tie_closeness (measure_central_close), 113
- tie_cohesion (measure_holes), 143
- tie_degree (measure_central_degree), 117
- tie_eigenvector
 - (measure_central_eigen), 121
- tie_is_bridge (mark_ties), 105
- tie_is_cyclical (mark_triangles), 107
- tie_is_feedback (mark_ties), 105
- tie_is_forbidden (mark_triangles), 107
- tie_is_imbalanced (mark_triangles), 107
- tie_is_loop (mark_ties), 105
- tie_is_max (mark_tie_select), 106
- tie_is_min (mark_tie_select), 106
- tie_is_multiple (mark_ties), 105
- tie_is_path (mark_ties), 105
- tie_is_random (mark_tie_select), 106
- tie_is_reciprocated (mark_ties), 105
- tie_is_simmelian (mark_triangles), 107
- tie_is_transitive (mark_triangles), 107
- tie_is_triangular (mark_triangles), 107
- tie_is_triplet (mark_triangles), 107
- tie_is_twomode
 - (measure_attributes_ties), 109
- tie_signs (measure_attributes_ties), 109
- tie_weights (measure_attributes_ties), 109

- to_acyclic (manip_direction), 72
- to_anti (manip_reformat), 87
- to_blocks (manip_scope), 88
- to_components (manip_split), 90
- to_correlation (manip_correlation), 70
- to_cosine (manip_correlation), 70
- to_directed (manip_direction), 72
- to_dominating (manip_paths), 80
- to_ego (manip_scope), 88
- to_egos (manip_split), 90
- to_eulerian (manip_paths), 80
- to_giant (manip_scope), 88
- to_matching (manip_paths), 80
- to_mentoring (manip_paths), 80
- to_mode1 (manip_project), 85
- to_mode2 (manip_project), 85
- to_multilevel (manip_levels), 76
- to_named (manip_preformat), 84
- to_no_isolates (manip_scope), 88
- to_no_missing (manip_scope), 88
- to_onemode (manip_levels), 76
- to_permuted (manip_permutation), 83
- to_reciprocated (manip_direction), 72
- to_redirected (manip_direction), 72
- to_signed (manip_preformat), 84
- to_simplex (manip_deformat), 71
- to_slices (manip_split), 90
- to_subgraph (manip_scope), 88
- to_subgraphs (manip_split), 90
- to_ties (manip_project), 85
- to_time (manip_scope), 88
- to_time(), 69
- to_tree (manip_paths), 80
- to_twomode (manip_levels), 76
- to_undirected (manip_direction), 72
- to_undirected(), 110, 113, 118, 120, 121

to_uniplex (manip_deformat), 71
to_unnamed (manip_deformat), 71
to_unsigned (manip_deformat), 71
to_unweighted (manip_deformat), 71
to_unweighted(), 120
to_waves (manip_split), 90
to_weighted (manip_preformat), 84
tutorials, 169

write_edgelist (make_write), 64
write_graphml (make_write), 64
write_matrix (make_write), 64
write_nodelist (make_write), 64
write_pajek (make_write), 64
write_ucinet (make_write), 64