Package ‘netseg’

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Title Measures of Network Segregation and Homophily

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Description Segregation is a network-level property such that edges between predefined groups of vertices are relatively less likely. Network homophily is a individual-level tendency to form relations with people who are similar on some attribute (e.g. gender, music taste, social status, etc.). In general homophily leads to segregation, but segregation might arise without homophily. This package implements descriptive indices measuring homophily/segregation. It is a computational companion to Bojanowski & Corten (2014) <doi:10.1016/j.socnet.2014.04.001>.

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- netseg-package
- assort
- Catania
Description

Segregation is a network-level property such that edges between predefined groups of vertices are relatively less likely. Network homophily is an individual-level tendency to form relations with people who are similar on some attribute (e.g., gender, music taste, social status, etc.). In general, homophily leads to segregation, but segregation might arise without homophily. This package implements descriptive indices measuring homophily/segregation. It is a computational companion to Bojanowski & Corten (2014) <doi:10.1016/j.socnet.2014.04.001>.

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References


See Also

Useful links:

- Package homepage: https://mbojan.github.io/netseg
- Bug reports: https://github.com/mbojan/netseg/issues
Description

Assortativity coefficient is a measure of segregation for social networks due to Newman & Girvan (2002).

Usage

```r
assort(object, ...)  
## S3 method for class 'table'  
assort(object, ...)  
## S3 method for class 'igraph'  
assort(object, vattr, ...)  
## Default S3 method:  
assort(object, ...)  
```

Arguments

- `object` R object, see available methods
- `...` other arguments to/from other methods
- `vattr` character, name of the vertex attribute for which the measure is to be calculated

Details

The measure evaluates the relative prevalence of within-group ties. It is based on the contact layer of the mixing matrix.

Assortativity coefficient is 1 if all ties are within-group. The minimum can be negative, but not less than -1, and depends on the relative number of ties of nodes in different groups. If the network conforms to "proportionate mixing", the coefficient is 0.

If `object` is a table it is interpreted as a mixing matrix. Two-dimensional table is interpreted as a contact layer. Three-dimensional table is interpreted as a full mixing matrix $m_{ghy}$ cross-classifying all dyads, in which $g$ and $h$ correspond to group membership of ego and alter respectively. Layers $y = 1$ and $y = 2$ are assumed to be non-contact and contact layers respectively.

If `object` is of class "igraph" it is required to supply `vattr` with the name of the vertex attribute to calculate intermediate mixing matrix.

For any other classes, `object` is coerced to a table and the table method is called.

Value

Numeric value of the index.
References


See Also

Mixing matrices: mixingm()
Other segregation measures: coleman(), ei(), freeman(), gamix(), orwg(), smi(), ssi()

Examples

```r
assort(WhiteKinship, "gender")
assort(EF3, "type")

# Values of 'assort()' for full networks of different sizes
if( requireNamespace("igraph", quietly = TRUE) ) {
  f <- function(n) {
    gfull <- igraph::make_full_graph(n, directed=FALSE)
    igraph::V(gfull)$type <- rep(1:2, length = igraph::vcount(gfull))
    assort(gfull, "type")
  }
  set.seed(1)
  x <- sort(sample(5:100, 25) * 2)
  y <- sapply(x, f)
  plot(x, y, type="o",
       xlab="Network size", ylab="Assortativity coefficient",
       main="Assortativity coef. for full networks of different sizes")
}
```

Catania

Pattern of sexual contacts in AMEN study

Description


Usage

Catania

Format

Four-by-four numeric matrix with dimnames.
## female
## male  black  hispanic  other  white
##    black  506     32     26     69
##  hispanic  23    308     38    114
##  other  10     14     32     47
##   white  26     46     68    599

### Source


### References

Catania et al. (1992) "The population-based AMEN (AIDS in Multi-Ethnic Neighborhoods) study" *American Journal of Public Health* 82, 284-287


### Examples

data(Catania)

# assortativity
ep <- sum(Catania %*% Catania)
( sum(diag(Catania)) - ep ) / ( 1 - ep )

### Description

A directed network of ties "with whom do you like to play with?" collected in a school class of 9-year olds. The data comes from a study undertook by Educational Research Institute (Dolata 2014).

### Usage

Classroom

### Format

Object of class "igraph" with a directed network of size 26. Vertex attributes:

- gender – with values "Boy" or "Girl".
References


Description

Coleman's homophily index for directed networks.

Usage

coleman(object, ...)

## S3 method for class 'table'
coleman(object, gsizes = NULL, loops = FALSE, ...)

## S3 method for class 'igraph'
coleman(object, vattr, ...)

## Default S3 method:
coleman(object, ...)

Arguments

object R object, see Details for available methods

... other arguments passed to/from methods

gsizes numeric vector of group sizes

loops logical, whether loops are allowed

vattr character, vertex attribute

Details

Coleman's homophily index computes homophily scores for each group defined by a vertex attribute.

If object is a table it is interpreted as a mixing matrix. Two-dimensional table is interpreted as a contact layer. Three-dimensional table is interpreted as a full mixing matrix \( m_{ghy} \) cross-classifying all dyads, in which \( g \) and \( h \) correspond to group membership of ego and alter respectively. Layers \( y = 1 \) and \( y = 2 \) are assumed to be non-contact and contact layers respectively.

If object is of class "igraph" it is required to supply vattr with the name of the vertex attribute to calculate intermediate mixing matrix.
Value

Vector of numeric values of the index for each group

References


See Also

Other segregation measures: `assort()`, `ei()`, `freeman()`, `gamix()`, `orwg()`, `smi()`, `ssi()`

Examples

```r
if(requireNamespace("igraph", quietly = TRUE)) {
  # Converting networks to directed
  coleman(igraph::as.directed(WhiteKinship, "mutual"), "gender")
  coleman(igraph::as.directed(EF3, "mutual"), "race")
}
```

### Description

Artificial example data from Echenique & Fryer (2006) Figure III representing a city with black and white neighbourhoods.

### Usage

`EF3`

### Format

Object of class "igraph". An undirected network with vertex attributes:

- **name** – vertex names of the form "A1" in which letter and number indicate the position in the lattice
- **race** – values 1 or 2 indicate the two groups

### Details

This data is taken from Echenique & Fryer (2006, figure III). The data represent a fictional city composed of 30 neighborhoods that are either black or white.

### Source

Examples

```r
if(requireNamespace("igraph", quietly = TRUE)) {
  set.seed(1)
  plot(
    EF3,
    layout = igraph::layout.fruchterman.reingold,
    vertex.color = igraph::V(EF3)$type+1,
    vertex.label.family = "",
    sub = "Source: Echenique & Fryer (2006)",
    main = "Neighborhood racial segregation in a fictional city"
  )
}
```

---

**ei**

*Krackhard and Stern’s E-I index*

### Description

An index proposed by Krackhard and Stern (1988) to capture relative prevalence of between- and within-group ties. From that perspective it can be interpreted as a measure of network segregation.

### Usage

```r
ei(object, ...)
```

#### S3 method for class 'table'

```r
ei(object, ...)
```

#### S3 method for class 'igraph'

```r
ei(
  object,
  vattr,
  directed = is.directed(object),
  loops = any(is.loop(object)),
  ...
)
```

#### Default S3 method:

```r
ei(object, ...)
```

### Arguments

- **object**
  - R object, see Details for available methods
  - ... other arguments passed to/from other methods
- **vattr**
  - character scalar or vector of length equal to the size of `object`, vertex attribute for which mixing matrix is to be computed
- **directed**
  - logical whether the network is directed
- **loops**
  - logical, whether loops are allowed
Details

If object is a table it is interpreted as a mixing matrix. Two-dimensional table is interpreted as a contact layer. Three-dimensional table is interpreted as a full mixing matrix $m_{ghy}$ cross-classifying all dyads, in which $g$ and $h$ correspond to group membership of ego and alter respectively. Layers $y = 1$ and $y = 2$ are assumed to be non-contact and contact layers respectively.

If object is of class "igraph" it is required to supply vattr with the name of the vertex attribute to calculate intermediate mixing matrix.

Value

Numerical value of the E-I index.

References


See Also

Other segregation measures: assort(), coleman(), freeman(), gamix(), orwg(), smi(), ssi()

Examples

ei(WhiteKinship, "gender")

fold

Folding square matrices around the diagonal

Description

Fold a square matrix by collapsing lower triangle on upper triangle, or vice versa, through addition.

Usage

fold(x, direction = c("upper", "lower"))

Arguments

x

square numeric matrix

direction

character, one of "upper" or "lower", direction of folding

Details

By default, for direction="upper", the function takes the values in the lower triangle of x and adds them symmetrically to the values in the upper triangle. The values on the diagonal remain unchanged. The lower triangle is filled with 0s. If direction="lower" the upper triangle is collapsed on to the lower triangle.
Value

Square matrix of the same dim as x with the lower (upper) triangle folded onto the upper (lower) triangle.

See Also

upper.tri(), lower.tri(), symmetrize()

Examples

(m <- matrix(1:4, 2, 2))
(f1 <- fold(m))
(f2 <- fold(m, "lower"))

stopifnot( all.equal(diag(m), diag(f1)) )
stopifnot( all.equal(diag(m), diag(f2)) )
stopifnot( all.equal(f1[1,2], m[2,1] + m[1,2]) )
stopifnot( all.equal(f2[2,1], m[2,1] + m[1,2]) )

---

freeman

Generalized Freeman’s segregation index

Description

Calculate Freeman’s segregation index for undirected networks with arbitrary number of groups.

Usage

freeman(object, ...)

## S3 method for class 'table'
freeman(object, gsizes = NULL, loops = FALSE, ...)

## S3 method for class 'igraph'
freeman(object, vattr, gsizes = NULL, loops = any(is.loop(object)), ...)

## Default S3 method:
freeman(object, ...)

Arguments

object R object, see Details for available methods
...
other arguments passed to/from other methods
gsizes numeric, optional true distribution of types, see Details
loops logical, whether loops are allowed
vattr character scalar or any vector of length equal to vcount(object), name of the vertex attribute in object designating the groups or a vector with the attribute itself
Details

Freeman’s segregation index (Freeman, 1978) is designed to capture the extent to which the defined groups of vertices tend to have more edges with vertices from the same group than with other groups. Formally, the index compares the observed number of between-group ties with the number of between-group ties that would be expected if ties would be created randomly.

Originally the index has a discontinuity for network and group size configurations that are characterized by the higher number of between-group ties that is expected under a random graph, for which it returns 0 (as originally described by Freeman (1978)). We removed that truncation such that it returns values between -1 and 1.

The original Freeman’s formulation involves two groups of vertices. Here it is extended to the arbitrary number of groups. The generalization affects the way in which the expected number of between-group edges under pure random graph is calculated, see Bojanowski & Corten (2014) for details.

The function internally calculates the sizes of groups of vertices in the supplied attribute `vattr`. However, it is possible to override this by specifying "true" type distribution with the `gsizes` argument. It is assumed to be a table (as returned by `table()`) or a numeric vector with the group sizes. This may be especially useful when dealing with large graphs and/or with large number of isolates.

If `object` is a table it is interpreted as a mixing matrix. Two-dimensional table is interpreted as a contact layer. Three-dimensional table is interpreted as a full mixing matrix `mghy` cross-classifying all dyads, in which `g` and `h` correspond to group membership of ego and alter respectively. Layers `y = 1` and `y = 2` are assumed to be non-contact and contact layers respectively.

If `object` is of class "igraph" it is required to supply `vattr` with the name of the vertex attribute to calculate intermediate mixing matrix.

Method for mixing matrices

Method for "igraph"s

Value

The value of the Freeman’s index.

References


See Also

Other segregation measures: `assort()`, `coleman()`, `ei()`, `gamix()`, `orwg()`, `smi()`, `ssi()`

Examples

```r
## White's data from Freeman's article segregation level
freeman(WhiteKinship, "gender")
```
# using 'more' argument
freeman(WhiteKinship, "gender")

## S3 method for class 'table'
gamix(object, ...)

## S3 method for class 'igraph'
gamix(object, vattr, ...)

## Default S3 method:
gamix(object, ...)

### Arguments

- **object**  
  R object, see Details for available methods
- **...**  
  other objects passed to/from other methods
- **vattr**  
  character, name of vertex attribute

### Details

The measure varies between $-1/v\text{count}(g)$ for dissassortative mixing and 1 for perfect within-group mixing. It takes a value of 0 for proportionate mixing.

If object is a table it is interpreted as a mixing matrix. Two-dimensional table is interpreted as a contact layer. Three-dimensional table is interpreted as a full mixing matrix $m_{ghy}$ cross-classifying all dyads, in which $g$ and $h$ correspond to group membership of ego and alter respectively. Layers $y = 1$ and $y = 2$ are assumed to be non-contact and contact layers respectively.

If object is of class "igraph" it is required to supply vattr with the name of the vertex attribute to calculate intermediate mixing matrix.

### Value

Numerical value of the measure.

### References

See Also

Other segregation measures: `assort()`, `coleman()`, `ei()`, `freeman()`, `orwg()`, `smi()`, `ssi()`

Examples

```r
gamix(WhiteKinship, "gender")
gamix(EF3, "race")
```

Description

`group_sizes()` recomputes group sizes from a full mixing matrix. This is only limited to square (single-attribute) mixing matrices.

Usage

```r
group_sizes(mm, directed = TRUE, loops = FALSE)
```

Arguments

- `mm` numeric array with `dim` of `(k, k, 2)` for some `k`
- `directed` logical, whether network is directed
- `loops` logical, whether loops are allowed

Value

A numeric vector of group sizes

Description

Creating network mixing matrices (`mixingm()`) and data frames (`mixingdf()`).
mixingm

Usage

mixingm(object, ...)

## S3 method for class 'igraph'
mixingm(
  object,
  rattr,
  cattr = rattr,
  full = FALSE,
  directed = is.directed(object),
  loops = any(is.loop(object)),
  ...
)

mixingdf(object, ...)

## S3 method for class 'table'
mixingdf(object, ...)

## S3 method for class 'igraph'
mixingdf(object, ...)

Arguments

object 
R object, see Details for available methods
...
other arguments passed to/from other methods
rattr 
name of the vertex attribute or an attribute itself as a vector. If cattr is not NULL, rattr is used for rows of the resulting mixing matrix.
cattr 
name of the vertex attribute or an attribute itself as a vector. If supplied, used for columns in the mixing matrix.
full 
logical, whether two- or three-dimensional mixing matrix should be returned.
directed 
logical, whether the network is directed. By default, directedness of the network is determined with igraph::is_directed().
loops 
logical, whether loops are allowed. By default it is TRUE whenever there is at least one loop in object.

Details

Network mixing matrix is, traditionally, a two-dimensional cross-classification of edges depending on the values of a specified vertex attribute for tie sender and tie receiver. It is an important tool for assessing network homophily or segregation.

Let $G$ be the number of distinct values of the vertex attribute in question. We may say that we have $G$ mutually exclusive groups in the network. The mixing matrix is a $G \times G$ matrix such that $m_{ij}$ is the number of ties send by vertices in group $i$ to vertices in group $j$. The diagonal of that matrix is of special interest as, say, $m_{ii}$ is the number of ties within group $i$.

A full mixing matrix is a three-dimensional array that cross-classifies all network dyads depending on:
1. the value of the vertex attribute for tie sender
2. the value of the vertex attribute for tie receiver
3. the status of the dyad, i.e. whether it is connected or not

The two-dimensional version is a so-called "contact layer" of the three-dimensional version.

If object is of class "igraph," mixing matrix is created for the network in object based on vertex attributes supplied in arguments rattr and optionally cattr.

If only rattr is specified (or, equivalently, rattr and cattr are identical), the result will be a mixing matrix $G \times G$ if full is FALSE or $G \times G \times 2$ if full is TRUE. Where $G$ is the number of categories of vertex attribute specified by rattr.

If rattr and cattr can be used to specify different vertex attributes for tie sender and tie receiver.

Value

Function `mixingm()`, depending on full argument, a two- or three-dimensional array crossclassifying connected or all dyads in object. For undirected network and if foldit is TRUE (default), the matrix is folded onto the upper triangle (entries in lower triangle are 0).

Function `mixingdf()` returns non-zero entries of a mixing matrix (as returned by `mixingm()`), but organized in a data frame with columns:

- ego, alter – group membership of ego an alter
- tie – present only if full=TRUE, with TRUE or FALSE for connected and disconnected dyads respectively
- n – counts

Examples

```r
if(requireNamespace("igraph", quietly = TRUE)) {
  # some directed network
  net <- igraph::make_graph(c(1,2, 1,3, 2,3, 4,5, 1,4, 1,5, 4,2, 5,3))
  igraph::V(net)$type <- c(1,1,1, 2,2)
  mixingm(net, "type")
  mixingm(net, "type", full=TRUE)
  # as undirected
  mixingm(igraph::as.undirected(net), "type")
  mixingm(net, "type")
  mixingm(net, "type", full=TRUE)
}
```

---

**orwg**

*Odds ratio of existence of within-group ties*

**Description**

Odds ratio for connected, as opposed to disconnected, dyads depending whether it is between- or within-group, i.e. how much more likely the dyad will be connected if it is within-group.
Usage

orwg(object, ...)

## S3 method for class 'table'
orwg(object, ...)

## S3 method for class 'igraph'
orwg(object, vattr, ...)

## Default S3 method:
orwg(object, ...)

Arguments

object R object, see Details for available methods
... other arguments passed to/from other methods
vattr character scalar or any vector, name of the vertex attribute or the attribute itself (as a vector)

Details

The measure takes values, like all odds ratios, from \((0; \infty)\).

If object is a table it is interpreted as a mixing matrix. Two-dimensional table is interpreted as a contact layer. Three-dimensional table is interpreted as a full mixing matrix \(m_{ghy}\) cross-classifying all dyads, in which \(g\) and \(h\) correspond to group membership of ego and alter respectively. Layers \(y = 1\) and \(y = 2\) are assumed to be non-contact and contact layers respectively.

If object is of class "igraph" it is required to supply vattr with the name of the vertex attribute to calculate intermediate mixing matrix.

Value

Numeric value of the measure.

References


See Also

Other segregation measures: assort(), colem(), ei(), freeman(), gamix(), smi(), ssi()

Examples

orwg(WhiteKinship, "gender")
smi

Segregation Matrix Index

Description

Segregation Matrix Index due to Freshtman (1997). A measure of network segregation. Currently (and originally) supports only two groups.

Usage

smi(object, ...)

## S3 method for class 'table'
smi(object, normalize = TRUE, ...)

## S3 method for class 'igraph'
smi(object, vattr, ...)

## Default S3 method:
smi(object, ...)

Arguments

object       R object, see Details for available methods
...
other arguments passed to/from other methods
normalize   logical, whether normalized values should be returned, defaults to TRUE
vattr       character, name of the node attribute designating groups

Details

The Segregation Matrix Index (SMI) is calculated for every group separately. It compares the density within group to the density of between group ties of nodes belonging to that group.

Non-normalized version is the ratio of the within-group density to the between-group density, so vary between 0 and infinity. The normalized version varies between 0 and 1.

If object is a table it is interpreted as a mixing matrix. Two-dimensional table is interpreted as a contact layer. Three-dimensional table is interpreted as a full mixing matrix \( m_{ghy} \) cross-classifying all dyads, in which \( g \) and \( h \) correspond to group membership of ego and alter respectively. Layers \( y = 1 \) and \( y = 2 \) are assumed to be non-contact and contact layers respectively.

If object is of class "igraph" it is required to supply vattr with the name of the vertex attribute to calculate intermediate mixing matrix.

Value

Numeric vector of length equal to the number of groups in \( g \) according to vattr with the values of SMI for the groups.


References


See Also

Other segregation measures: assort(), coleman(), ei(), freeman(), gamix(), orwg(), ssi()

Examples

# ssi() needs a directed network
smi( igraph::as.directed(WhiteKinship, "mutual"), "gender"

### ssi  
\textit{Spectral Segregation Index for Social Networks}

Description

These functions implement Spectral Segregation Index as proposed by Echenique & Fryer (2006). This index is a node-level measure of segregation in a given network.

Usage

ssi(g, vattr)

Arguments

- **g**: object of class "igraph" representing a network
- **vattr**: character, name of the vertex attribute

Details

For a full description and axiomatization see Echenique & Fryer (2006).

The network g is converted to adjacency matrix and normalized so that all rows sum-up to 1.

The procedure essentially consists of creating a submatrix, say, \( B \) of the adjacency matrix, say \( A \). This submatrix \( B \) contains only vertices of the given type. It may be viewed as a type-homogeneous subnetwork of \( A \). This subnetwork is further decomposed into connected components. Then, for every component, an eigenvalue decomposition is applied. The value of the index for the component is simply the largest eigenvalue, and the individual-level indices are obtained by distributing it according to the corresponding eigenvector.

Value

Named vector of individual level values of SSI. Names correspond to vertex ids in g.
symmetrize

(De)symmetrize square numeric matrix

References


See Also

Other segregation measures: assort(), coleman(), ei(), freeman(), gamix(), orwg(), smi()

Examples

```r
if(requireNamespace("igraph", quietly = TRUE)) {

### artificial EF data
x <- ssi(EF3, "race")
xx

# show it on picture
a <- igraph::V(EF3)$race
# rescale SSI values to use as shades of gray
k <- 1 - scale(x, center=min(x), scale=max(x) - min(x))
plot( EF3, layout=igraph::layout.fruchterman.reingold,
vertex.color= gray(k),
vertex.label.family="", vertex.label=igraph::V(WhiteKinship)$name,
vertex.shape=c("circle", "square")[a], vertex.label.color=gray( (1-k) > .4 )
)

### For White's kinship data
x <- ssi(WhiteKinship, "gender")
xx

# plot it
a <- match(igraph::V(WhiteKinship)$gender, unique(igraph::V(WhiteKinship)$gender))
k <- 1 - scale(x, center=min(x), scale=max(x) - min(x))
set.seed(1234)
plot( WhiteKinship, layout=igraph::layout.fruchterman.reingold,
main="Node segregation in White's kinship data",
vertex.label=igraph::V(WhiteKinship)$name,
vertex.shape=c("circle", "csquare")[a],
vertex.label.color="black")
legend( "topleft", legend=c("Men", "Women"), pch=c(0,1), col=1)
}
```
Description

(De)symmetrize square binary matrix in various ways.

Usage

symmetrize(mat, rule = c("upper", "lower", "div", "intdiv"))

Arguments

- mat: square numeric matrix
- rule: character, direction of copying, see Details

Details

Argument mat is to be a square numeric matrix. The way it is made symmetric, or asymmetric, depends on the value of the rule argument.

If rule is "upper" or "lower" then mat is made symmetric by copying, respectively, upper triangle onto lower, or lower onto upper. The value of rule specifies values of which triangle will stay in the returned value.

If rule is "intdiv" then the off-diagonal values are distributed approximately equally between the lower/upper triangles. If r is the computed result, then r[i,j] will be equal to (x[i,j] + x[j,i]) \%/\% 2 if r[i,j] is in the lower triangle. It will be equal to (x[i,j] + x[j,i]) \%/\% 2 + 1 if in the upper triangle.

If rule is "div" then the off-diagonal values are distributed equally between the lower/upper triangles: as with "intdiv" but using normal / division.

Value

A matrix: symmetrized version of mat.

See Also

fold()

Examples

m <- matrix(1:16, 4, 4)

# copy upper triangle onto lower symmetrically
symmetrize(m, "upper")

# copy lower triangle onto upper symmetrically
symmetrize(m, "lower")

# distribute off-diagonal values exactly
# r[i,j] = (m[i,j] + m[j,i]) / 2
r1 <- symmetrize(m, "div")
r1
all.equal(sum(m), sum(r1))
# distribute off-diagonal values using integer division
r2 <- symmetrize(m, "intdiv")

all.equal(sum(m), sum(r2))

---

### WhiteKinship

- **Description**
  - This data is taken from Freeman (1978) who uses data from White (1975) to illustrate the segregation measure.

- **Usage**
  - `WhiteKinship`

- **Format**
  - Object of class "igraph" with an undirected network of size 10. Vertex attribute gender, takes values "male" or "female".

- **Details**
  - Based on Freeman (1978):
    - White dealt with the problem of segregation among social positions rather than among individual persons. He specified a set of standard kinship positions that he called the “effective kinship network”.
    - Traditional analysis (e.g. Murdock, 1971) have argued that societies sometimes proscribe interaction among some kinship positions as an extension of icest taboos. Thus, given this reasoning, kinship positions should be segregated according to the gender of their occupants. White’s data provide possibility to test of this hypothesis.
    - White collected data on the rules governing various kinds of interaction among occupants of his ten standard kinship positions for a sample of 219 societies. For every pair of positions White specified whether or not interaction between their occupants was ever restricted in any society in the sample.

- **Source**
References


White, D. R. (1975) "Communicative Avoidance in Social Networks". University of California, Irvine. (mimeo)

Examples

```r
if( requireNamespace("igraph", quietly = TRUE) ) {
  set.seed(2992)
  plot(
    WhiteKinship, layout=igraph::layout.fruchterman.reingold,
    vertex.color= match(igraph::V(WhiteKinship)$gender, unique(igraph::V(WhiteKinship)$gender)),
    vertex.label=igraph::V(WhiteKinship)$name, vertex.label.family="",
    main="White's (1975) data on kinship networks"
  )
  legend("topleft", col=2:3, legend=c("Woman", "Man"), pch=19)
}
```
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