Package ‘spreadr’

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Title Simulating Spreading Activation in a Network
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**Description**

Small example of a phonological network as an igraph object

**Usage**

```r
pnet
```

**Format**

igraph object representing an unweighted undirected graph with 34 vertices and 96 edges. There are no self-loops.

**Source**


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**Description**

Small example of a phonological network as an adjacency matrix

**Usage**

```r
pnetm
```
spreadr

Format

Adjacency matrix representing an unweighted undirected graph with 34 vertices and 96 edges. There are no self-loops.

Source


spreadr

Simulate spreading activation in a network

Description

Simulate spreading activation in a network

Usage

spreadr(
  network,
  start_run,
  retention = 0.5,
  time = 10,
  threshold_to_stop = NULL,
  decay = 0,
  suppress = 0,
  include_t0 = FALSE,
  create_names = TRUE,
  never_stop = FALSE
)

Arguments

network Adjacency matrix or igraph object representing the network in which to simulate spreading activation.

start_run Non-empty data.frame with mandatory columns node, activation; and optional columns time. If the time column is present, activation is added to node at each time. Otherwise, the activations are added to their corresponding nodes at t = 0.

retention Number from 0 to 1 (inclusive) or a numeric vector of such numbers of length equals number of nodes in the network. This represents the proportion of activation that remains in the node (not spread) at each time step. Then, 1 -retention of the activation at each node is spread to neighbouring nodes. If a numeric vector, retentions are assigned to nodes according to the order given by V(network) if network is an igraph object or nrow(network) if network is an adjacency matrix.
time Positive non-zero integer, or NULL. If not NULL, the number of time steps to simulate before stopping. Otherwise, stop with the threshold_to_stop parameter.

threshold_to_stop Number or NULL. If not NULL, stop the simulation only when all nodes have activation value less than threshold_to_stop. Otherwise, stop with the time parameter.

decay Number from 0 to 1 (inclusive) representing the proportion of activation that is lost at each time step.

suppress Number representing the maximum amount of activation in a node for it to be set to 0, at each time step.

include_t0 Boolean flag indicating if activation at $t = 0$ should be prepended to the output data.frame. This is FALSE by default for back-compatibility.

create_names Boolean flag indicating if nodes should be automatically named (1:n, where n is the number of nodes) in case they are missing.

never_stop Boolean flag indicating if the simulation should be stopped if there have been too many iterations (so that there might be an infinite loop).

Details
At least one of parameters time or threshold_to_stop must be non-NULL. If both are non-NULL, the simulation stops at the earliest time possible.

The simulation iterates like so: for every $i$ in $[0, \text{time}]$,

- Spread activation from node to node
- Decay the activation at each node by the proportion specified by decay
- Set the activation at nodes with activation less than suppress to 0
- Add the activations in start_run with time $= i$ to their corresponding nodes
- Save the activations at each node for output
- Check the terminating conditions time and threshold_to_stop. If any are satisfied, terminate the simulation.

Value
A data.frame with node, activation and time columns representing the spread of activation in the network over time.

Examples

```r
# make an adjacency matrix and randomly fill some cells with 1s
mat <- matrix(sample(c(0,1), 100, replace=TRUE), 10, 10)
diag(mat) <- 0 # remove self-loops
initial_df <- data.frame(node=1, activation=20, stringsAsFactors=FALSE)
results <- spreadr(mat, initial_df)

head(results, 10)
tail(results, 10)
```
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