Package 'spreadr'

November 19, 2018

Type Package

Title Simulating Spreading Activation in a Network

Version 0.1.0

Description The notion of spreading activation is a prevalent metaphor in the cognitive sciences.
This package provides the tools for cognitive scientists and psychologists to conduct computer simulations
that implement spreading activation in a network representation. The algorithmic method implemented in 'spreadr'
subroutines follows the approach described in Vitevitch, Ercal, and Adagarla (2011, Frontiers),
who viewed activation as a fixed cognitive resource that could spread among nodes that were connected to
each other via edges or connections (i.e., a network). See Vitevitch, M. S., Ercal, G., & Adagarla, B. (2011).
Simulating retrieval from a highly clustered network: Implications for spoken word recognition.
Frontiers in Psychology, 2, 369. <doi:10.3389/fpsyg.2011.00369>.

License GPL-3

Encoding UTF-8

LazyData true

Depends Rcpp (>= 0.12.5)

RoxygenNote 6.1.0

Imports igraph, extrafont, ggplot2

Suggests knitr, rmarkdown

VignetteBuilder knitr

LinkingTo Rcpp

NeedsCompilation yes

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Repository CRAN

Date/Publication 2018-11-19 19:20:03 UTC

1

R topics documented:

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spreadr   *Spread of activation process to determine activation of network nodes.*

Description

This function takes in a dataframe with 'node' and 'activation' columns, and simulates the spread of activation among nodes in a specified network structure.

Usage

```
spreadr(network, start_run, retention = 0.5, time = 10, decay = 0,
  suppress = 0, create_names = TRUE)
```

Arguments

network	Network where the spreading occurs. Must be specified. Must be an igraph object with a "name" property or an adjacency matrix.
start_run	A non-empty dataframe with 'node' and 'activation' columns. Must be specified.
retention	Proportion of activation that remains in the node from which activation is being spread from. Ranges from 0 to 1. Default is 0.5.
time	Number of time steps to run the spreadr() function for. Default is 10.
decay	Proportion of activation that is lost at each time step. Ranges from 0 to 1. Default is 0.
suppress	Suppress nodes with a final activation of < x units at each time step to an activation value of 0. Default is 0.
create_names	Name nodes 1:number_of_nodes in case network is missing node names.

Value

A compiled dataframe with 'node', 'activation' and 'time' columns showing the spread of activation in the network over time.

Examples

```
g_d_mat <- matrix(sample(c(0,1), 100, replace = TRUE), 10, 10)
# make an adjacency matrix and randomly fill some cells with 1s
diag(g_d_mat) <- 0 # remove self-loops
library(spreadr)
initial_df <- data.frame(node = 1, activation = 20, stringsAsFactors = FALSE)
result_d <- spreadr(start_run = initial_df, decay = 0, retention = 0.5,
suppress = 0, network = g_d_mat, time = 10)
head(result_d, 10)
tail(result_d, 10)
```

spreadr_2	*Spread of activation process to determine activation of network nodes.*

Description

This function takes in a dataframe with 'node' and 'activation' columns, and simulates the spread of activation among nodes in a specified network structure. Note that spreadr_2 is identical to spreadr, except that there is an additonal option for the user to

Usage

```
spreadr_2(network, start_run, retention = 0.5, time = 10, decay = 0,
  suppress = 0, ignore_time = F, threshold_to_stop = 0.01,
  create_names = TRUE)
```

Arguments

network	Network where the spreading occurs. Must be specified. Must be an igraph object with a "name" property or an adjacency matrix.
start_run	A non-empty dataframe with 'node' and 'activation' columns. Must be specified.
retention	Proportion of activation that remains in the node from which activation is being spread from. Ranges from 0 to 1. Default is 0.5.
time	Number of time steps to run the spreadr() function for. Default is 10.
decay	Proportion of activation that is lost at each time step. Ranges from 0 to 1. Default is 0.
suppress	Suppress nodes with a final activation of < x units at each time step to an activation value of 0. Default is 0.
ignore_time	Indicate whether to ignore the number of time steps listed and allow for the spreading activation process to continue until the value listed in threshold_to_stop is achieved. Default = F
threshold_to_stop	
	Stop spreading activation when the proportion of total activation in start_run is below the threshold. Default = 0.01
create_names	Name nodes 1:number_of_nodes in case network is missing node names.

Value

A compiled dataframe with 'node', 'activation' and 'time' columns showing the spread of activation in the network over time.

Examples

```
g_d_mat <- matrix(sample(c(0,1), 100, replace = TRUE), 10, 10)
# make an adjacency matrix and randomly fill some cells with 1s
diag(g_d_mat) <- 0 # remove self-loops
library(spreadr)
initial_df <- data.frame(node = 1, activation = 20, stringsAsFactors = FALSE)
result_d <- spreadr_2(start_run = initial_df, decay = 0, retention = 0.5,
suppress = 0, network = g_d_mat, ignore_time = TRUE, threshold_to_stop = 0.01)
head(result_d, 10)
tail(result_d, 10)
```

Index