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
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

```r
g_d_mat <- matrix(sample(c(0L, 1L), 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 = 1L, activation = 0L, 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 additional option for the user to

Usage

```r
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)
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