Package 'ScriptMapR'

November 13, 2023

Type Package

Title R Script Visualization in Cytoscape

Version 0.0.3

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Description Displays the content of a R script into the 'Cytoscape' network-visualization app <https://cytoscape.org/>.

Depends R (>= 3.5.0)

BugReports https://github.com/peyronlab/ScriptMapR/issues

biocViews

Imports RCy3, formatR, dplyr, stringr, utils, grDevices

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

NeedsCompilation no

Repository CRAN

Date/Publication 2020-09-24 09:20:10 UTC

R topics documented:

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scriptmapr   *Display content of input script in 'Cytoscape'*

Description

This function allows the user to represent the content of a given script in 'Cytoscape' (<https://cytoscape.org/>). Therefore it requires to have a functioning version of 'Cytoscape' 3.6.1 or greater.

Each variable is represented as a node and edges represent commands that call the variable. Functions can also be represented.

A color code is associated to each nodes:

- white: intermediate variables (that are created and used to create new ones),

- pink: subsets of a variable (ex: var2 in var1$var2),

- green: final variables (that are created and not used afterwards),

- red: warnings, message and stop functions,

- yellow: if, else if, else and ifelse functions,

- orange: for, foreach and while functions,

- blue: *print, cat or other functions at beginning of line,

- gray: packages import and session info (wd)

Edge color reports the sequence of command on a blue scale (light: early in the script -to- dark: late in the script) Node color code extend to edges in case of loops or tests (orange and yellow)

Edges of type sinewave represent the connection between a node and itself when used as an indice. Edges of type dots represent the commands within a if, else, else if, ifelse or loop condition.

User created functions are represented and pooled as a group, collapsed and extracted to a subnetwork to avoid latency.

Usage

```
scriptmapr(path)
```

Arguments

path   path of the R file to plot in Cytoscape

Value

Cytoscape network visualization

Examples

```
# load example script path
file.path <- system.file("extdata", "example.R", package = "ScriptMapR")

scriptmapr(path=file.path)
```

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