

Package: ScriptMapR (via r-universe)

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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>

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

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Repository <https://peyronlab.r-universe.dev>

RemoteUrl <https://github.com/peyronlab/scriptmapr>

RemoteRef HEAD

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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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