Package 'transomics2cytoscape'

March 30, 2021

Title A tool set for 3D Trans-Omic network visualization with
Cytoscape

Version 1.0.0

Description transomics2cytoscape generates a file for 3D transomics
visualization by providing input that specifies the IDs of multiple
KEGG pathway layers, their corresponding Z-axis heights, and an input that
represents the edges between the pathway layers.
The edges are used, for example, to describe the relationships between
kinase on a pathway and enzyme on another pathway.
This package automates creation of a transomics network as
shown in the figure in Yugi.2014
(https://doi.org/10.1016/j.celrep.2014.07.021)
using Cytoscape automation
(https://doi.org/10.1186/s13059-019-1758-4).

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Imports RCy3, KEGGREST, dplyr

Suggests testthat, roxygen2, knitr, BiocStyle, rmarkdown

Encoding UTF-8

LazyData true

biocViews Network, Software, Pathways, DataImport, KEGG

VignetteBuilder knitr

SystemRequirements Java 11, Cytoscape 3.8.*, Cy3D >= 1.1.2

RoxygenNote 7.1.1

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R topics documented:

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create3Dnetwork   *Create 3D network view for transomics visualization.*

Description

Import multiple KEGG pathways and integrate the pathways into Cy3D renderer

Usage

```
create3Dnetwork(networkDataDir, networkLayers, transomicEdges, stylexml)
```

Arguments

networkDataDir	Path of a directory to put the network files of the second column of networkLayers TSV.
networkLayers	Path of a TSV file with the 3 columns (layer index, the network file name in networkDataDir, Z-height of the network).
transomicEdges	Path of a TSV file with the 5 columns (layer index of a source node, name or KEGG object ID that the source node should have, layer index of a target node, name or KEGG object ID that the target node should have, interaction type).
stylexml	Path of a XML file for Cytoscape style

Value

A SUID of the 3D network.

Author(s)

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Examples

```
## Not run:
networkDataDir <- tempfile(); dir.create(networkDataDir)
sif <- system.file("extdata","galFiltered.sif",package="RCy3")
file.copy(sif, networkDataDir)
networkLayers <- system.file("extdata", "networkLayers.tsv",
    package = "transomics2cytoscape")
transomicEdges <- system.file("extdata", "transomicEdges.tsv",
    package = "transomics2cytoscape")
stylexml <- system.file("extdata", "transomics.xml",
    package = "transomics2cytoscape")
create3Dnetwork(networkDataDir, networkLayers, transomicEdges, stylexml)

## End(Not run)
```

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