

Package ‘transomics2cytoscape’

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

Version 1.2.1

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 3.8.2, Cy3D >= 1.1.3

RoxygenNote 7.1.1

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Author Kozo Nishida [aut, cre] (<<https://orcid.org/0000-0001-8501-7319>>), Katsuyuki Yugi [aut] (<<https://orcid.org/0000-0002-2046-4289>>)

Maintainer Kozo Nishida <kozo.nishida@gmail.com>

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create3Dnetwork	<i>Create 3D network view for transomics visualization.</i>
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Description

Import multiple KEGG pathways and integrate the pathways into Cy3D renderer

Usage

```
create3Dnetwork(networkDataDir, networkLayers, 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).
stylexml	Path of a XML file for Cytoscape style

Value

A SUID of the 3D network.

Author(s)

Kozo Nishida

Examples

```
## Not run:
networkDataDir <- tempfile(); dir.create(networkDataDir)
networkLayers <- system.file("extdata", "yugi2014.tsv",
  package = "transomics2cytoscape")
stylexml <- system.file("extdata", "transomics.xml",
  package = "transomics2cytoscape")
suid <- create3Dnetwork(networkDataDir, networkLayers, stylexml)

## End(Not run)
```

createTransomicEdges *Create Trans-Omic edges between layers of the network.*

Description

Create Trans-Omic edges between layers of the network

Usage

```
createTransomicEdges(suid, transomicEdges)
```

Arguments

suid A SUID of Cytoscape network

transomicEdges Path of a TSV file with the 9 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).

Value

A SUID of the 3D network.

Author(s)

Kozo Nishida

Examples

```
## Not run:
transomicEdges <- system.file("extdata", "allosteric.tsv",
  package = "transomics2cytoscape")
createTransomicEdges(suid, transomicEdges)

## End(Not run)
```

ec2reaction *Convert KEGG enzyme IDs to KEGG reaction IDs.*

Description

Convert KEGG enzyme IDs to KEGG reaction IDs

Usage

```
ec2reaction(tsvFilePath, columnIndex, outputFilename)
```

Arguments

tsvFilePath Path of a TSV file with the 9 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).

columnIndex The column number

outputFilename The output filename

Value

None

Author(s)

Kozo Nishida

Examples

```
## Not run:  
ec = system.file("extdata", "allosteric_ecnumber.tsv",  
  package = "transomics2cytoscape")  
ec2reaction(ec, 8, "allosteric.tsv")  
  
## End(Not run)
```

installCyApps

Install the Cytoscape Apps the transomics2cytoscape depends.

Description

Install the Cytoscape Apps the transomics2cytoscape depends

Usage

```
installCyApps()
```

Value

None

Author(s)

Kozo Nishida

Examples

```
## Not run:  
installCyApps()  
  
## End(Not run)
```

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