Package 'transomics2cytoscape'

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

Version 1.22.0

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, purrr, tibble, pbapply

Suggests testthat, roxygen2, knitr, BiocStyle, rmarkdown

Encoding UTF-8

LazyData false

biocViews Network, Software, Pathways, DataImport, KEGG

VignetteBuilder knitr

SystemRequirements Cytoscape >= 3.10.0

RoxygenNote 7.1.2

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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, 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 4 columns (layer index, the network file name in networkDataDir, Z-height of the network, whether to interact not only with the nodes of each network layer but also with the edges).
`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/usecase1", "yugi2014.tsv",
    package = "transomics2cytoscape")
stylexml <- system.file("extdata/usecase1", "yugi2014.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 7 columns (layer index of the source node, the column name for which you want to find the attribute value of the source node, the attribute value of the source node should have, layer index of a target node name or KEGG object ID that the source node should have, layer index of the target node, the column name for which you want to find the attribute value of the target node, the attribute value of the target node should have, 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:
layer1to2 <- system.file("extdata/usecase1", "k2e.tsv",
    package = "transomics2cytoscape")
suid <- createTransomicEdges(suid, layer1to2)

## End(Not run)
```

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

Description

Convert a EC number column to a KEGG reaction ID column

Usage

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

Arguments

tsvFilePath	Path of a TSV file with column of EC number
columnIndex	Index number of the column with the EC number you want to convert
outputFilename	The output file name

Value

None

Author(s)

Kozo Nishida

Examples

```
## Not run:
layer3to2 <- system.file("extdata/usecase1", "allosteric_ecnumber.tsv",
    package = "transomics2cytoscape")
ec2reaction(layer3to2, 6, "allosteric_ec2rea.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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