

Package ‘flowCL’

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Type Package

Title Semantic labelling of flow cytometric cell populations

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Author Justin Meskas, Radina Droumeva

Maintainer Justin Meskas <jmeskas@bccrc.ca>

Depends R (>= 3.0.2), Rgraphviz, SPARQL

Description Semantic labelling of flow cytometric cell populations.

biocViews FlowCytometry

Suggests RUnit, BiocGenerics

License Artistic-2.0

LazyLoad yes

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flowCL-package	<i>Semantic labelling of flow cytometric cell populations.</i>
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Description

flowCL uses SPARQL to match a phenotype to a cell type from the cell ontology. If the match is not unique, then the best alternative is returned.

Details

```

Package:    flowCL
Type:      Package
License:   Artistic-2.0
LazyLoad:  yes
Depends:   Rgraphviz, SPARQL

```

flowCL executes queries against the Cell Ontology (CL), available at <http://cellontology.org>. The CL file is hosted on a triplestore, i.e., a database for storage and retrieval of Resource Description Framework (RDF) triples. The SPARQL endpoint at <http://cell.ctde.net:8080/openrdf-sesame/repositories/CL> is used to execute the SPARQL queries retrieving the correct matches from the CL. While other SPARQL endpoints can be used, users should be aware that in our case the CL file has been reasoned upon, and resulting extra inferred axioms have been added to the triplestore, providing a more complete result set.

Author(s)

Maintainer: Justin Meskas <jmeskas@bccrc.ca>

Authors: Justin Meskas, Radina Droumeva

Examples

```

# Load a pre-loaded archive. Skipping this chunk will cause flowCL to
## slowly build a new one.
flowCL("archive")

# Simple two marker example
Res <- flowCL("CCR7+CD45RA+")
tmp <- Res$CCR7+CD45RA+
plot(tmp[[1]], nodeAttrs=tmp[[2]], edgeAttrs=tmp[[3]], attrs=tmp[[4]])
Res$Table

# Exact match example
Res <- flowCL("CCR7+CD45RA+CD8+", CompInfo = TRUE, OntolNamesTD = TRUE)
tmp <- Res$CCR7+CD45RA+CD8+
plot(tmp[[1]], nodeAttrs=tmp[[2]], edgeAttrs=tmp[[3]], attrs=tmp[[4]])
Res$Table

# Cell Label Example
x <- "CCR7+CD45RA+CD8+"
Res <- flowCL(x)
Res$Cell_Label[[x]][[1]]

# As a secondary way to view the results,
## see "[current directory]/flowCL_results/".
# Figures created called tree_(phenotype).pdf give the cell hierarchy
## dependent on the markers in the phenotype.
# A list of results from Res$Table are stored in listPhenotypes.csv.

```


Details

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Value

A list containing $N + 5$ elements. Where N is the number of phenotypes queried. Each of these N elements contains information for plotting the results. The other five elements show the cell labels (Cell_Labels), the matching markers in a list form (Marker_Groups) and a bracket form (Markers), ranking scores (Ranking) and a table (Table). The cell labels element lists the cell labels in order of highest score based on their ranking, which is in a form easily extracted and used by other R packages and functions. Marker_Groups and Markers list markers that were queried and that are part of a certain cell type. In Markers these markers are displayed in the form of A B (C) [D]. A and B together make up the markers input for the query. B, C and D together are the markers that make up the definition of the particular cell type. C lists the markers that were part of the experiment that were not part of the query, while D lists all other markers that make up the cell type that were not part of the experimental markers. A lists all the markers in the input for the query that were not required for that particular cell type. The table is a list of all the related information of each phenotype queried. This table is mainly for users to see the results in R.

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Res$Cell_Label[[x]][[1]]

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# Figures created called tree_(phenotype).pdf give the cell hierarchy
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# A list of results from Res$Table are stored in listPhenotypes.csv.
```

flowCL_archive *A list of data used to build a local archive.*

Description

A list of data used to build a local archive.

Usage

```
data(flowCL_archive)
```

Author(s)

Justin Meskas

test.flowCL.connection *A function to check that a connection exists between the user and the ontology server.*

Description

A function to check that a connection exists between the user and the ontology server.

Usage

```
test.flowCL.connection()
```

Author(s)

Justin Meskas

Examples

```
test.flowCL.connection()
```

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