

Package ‘LINCSDataportal’

September 30, 2016

Title Query LINCS (Library of Integrated Network-
based Cellular Signatures) Data and Metadata from LINCS Data Portal

Version 0.0.0.9000

Author person("Michele", "Forlin", email = "mxf854@med.miami.edu", role = c("aut", "cre"))

Maintainer person("Michele", "Forlin", email = "mxf854@med.miami.edu")

Description Access, query and download of LINCS data and metadata from LINCS

Depends R (>= 3.3.1)

Imports httr, jsonlite

License public

Encoding UTF-8

LazyData true

RoxygenNote 5.0.1.9000

R topics documented:

cell_metadata	2
datalevels	2
dataset_entities	3
download_dataset	3
find_dataset	4
gene_metadata	4
protein_metadata	5
SM_metadata	5
Index	7

cell_metadata	<i>Retrieve metadata associated with a cell (cl) used in LINCS experiments.</i>
---------------	---

Description

Retrieve metadata associated with a cell (cl) used in LINCS experiments.

Usage

```
cell_metadata(cl)
```

Arguments

cl	String representing a cell of interest
----	--

Value

data frame with available cell metadata

Examples

```
cell_metadata("mcf7")
```

datalevels	<i>Retrieve all available data level and associated dataset id for a given dataset id.</i>
------------	--

Description

Retrieve all available data level and associated dataset id for a given dataset id.

Usage

```
datalevels(lds_id)
```

Arguments

lds_id	String representing a dataset id (LDS-xxxx)
--------	---

Value

data frame with available data level and associated dataset id

Examples

```
datalevels("LDS-1233")
```

dataset_entities	<i>Retrieve entities (gene, protein, small molecule, etc.) associated with a specific LINCS dataset</i>
------------------	---

Description

Retrieve entities (gene, protein, small molecule, etc.) associated with a specific LINCS dataset

Usage

```
dataset_entities(lds_id)
```

Arguments

lds_id	String representing the dataset id (LDS-xxxx)
--------	---

Value

list of vectors with entities, measured or used to perturb the experiment associated to a given dataset.
One vector per entity type.

Examples

```
dataset_entities("LDS-1266")  
dataset_entities("LDS-1173")
```

download_dataset	<i>Download LINCS dataset packages, given dataset id's, from Lincs Data Portal.</i>
------------------	---

Description

Download LINCS dataset packages, given dataset id's, from Lincs Data Portal.

Usage

```
download_dataset(lds_id, path = ".")
```

Arguments

lds_id	Vector of dataset ids (LDS-xxxx)
path	Path to local folder where the dataset package will be downloaded, default = current directory

Examples

```
download_dataset("LDS-1266")
download_dataset("LDS-1173", path = "/datasets")
```

find_dataset	<i>Retrieve datasets from LINCS data portal associated with a term of interest (gene, protein, small molecule)</i>
--------------	--

Description

Retrieve datasets from LINCS data portal associated with a term of interest (gene, protein, small molecule)

Usage

```
find_dataset(searchterm)
```

Arguments

searchterm	String representing the search term
------------	-------------------------------------

Value

data.frame containing dataset id and description

Examples

```
find_dataset("afatinib")
find_dataset("mcf7")
```

gene_metadata	<i>Retrieve metadata associated with a gene measured in LINCS experiments.</i>
---------------	--

Description

Retrieve metadata associated with a gene measured in LINCS experiments.

Usage

```
gene_metadata(ge)
```

Arguments

ge	String representing a gene of interest
----	--

Value

data frame with available gene metadata

Examples

```
gene_metadata("BRCA1")
```

protein_metadata	<i>Retrieve metadata associated with a protein measured or used in LINCS experiments.</i>
------------------	---

Description

Retrieve metadata associated with a protein measured or used in LINCS experiments.

Usage

```
protein_metadata(pr)
```

Arguments

pr String representing a protein of interest

Value

data frame with available protein metadata

Examples

```
protein_metadata("ACK")
```

SM_metadata	<i>Retrieve metadata associated with a Small Molecule (SM) used in LINCS experiments.</i>
-------------	---

Description

Retrieve metadata associated with a Small Molecule (SM) used in LINCS experiments.

Usage

```
SM_metadata(sm)
```

Arguments

sm String representing a small molecule of interest

Value

data frame with available small molecule metadata

Examples

```
SM_metadata("afatinib")
```

Index

cell_metadata, [2](#)

datalevels, [2](#)

dataset_entities, [3](#)

download_dataset, [3](#)

find_dataset, [4](#)

gene_metadata, [4](#)

protein_metadata, [5](#)

SM_metadata, [5](#)