

Package ‘cellxgenedp’

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Title Discover and Access Single Cell Data Sets in the cellxgene Data Portal

Version 1.0.0

Description The cellxgene data portal (<https://cellxgene.cziscience.com/>) provides a graphical user interface to collections of single-cell sequence data processed in standard ways to 'count matrix' summaries. The cellxgenedp package provides an alternative, R-based interface, allowing data discovery, viewing, and downloading.

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Encoding UTF-8

Collate db.R collections.R datasets.R files.R facets.R keys.R cellxgene.R utilities.R cpp11.R jmespath.R cxg.R

Imports dplyr, httr, curl, jsonlite, utils, tools, parallel, shiny, DT

LinkingTo cpp11

Suggests zellkonverter, SingleCellExperiment, HDF5Array, BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0), mockery

biocViews SingleCell, DataImport, ThirdPartyClient

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collections	<i>Query cellxgene collections, datasets, and files</i>
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Description

files_download() retrieves one or more cellxgene files to a cache on the local system.

Usage

```
collections(cellxgene_db = db())
```

```
datasets(cellxgene_db = db())
```

```
datasets_visualize(tbl)
```

```
files(cellxgene_db = db())
```

```
files_download(tbl, dry.run = TRUE)
```

Arguments

cellxgene_db	an optional 'cellxgene_db' object, as returned by db().
tbl	a tibble() typically derived from datasets(db) or files(db) and containing columns dataset_id (for datasets_visualize()), or columns dataset_id, file_id, and filetype (for files_download()).
dry.run	logical(1) indicating whether the (often large) file(s) in tbl should be downloaded to a local cache. Files are not downloaded when dry.run = TRUE (default).

Value

Each function returns a tibble describing the corresponding component of the database.

files_download() returns a character() vector of paths to the local files.

Examples

```
db <- db()

collections(db)

collections(db) |>
  dplyr::glimpse()

datasets(db) |>
  dplyr::glimpse()

## visualize the first dataset
datasets(db) |>
  dplyr::slice(1) |>
  datasets_visualize()

files(db) |>
  dplyr::glimpse()

## Not run:
files(db) |>
  dplyr::slice(1) |>
  files_download(dry.run = FALSE)

## End(Not run)
```

cxg

Shiny application for discovering, viewing, and downloading cellxgene data

Description

Shiny application for discovering, viewing, and downloading cellxgene data

Usage

```
cxg(as = c("tibble", "sce"))
```

Arguments

as character(1) Return value when quitting the shiny application. "tibble" returns a tibble describing selected datasets (including the location on disk of the downloaded file). "sce" returns a list of dataset files imported to R as SingleCellExperiment objects.

Value

`cxg()` returns either a tibble describing datasets selected in the shiny application, or a list of datasets imported into R as `SingleCellExperiment` objects.

Examples

```
cxg()
```

db	<i>Retrieve updated cellxgene database metadata</i>
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Description

Retrieve updated cellxgene database metadata

Usage

```
db(overwrite = .db_online() && .db_first())
```

Arguments

overwrite	logical(1) indicating whether the database of collections should be updated from the internet (the default, when internet is available and, in an interactive session, the user requests the update), or read from disk (assuming previous successful access to the internet). <code>overwrite = FALSE</code> might be useful for reproducibility, testing, or when working in an environment with restricted internet access.
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Details

The database is retrieved from the cellxgene data portal web site. 'collections' metadata are retrieved on each call; metadata on each collection is cached locally for re-use.

Value

`db()` returns an object of class `'cellxgene_db'`, summarizing available collections, datasets, and files.

Examples

```
db()
```

FACETS

Facets available for querying cellxgene data

Description

FACETS is a character vector of common fields used to subset cellxgene data.

`facets()` is used to query the cellxgene database for current values of one or all facets.

`facets_filter()` provides a convenient way to filter facets based on label or ontology term.

Usage

FACETS

```
facets(cellxgene_db = db(), facets = FACETS)
```

```
facets_filter(facet, key = c("label", "ontology_term_id"), value, exact = TRUE)
```

Arguments

<code>cellxgene_db</code>	an (optional) <code>cellxgene_db</code> object, as returned by <code>db()</code> .
<code>facets</code>	a <code>character()</code> vector corresponding to one of the facets in FACETS.
<code>facet</code>	the column containing faceted information, e.g., <code>sex</code> in <code>datasets(db)</code> .
<code>key</code>	<code>character(1)</code> identifying whether value is a <code>label</code> or <code>ontology_term_id</code> .
<code>value</code>	<code>character()</code> value of the label or ontology term to filter on. The value may be a vector with <code>length(value) > 0</code> for exact matches (<code>exact = TRUE</code> , default), or a <code>character(1)</code> regular expression.
<code>exact</code>	<code>logical(1)</code> whether values match exactly (default, <code>TRUE</code>) or as a regular expression (<code>FALSE</code>).

Format

FACETS is an object of class `character` of length 8.

Value

`facets()` returns a tibble with columns `facet`, `label`, `ontology_term_id`, and `n`, the number of times the facet label is used in the database.

`facets_filter()` returns a logical vector with length equal to the length (number of rows) of `facet`, with `TRUE` indicating that the value of `key` is present in the dataset.

Examples

```
f <- facets()

## levels of each facet
f |>
  dplyr::count(facet)

## same as facets(, facets = "organism")
f |>
  dplyr::filter(facet == "organism")

db <- db()
ds <- datasets(db)

## datasets with African American females
ds |>
  dplyr::filter(
    facets_filter(ethnicity, "label", "African American"),
    facets_filter(sex, "label", "female")
  )

## datasets with non-European, known ethnicity
facets(db, "ethnicity")
ds |>
  dplyr::filter(
    !facets_filter(ethnicity, "label", c("European", "na", "unknown"))
  )
```

jmespath_version

Use JMESpath to query JSON files

Description

``jmespath_version()`` reports the version of the C++ jsoncons library in use.

``jmespath()`` executes a query against a json string using the 'jmespath' specification.

Usage

```
jmespath_version()

jmespath(data, path)
```

Arguments

data	character(1) JSON string.
path	character(1) JMESpath query string.

Details

`jmespath()` is implemented in the `jsoncons` C++ library.

Value

``jmespath_version()`` returns a character(1) major.minor.patch version string describing the version of the `jsoncons` library on which `jmespath` is implemented.

``jmespath()`` returns a character(1) json string representing the result of the query.

See Also

<https://danielparker.github.io/jsoncons/>

Examples

```
jmespath_version()

json <- '{
  "locations": [
    {"name": "Seattle", "state": "WA"},
    {"name": "New York", "state": "NY"},
    {"name": "Bellevue", "state": "WA"},
    {"name": "Olympia", "state": "WA"}
  ]
}'

jmespath(json, "locations[?state == 'WA'].name | sort(@)") |>
  cat("\n")
```

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