Package ‘HCAMatrixBrowser’

December 23, 2020

Title Extract and manage matrix data from the Human Cell Atlas project

Version 1.0.1

Description The HCAMatrixBrowser queries the HCA matrix endpoint to download expression data and returns a standard Bioconductor object. It uses the LoomExperiment package to serve matrix data that is downloaded as HDF5 loom format.

License Artistic-2.0

Depends R (>= 4.0.0), AnVIL

Imports BiocFileCache, digest, dplyr, httr, jsonlite, Matrix, methods, progress, rlang, SingleCellExperiment, stats, utils

Suggests BiocStyle, knitr, HCABrowser, LoomExperiment (>= 1.5.3), readr

BugReports `https://github.com/Bioconductor/HCAMatrixBrowser`

biocViews Infrastructure, DataRepresentation, Software

Encoding UTF-8

VignetteBuilder knitr

RoxygenNote 7.1.1

git_url https://git.bioconductor.org/packages/HCAMatrixBrowser

git_branch RELEASE_3_12

git_last_commit f9c47ee

git_last_commit_date 2020-10-28

Date/Publication 2020-12-22

Author Marcel Ramos [aut, cre] (<https://orcid.org/0000-0002-3242-0582>), Martin Morgan [aut] (0000-002-5874-8148)

Maintainer Marcel Ramos <`marcel.ramos@roswellpark.org`>

R topics documented:

`filtering` *Manipulating HCAMatrix filters*

Description

Manipulating HCAMatrix filters

Usage

```
filter(x, expr)

filters(x)

filters(x) <- value

## S4 method for signature 'HCAMatrix'
filter(x, expr)

## S4 method for signature 'HCAMatrix'
filters(x)

## S4 replacement method for signature 'HCAMatrix'
filters(x) <- value
```

Arguments

`x`	the object on which to set the filter list member
`expr`	a filter expression in the form of the right hand side of a formula, where bare names (without quotes) are allowed if they are available fields associated with the HCAMAtrix object, `x`
`value`	A list of structured filters (internal use)

Value

A `HCAMatrix` object with the filter field replaced by the specified filter expression

filter

The `filter` is a convenient setter for the filter element in `HCAMatrix` objects.

filters

The `filters` (plural) function is a safe accessor for the filters already present in the ‘HCAMAtrix‘ API object. The filter can also be set using the ‘filters<-‘ function setter (advanced use).

Note

Filtering documentation provided by the ‘GenomicDataCommons‘ package

Examples

```
# make an HCAMatrix object to start
hca <- HCAMatrix()

head(available_filters(hca))

hca1 <- filter(hca, genes_detected >= 500)
filters(hca1)
```

`HCAMatrix` *API Entry function for the Human Cell Atlas Matrix service*

Description

This function allows the use of the HCA Matrix API

Usage

```
HCAMatrix()

available_filters(api)

filter_detail(api, filter_name)

available_formats(api)

format_detail(api, format_name)

available_features(api)

feature_detail(api, feature_name)
```

Arguments

`api`	An HCAMatrix API object
`filter_name`	character(1) The name of the filter to get more detail on
`format_name`	character(1) The format for which to obtain more detail on
`feature_name`	character(1) The feature for which to obtain more detail on

Value

An object of class 'HCAMatrix'

Filters

* available_filter - Get a list of filters within the API to filter with * filter_detail - Obtain more detail on a particular filter name

Formats

* available_formats - Get a list of matrix format outputs * format_detail - Obtain more detail on a particular matrix file format

Features

* available_features - Get a list of feature outputs, either genes or transcripts * feature_detail - Obtain more information on a matrix feature type

Examples

```
hca <- HCAMatrix()
```

`HCAMatrix-class` *A class for representing the HCAMatrix API*

Description

The ‘HCAMatrix‘ class is a representation of the ‘HCAMatrix‘ API protocol via OAS version 2.0. The original version OAS 3 was converted using the APIMatic converter (`apimatic.io`).

See Also

HCAMatrix, Service

Examples

```
HCAMatrix()
```

`loadHCAMatrix` *Obtain expression matrix data from the Human Cell Atlas API service*

Description

Using a vector of data bundle identifiers (‘bundle_fqids‘), users can request the associated matrix of expression values. The query submitted by ‘loadHCAMatrix‘ may take some time to be completed. Once the query is completed, either a ‘LoomExperiment‘, ‘SingleCellExperiment‘, or ‘tibble‘ table is returned (depending on the value of ‘format‘).

Usage

```
loadHCAMatrix(
  api,
  bundle_fqids,
  verbose = FALSE,
  names.col = "CellID",
  format = c("loom", "mtx", "csv"),
  feature = c("gene", "transcript")
)
```

Arguments

`api`	An API object of class ‘HCAMatrix‘ from the ‘HCAMatrix‘ function
`bundle_fqids`	character() v0 Bundle identifiers
`verbose`	logical (default FALSE) whether to output stepwise messages
`names.col`	character (default "CellID") The column name in the ‘colData‘ metadata to use as column names of the `LoomExperiment` object when ‘format = "loom"‘
`format`	character(1) Data return format, one of: c("loom", "mtx", "csv"); (default: "loom")
`feature`	character(1) Provide either cell by "gene" or "transcript" matrices (default: "gene")

Value

A ‘LoomExperiment‘, ‘SingleCellExperiment‘ or ‘tibble‘ object

Examples

```
hca <- HCAMatrix()

## with an bundle_fqid character vector

bundle_fqids <-
    c("ffd3bc7b-8f3b-4f97-aa2a-78f9bac93775.2019-05-14T122736.345000Z",
    "f69b288c-fabc-4ac8-b50c-7abcae3731bc.2019-05-14T120110.781000Z",
    "f8ba80a9-71b1-4c15-bcfc-c05a50660898.2019-05-14T122536.545000Z")

loadHCAMatrix(hca, bundle_fqids)

## using filtering operation

hca2 <- filter(hca, dss_bundle_fqid %in% bundle_fqids)
filters(hca2)
loadHCAMatrix(hca2)
```

Index