

# Package ‘HCAMatrixBrowser’

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**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>

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**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)
```

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HCAMatrix

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

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**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()
```

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HCAMatrix-class	<i>A class for representing the HCAMatrix API</i>
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**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](https://apimatic.io)).

**See Also**

[HCAMatrix, Service](#)

**Examples**

```
HCAMatrix()
```

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loadHCAMatrix	<i>Obtain expression matrix data from the Human Cell Atlas API service</i>
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**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)
```

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