Package 'HuBMAPR'

November 12, 2026

Title Interface to 'HuBMAP'

Version 1.6.2

Description 'HuBMAP' provides an open, global bio-molecular atlas of the human body at the cellular level. The `datasets()`, `samples()`, `donors()`, `publications()`, and `collections()` functions retrieves the information for each of these entity types. `*_details()` are available for individual entries of each entity type. `*_derived()` are available for retrieving derived datasets or samples for individual entries of each entity type. Data files can be accessed using `bulk_data_transfer()`.

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Depends R (>= 4.4.0)

Imports httr2, dplyr, tidyr, tibble, rjsoncons, utils, stringr, whisker, purrr, rlang

Collate query.R datasets.R samples.R donors.R utilities.R publications.R publication_information.R collections.R collection_information.R provenance.R files.R organ.R template.R utils-globals.R

Encoding UTF-8

Roxygen list(markdown = TRUE)

Suggests testthat (>= 3.0.0), knitr, ggplot2, rmarkdown, BiocStyle

VignetteBuilder knitr

biocViews Software, SingleCell, DataImport, ThirdPartyClient, Spatial, Infrastructure

URL https://christinehou11.github.io/HuBMAPR/, https://github.com/christinehou11/HuBMAPR

BugReports https://github.com/christinehou11/HuBMAPR/issues

Config/testthat/edition 3

Config/roxygen2/version 8.0.0

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

git_branch RELEASE_3_23

git_last_commit e770872

git_last_commit_date 2026-07-01

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`bulk_data_transfer` *HuBMAP File Querying*

Description

`bulk_data_transfer()` takes a unique dataset or publication UUID to be used to query the HuBMAP API for information about available files.

Usage

```
bulk_data_transfer(uuid)
```

Arguments

`uuid`	character(1) corresponding to the HuBMAP Dataset UUID string. This is expected to be a 32-digit hex number. One unique Dataset UUID corresponds to one specific URL on Globus. Files corresponding to unique Dataset UUID are saved on Globus HuBMAP Public Collection webpage.

Details

Additional details are provided on the HuBMAP consortium webpage, https://software.docs.hubmapconsortium.org/apis

Value

bulk_data_transfer() display information about how to bulk download all files related to the dataset or publication.

Examples

```
# Globus available
uuid_globus <- "2d3dbd5e5a3d9d5cfc7a46f06815a4eb"
uuid_sra_dbGaP <- "5ba6a5b81e95c93c26a33980f6e957d7"
uuid_not_available <- "0eb5e457b4855ce28531bc97147196b6"

# bulk_data_transfer(*_globus)
```

---

collections *HuBMAP Collections*

Description

collections() returns details about available collections, ordered by last modified dates
*_columns() returns a tibble or named character vector describing the content of the tibble returned by samples(), datasets(), donors(), collections(), or publications().

collection_detail() takes a unique collection_id and returns details about one specified collection as a tibble

collection_contacts() takes a unique collection_id and returns contacts information of one specified collection as a tibble

collection_data() takes a unique collection_id and returns related datasets of one specified collection as a tibble

collection_contributors() takes a unique collection_id and returns contributors information of one specified collection as a tibble

Usage

```
collections()

collections_default_columns(as = c("tibble", "character"))

collection_detail(uuid)

collection_contacts(uuid)

collection_data(uuid)

collection_contributors(uuid)
```

Arguments

as	character(1) return format. One of "tibble" (default), or "character".
uuid	character(1) corresponding to the HuBMAP Collection UUID string. This is expected to be a 32-digit hex number.

Details

Additional details are provided on the HuBMAP consortium webpage, https://software.docs.hubmapconsortium.org/apis

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Value

*_columns() returns a named list name containing the column name used in the tibble returned by samples(), datasets(), donors(), collections(), or publications(). When as = "tibble",the return value is a tibble with paths as elements and abbreviations as names.

Examples

```
collections()
collections_default_columns()

uuid <- "a320abcf56241be2e5e453401efeaaf3"
collection_detail(uuid)
uuid <- "381f65e58d5e2c1d16a9cef2cc203aab"
collection_contacts(uuid)
uuid <- "381f65e58d5e2c1d16a9cef2cc203aab"
collection_data(uuid)
uuid <- "590b0485a196956284b8f3344276bc50"
collection_contributors(uuid)
```

---

collection_information

Collection Information Summaries from Collection UUID

Description

collection_information() queries the HuBMAP collection for title, description, DOI, URL, creation date, and last modified time date.

print.collection_information() organizes the returned tibble from collection_information() in a more legible format.

Usage

```
collection_information(uuid)

## S3 method for class 'collection_information'
print(x, ...)
```

Arguments

uuid	character(1) corresponding to the HuBMAP Collection UUID string. This is expected to be a 32-digit hex number.
x	an object of class collection_information, the result of a call to collection_information().
...	additional arguments, required to conform with the print generic but not used.

Value

collection_information() returns a tibble, and columns containing information about the collection. The tibble is of class collection_information and is printed in character.

print.collection_information() is invoked automatically when the result of collection_information() is displayed for it's side effect of displaying the object.

Examples

```
uuid <- "90399057f6ff0ff18d4c46a378f0b069"
collection_information(uuid)
```

---

datasets *HuBMAP Datasets*

Description

datasets returns the details available datasets, ordered by last modified dates
*_columns() returns a tibble or named character vector describing the content of the tibble returned by samples(), datasets(), donors(), collections(), or publications().

dataset_detail() takes a unique dataset_id and returns details about one specified dataset as a tibble

dataset_derived() takes a unique sample_id and returns the derived (support) dataset details. Support datasets normally belong to Image Pyramid, with image files available to download via Globus Collection. See details to download in files_globus_url().

dataset_metadata() takes a unique dataset_id and returns the metadata of the dataset.

dataset_contributors() takes a unique dataset_id and returns the contributors of the dataset. For questions for this dataset, reach out to the individuals listed as contacts, either via the email address listed in the table or contact information provided on their ORCID profile page.

Usage

```
datasets()

datasets_default_columns(as = c("tibble", "character"))

dataset_detail(uuid)

dataset_derived(uuid)

dataset_metadata(uuid)

dataset_contributors(uuid)
```

Arguments

as	character(1) return format. One of "tibble" (default), or "character".
uuid	character(1) corresponding to the HuBMAP Donor UUID string. This is expected to be a 32-digit hex number.

Details

Additional details are provided on the HuBMAP consortium webpage, https://software.docs.hubmapconsortium.org/apis

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Value

*_columns() returns a named list name containing the column name used in the tibble returned by samples(), datasets(), donors(), collections(), or publications(). When as = "tibble",the return value is a tibble with paths as elements and abbreviations as names.

Examples

```
datasets()
datasets_default_columns()

uuid <- "7754aa5ebde628b5e92705e33e74a4ef"
dataset_detail(uuid)
# no derived dataset
uuid <- "3acdb3ed962b2087fbe325514b098101"
dataset_derived(uuid)

# with derived dataset
uuid <- "2c77b1cdf33dbed3dbfb74e4b578300e"
dataset_derived(uuid)
uuid <- "564167adbbb2fdd64c24e7ea409c23f1"
dataset_metadata(uuid)
```

```
uuid <- "564167adbbb2fdd64c24e7ea409c23f1"
dataset_contributors(uuid)
```

---

donors *HuBMAP Donors*

Description

donors() returns details about available samples, ordered by last modified dates
*_columns() returns a tibble or named character vector describing the content of the tibble returned by samples(), datasets(), donors(), collections(), or publications().

donor_detail() takes a unique donor_id and returns details about one specified sample as a tibble

donor_derived() takes a unique donor_id and returns the derived dataset or/and sample details.

donor_metadata() takes a unique donor_id and returns the metadata of the donor.

Usage

```
donors()

donors_default_columns(as = c("tibble", "character"))

donor_detail(uuid)

donor_derived(uuid, entity_type = c("Dataset", "Sample"))

donor_metadata(uuid)
```

Arguments

as	character(1) return format. One of "tibble" (default), or "character".
uuid	character(1) corresponding to the HuBMAP Donor UUID string. This is expected to be a 32-digit hex number.
entity_type	character(1) selected derived entity type. One of "Sample" or "Dataset" (default).

Details

Additional details are provided on the HuBMAP consortium webpage, https://software.docs.hubmapconsortium.org/apis

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Value

`*_columns()` returns a named list `name` containing the column name used in the tibble returned by `samples()`, `datasets()`, `donors()`, `collections()`, or `publications()`. When `as = "tibble"`,the return value is a tibble with paths as elements and abbreviations as names.

Examples

```
donors()
donors_default_columns()

uuid <- "1dcde05aea3509b2cf89a41ceb3d700f"
donor_detail(uuid)
uuid <- "1dcde05aea3509b2cf89a41ceb3d700f"
donor_derived(uuid, "Sample")

uuid <- "d37df2cad4e80dc368763caefccf7140"
donor_metadata(uuid)
```

---

organ *HuBMAP Organs*

Description

`organ` retrieves available organ categories and abbreviations

Usage

```
organ()
```

Value

`organ` returns the tibble with all available organs' abbreviations and corresponding full name.

Examples

```
organs <- organ()
organs |>
    dplyr::select("name") |>
    dplyr::distinct()
```

publications *HuBMAP Samples*

Description

publications() returns details about available samples, ordered by last modified dates. publication_status == TRUE: peer reviewed publication; publication_status == FALSE: pre-print publication. *_columns() returns a tibble or named character vector describing the content of the tibble returned by samples(), datasets(), donors(), collections(), or publications().

publication_data() takes a unique publication_id and returns details about one specified publication.

publication_authors() takes a unique publication_id and returns authors information of one specified collection as a tibble

Usage

```
publications()

publications_default_columns(as = c("tibble", "character"))

publication_data(uuid, entity_type = c("Dataset", "Sample", "Donor"))

publication_authors(uuid)
```

Arguments

as	character(1) return format. One of "tibble" (default), or "character".
uuid	character(1) corresponding to the HuBMAP Publication UUID string. This is expected to be a 32-digit hex number.
entity_type	character(1) selected derived entity type. One of "Sample", "Donor" or "Dataset" (default).

Details

Additional details are provided on the HuBMAP consortium webpage, https://software.docs.hubmapconsortium.org/apis

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Value

*_columns() returns a named list name containing the column name used in the tibble returned by samples(), datasets(), donors(), collections(), or publications(). When as = "tibble",the return value is a tibble with paths as elements and abbreviations as names.

Examples

```
publications()
publications_default_columns()

uuid <- "3c7273660cdf9ab91a7901533b2cd9a5"
publication_data(uuid)

uuid <- "3c7273660cdf9ab91a7901533b2cd9a5"
publication_authors(uuid)
```

---

publication_information

Publication Information Summaries from Publication UUID

Description

`publication_information()` queries the HuBMAP publication for title, abstract, manuscript,corresponding authors, dataset types, and organ.

`publication_information()` organizes the returned tibble from `publication_information()` in a more legible format.

Usage

```
publication_information(uuid)

## S3 method for class 'publication_information'
print(x, ...)
```

Arguments

`uuid`	character(1) corresponding to the HuBMAP Publication UUID string. This is expected to be a 32-digit hex number.
`x`	an object of class `publication_information`, the result of a call to `publication_information()`.
`...`	additional arguments, required to conform with the `print` generic but not used.

Value

`publication_information()` returns a tibble, and columns containing information about the publication. The tibble is of class `publication_information` and is printed in character.

`print.publication_information()` is invoked automatically when the result of `publication_information()` is displayed for it's side effect of displaying the object.

Examples

```
uuid <- "e8338966c69e759157d6c6ad24847989"
publication_information(uuid)
```

samples *HuBMAP Samples*

Description

samples() returns details about available samples, ordered by last modified dates. There are multiple tissue sample types displayed in sample_category column which are block, organ, suspension, and section.
*_columns() returns a tibble or named character vector describing the content of the tibble returned by samples(), datasets(), donors(), collections(), or publications().

sample_detail() takes a unique sample_id and returns details about one specified sample as a tibble

sample_derived() takes a unique sample_id and returns the derived dataset or/and sample details.

sample_metadata() takes a unique donor_id and returns the metadata of the sample.

Usage

```
samples()

samples_default_columns(as = c("tibble", "character"))

sample_detail(uuid)

sample_derived(uuid, entity_type = c("Dataset", "Sample"))

sample_metadata(uuid)
```

Arguments

as	character(1) return format. One of "tibble" (default), or "character".
uuid	character(1) corresponding to the HuBMAP Donor UUID string. This is expected to be a 32-digit hex number.
entity_type	character(1) selected derived entity type. One of "Sample" or "Dataset" (default).

Details

Additional details are provided on the HuBMAP consortium webpage, https://software.docs.hubmapconsortium.org/apis

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Value

`*_columns()` returns a named list `name` containing the column name used in the tibble returned by `samples()`, `datasets()`, `donors()`, `collections()`, or `publications()`. When `as = "tibble"`,the return value is a tibble with paths as elements and abbreviations as names.

Examples

```
samples()
samples_default_columns()

uuid <- "d3525d35f6d5ee3dc3186613b0ab1762"
sample_detail(uuid)
uuid <- "3e7dc14313262af577f686dcb09f5119"
sample_derived(uuid, "Sample")
uuid <- "8d7ce3aab7013e416263d23b0c048900"
sample_metadata(uuid)
```

---

uuid_provenance *HuBMAP Provenance*

Description

HuBMAP Provenance

Usage

```
uuid_provenance(uuid)
```

Arguments

`uuid`	character(1) corresponding to the HuBMAP Dataset or Sample UUID string. This is expected to be a 32-digit hex number.

Details

Additional details are provided on the HuBMAP consortium webpage, https://software.docs.hubmapconsortium.org/apis

Value

`uuid_provenance()` takes a Dataset or Sample UUID, and returns the provenance details as a list of characters, from the most recent ancestor to the furthest ancestor. The entity type of ancestors include Dataset, Sample, and Donor. Note that there is no ancestor for Donor entity such that the returned result will be an empty list.

Examples

```
uuid <- "acf816bed56dd6ba55da82960d937ec4"
uuid_provenance(uuid)
```

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