Package ‘gemma.R’

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Title A wrapper for Gemma's Restful API to access curated gene expression data and differential expression analyses

Version 2.0.0

Description Low- and high-level wrappers for Gemma's RESTful API. They enable access to curated expression and differential expression data from over 10,000 published studies. Gemma is a web site, database and a set of tools for the meta-analysis, re-use and sharing of genomics data, currently primarily targeted at the analysis of gene expression profiles.


License Apache License (>= 2)

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.getResultSetFactors

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Description

Retrieve a single analysis result set by its identifier

Usage

```
.getResultSetFactors(
  resultSet = NA_character_,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

Arguments

- **resultSet**: An expression analysis result set numerical identifier.
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- **file**: The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
- **overwrite**: Whether or not to overwrite if a file exists at the specified filename.

Value

Varies
.getResultSets

Retrieve a single analysis result set by its identifier

Description
Retrieve a single analysis result set by its identifier

Usage

.getResultSets(
  resultSet = NA_character_,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

resultSet  An expression analysis result set numerical identifier.
raw         TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw
            results usually contain additional fields and flags that are omitted in the parsed
            results.
memoised    Whether or not to save to cache for future calls with the same inputs and use the
            result saved in cache if a result is already saved. Doing options(gemma.memoised
            = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised
            to clear the cache.
file        The name of a file to save the results to, or NULL to not write results to a file. If
            raw == TRUE, the output will be the raw endpoint from the API, likely a JSON
            or a gzip file. Otherwise, it will be a RDS file.
overwrite   Whether or not to overwrite if a file exists at the specified filename.

Value

Varies

accessField

Access the field in a list

Description
This function accesses named field within the elements of a list. If an element lacks the field, it’s
filled in by natype.
Usage

`accessField(d, field, natype = NA)`

Arguments

- **d**: Input data list
- **field**: Field name to access in each element
- **natype**: What to fill in when field is unavailable

Value

A vector of elements

---

`blank_processor`  
*A blank processor that returns data as is*

Description

A blank processor that returns data as is

Usage

`blank_processor(data)`

Arguments

- **data**: any data

Value

Data as is

---

`checkBounds`  
*Replace missing data with NAs*

Description

Replace missing data with NAs

Usage

`checkBounds(x, natype = NA)`
**Arguments**

- **x**: Data
- **natype**: type of NA to replace the missing data with

**Value**

Data or NA in case of an out of bounds error

---

**encode**

*URL encode a string safely*

---

**Description**

URL encode a string safely

**Usage**

```r
encode(url)
```

**Arguments**

- **url**: The string to URL encode. Vectors are delimited by a comma.

**Value**

A URL encoding of url

---

**filter_properties**

*Return all supported filter properties*

---

**Description**

Some functions such as `get_datasets` and `get_platforms_by_ids` include a filter argument that allows creation of more complex queries. This function returns a list of supported properties to be used in those filters

**Usage**

```r
filter_properties()
```

**Value**

A list of data.tables that contain supported properties and their data types

**Examples**

```r
filter_properties()
```
forget_gemma_memoised  
*Clear gemma.R cache*

**Description**

Forget past results from memoised calls to the Gemma API (ie. using functions with memoised = TRUE)

**Usage**

```r
forget_gemma_memoised()
```

**Value**

TRUE to indicate cache was cleared.

**Examples**

```r
forget_gemma_memoised()
```

---

**gemma.R**  
*gemma.R package: Access curated gene expression data and differential expression analyses*

**Description**

This package contains wrappers and convenience functions for Gemma’s RESTful API that enables access to curated expression and differential expression data from over 15,000 published studies (as of mid-2022). Gemma (https://gemma.msl.ubc.ca) is a web site, database and a set of tools for the meta-analysis, re-use and sharing of transcriptomics data, currently primarily targeted at the analysis of gene expression profiles.

**Details**

Most users will want to start with the high-level functions like `get_dataset_object`, `get_differential_expression_values` and `get_platform_annotations`. Additional lower-level methods are available that directly map to the Gemma RESTful API methods.

For more information and detailed usage instructions check the README, the function reference and the vignette.

All software-related questions should be posted to the Bioconductor Support Site: https://support.bioconductor.org

**Author(s)**

Javier Castillo-Arnemann, Jordan Sicherman, Ogan Mancarci, Guillaume Poirier-Morency
References

Lim, N. et al., Curation of over 10 000 transcriptomic studies to enable data reuse, Database, 2021. https://doi.org/10.1093/database/baab006

---

gemmaCache

**Gemma Cache**

**Description**

Gemma Cache

**Usage**

gemmaCache()

**Value**

A memoise filesystem

---

gemmaPath

**Get gemma path**

**Description**

Get gemma path

**Usage**

gemmaPath()

**Value**

Link to Gemma API
**gemma_call**  
*Custom gemma call*

### Description

A minimal function to create custom calls. Can be used to acquire unimplemented endpoints and/or raw output without any processing. Refer to the API documentation.

### Usage

```r
gemma_call(call, ..., json = TRUE)
```

#### Arguments

- `call`  
  Gemma API endpoint.

- `...`  
  Parameters included in the call

- `json`  
  If `TRUE` will parse the content as a list

### Value

A list if `json = TRUE` and an `httr` response if `FALSE`

### Examples

```r
# get singular value decomposition for the dataset
ghfix('datasets/(dataset)/svd', dataset = 1)
```

**get_all_pages**  
*Get all pages of a paginated call*

### Description

Given a Gemma.R output from a function with offset and limit arguments, returns the output from all pages. All arguments other than offset, limit

### Usage

```r
get_all_pages(
query,
step_size = 100,
binder = rbind,
directory = NULL,
file = getOption("gemma.file", NA_character_),
overwrite = getOption("gemma.overwrite", FALSE)
)
```
get_datasets

Arguments

query          Output from a `gemma.R` function with offset and query argument
step_size      Size of individual calls to the server. 100 is the maximum value
binder         Binding function for the calls. If `raw = FALSE` use `rbind` to combine the data.tables. If not, use `c` to combine lists
directory      Directory to save the output from the individual calls to. If provided, each page is saved to separate files.
file           The name of a file to save the results to, or `NULL` to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
overwrite      Whether or not to overwrite if a file exists at the specified filename.

Value

A data.table or a list containing data from all pages.

Description

Retrieve all datasets

Usage

```r
get_datasets(
  query = NA_character_,
  filter = NA_character_,
  taxa = NA_character_,
  uris = NA_character_,
  offset = 0L,
  limit = 20L,
  sort = "+id",
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

Arguments

query          The search query. Either plain text ("traumatic"), or an ontology term URI ("http://purl.obolibrary.org/obo/UBERON_0002048"). Datasets that contain the given string in their short or full name will also be matched.
Filter results by matching expression. Use `filter_properties` function to get a list of all available parameters. These properties can be combined using "and" "or" clauses and may contain common operators such as "=". (e.g. "taxon.commonName = human", "taxon.commonName in (human,mouse, rat)", "id < 1000")

taxa A vector of taxon common names (e.g. human, mouse, rat). Providing multiple species will return results for all species. These are appended to the filter and equivalent to filtering for `taxon.commonName` property

uris A vector of ontology term URIs. Providing multiple terms will return results containing any of the terms and their children. These are

offset The offset of the first retrieved result.

limit Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with offset and the `totalElements` attribute in the output to compile all data if needed.

sort Order results by the given property and direction. The '+' sign indicate ascending order whereas the '-' indicate descending.

raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

memoised Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

file The name of a file to save the results to, or NULL to not write results to a file. If `raw` == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

overwrite Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the queried dataset(s). A list if `raw` = TRUE. Returns an empty list if no datasets matched. A successful response may contain 'Geeq' information, which aims to provide a unified metric to measure experiments by the quality of their data, and their suitability for use in Gemma. You can read more about the geeq properties [here](#).

The fields of the output data.table are:

- `experiment.ShortName`: Shortname given to the dataset within Gemma. Often corresponds to accession ID
- `experiment.Name`: Full title of the dataset
- `experiment.ID`: Internal ID of the dataset.
- `experiment.Description`: Description of the dataset
- `experiment.Troubled`: Did an automatic process within gemma or a curator mark the dataset as "troubled"
- `experiment.Accession`: Accession ID of the dataset in the external database it was taken from
get_datasets_by_ids

- `experiment.Database`: The name of the database where the dataset was taken from
- `experiment.URI`: URI of the original database
- `experiment.SampleCount`: Number of samples in the dataset
- `experiment.batchEffect`: A text field describing whether the dataset has batch effects
- `geeq.batchCorrected`: Whether batch correction has been performed on the dataset.
- `geeq.batchConfound`: 0 if batch info isn't available, -1 if batch confound is detected, 1 if batch information is available and no batch confound found
- `geeq.batchEffect`: -1 if batch p value < 0.0001, 1 if batch p value > 0.1, 0 if otherwise and when there is no batch information is available or when the data is confounded with batches.
- `geeq.rawData`: -1 if no raw data available, 1 if raw data was available. When available, Gemma reprocesses raw data to get expression values and batches
- `geeq.qScore`: Data quality score given to the dataset by Gemma.
- `geeq.sScore`: Suitability score given to the dataset by Gemma. Refers to factors like batches, platforms and other aspects of experimental design
- `taxon.Name`: Name of the species
- `taxon.Scientific`: Scientific name for the taxon
- `taxon.ID`: Internal identifier given to the species by Gemma
- `taxon.NCBI`: NCBI ID of the taxon
- `taxon.Database.Name`: Underlying database used in Gemma for the taxon
- `taxon.Database.ID`: ID of the underlying database used in Gemma for the taxon

Examples

```r
get_datasets()
get_datasets(taxa = c("mouse", "human"), uris = "http://purl.obolibrary.org/obo/UBERON_0002048")
# filter below is equivalent to the call above
get_datasets(filter = "taxon.commonName in (mouse,human) and allCharacteristics.valueUri = http://purl.obolibrary"
get_datasets(query = "lung")
```

get_datasets_by_ids

Retrieves datasets by their identifiers

Description

Retrieves datasets by their identifiers
get_datasets_by_ids

Usage

```r
get_datasets_by_ids(
  datasets = NA_character_,
  filter = NA_character_,
  taxa = NA_character_,
  uris = NA_character_,
  offset = 0L,
  limit = 20L,
  sort = "+id",
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

Arguments

datasets  Numerical dataset identifiers or dataset short names. If not specified, all datasets will be returned instead appended to the filter and equivalent to filtering for allCharacteristics.valueUri

filter  Filter results by matching expression. Use `filter_properties` function to get a list of all available parameters. These properties can be combined using "and" "or" clauses and may contain common operators such as "=" "<" or "in". (e.g. "taxon.commonName = human", "taxon.commonName in (human,mouse), "id < 1000")

taxa  A vector of taxon common names (e.g. human, mouse, rat). Providing multiple species will return results for all species. These are appended to the filter and equivalent to filtering for taxon.commonName property

uris  A vector of ontology term URIs. Providing multiple terms will return results containing any of the terms and their children. These are

offset  The offset of the first retrieved result.

limit  Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with `offset` and the totalElements attribute in the output to compile all data if needed.

sort  Order results by the given property and direction. The '+' sign indicate ascending order whereas the '-' indicate descending.

raw  TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

memoised  Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

file  The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
overwrite  Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the queried dataset(s). A list if raw = TRUE. Returns an empty list if no datasets matched. A successful response may contain 'Geeq' information, which aims to provide a unified metric to measure experiments by the quality of their data, and their suitability for use in Gemma. You can read more about the geeq properties here.

The fields of the output data.table are:

- experiment.ShortName: Shortname given to the dataset within Gemma. Often corresponds to accession ID
- experiment.Name: Full title of the dataset
- experiment.ID: Internal ID of the dataset.
- experiment.Description: Description of the dataset
- experiment.Troubled: Did an automatic process within gemma or a curator mark the dataset as "troubled"
- experiment.Accession: Accession ID of the dataset in the external database it was taken from
- experiment.Database: The name of the database where the dataset was taken from
- experiment.URI: URI of the original database
- experiment.SampleCount: Number of samples in the dataset
- geeq.batchEffect: A text field describing whether the dataset has batch effects
- geeq.batchCorrected: Whether batch correction has been performed on the dataset.
- geeq.batchConfound: 0 if batch info isn't available, -1 if batch confound is detected, 1 if batch information is available and no batch confound found
- geeq.batchEffect: -1 if batch p value < 0.0001, 1 if batch p value > 0.1, 0 if otherwise and when there is no batch information is available or when the data is confounded with batches.
- geeq.rawData: -1 if no raw data available, 1 if raw data was available. When available, Gemma reprocesses raw data to get expression values and batches
- geeq.qScore: Data quality score given to the dataset by Gemma.
- geeq.sScore: Suitability score given to the dataset by Gemma. Refers to factors like batches, platforms and other aspects of experimental design
- taxon.Name: Name of the species
- taxon.Scientific: Scientific name for the taxon
- taxon.ID: Internal identifier given to the species by Gemma
- taxon.NCBI: NCBI ID of the taxon
- taxon.Database.Name: Underlying database used in Gemma for the taxon
- taxon.Database.ID: ID of the underlying database used in Gemma for the taxon

Examples

```r
get_datasets_by_ids("GSE2018")
get_datasets_by_ids(c("GSE2018", "GSE2872"))
```
get_dataset_annotations

Retrieve the annotations of a dataset

Description
Retrieve the annotations of a dataset

Usage
get_dataset_annotations(
  dataset,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

- **dataset**: A numerical dataset identifier or a dataset short name
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- **file**: The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
- **overwrite**: Whether or not to overwrite if a file exists at the specified filename.

Value
A data table with information about the annotations of the queried dataset. A list if `raw = TRUE`. A 404 error if the given identifier does not map to any object.

The fields of the output `data.table` are:

- **class.Type**: Type of the annotation class
- **class.Name**: Name of the annotation class (e.g. organism part)
- **class.URI**: URI for the annotation class
- **term.Name**: Name of the annotation term (e.g. lung)
- **term.URI**: URI for the annotation term
get_dataset_design

Examples

get_dataset_annotations("GSE2018")

generate_design

Retrieve the design of a dataset

Description

Retrieve the design of a dataset

Usage

get_dataset_design(
  dataset,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

dataset A numerical dataset identifier or a dataset short name

raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw
results usually contain additional fields and flags that are omitted in the parsed
results.

memoised Whether or not to save to cache for future calls with the same inputs and use the
result saved in cache if a result is already saved. Doing options(gemma.memoised
= TRUE) will ensure that the cache is always used. Use forget_gemma_memoised
to clear the cache.

file The name of a file to save the results to, or NULL to not write results to a file. If
raw == TRUE, the output will be the raw endpoint from the API, likely a JSON
or a gzip file. Otherwise, it will be a RDS file.

overwrite Whether or not to overwrite if a file exists at the specified filename.

Value

A data table of the design matrix for the queried dataset. A 404 error if the given identifier does
not map to any object

Examples

head(get_dataset_design("GSE2018"))
get_dataset_differential_expression_analyses

Retrieve annotations and surface level stats for a dataset’s differential analyses

Description

Retrieve annotations and surface level stats for a dataset’s differential analyses

Usage

get_dataset_differential_expression_analyses(
  dataset,
  offset = 0L,
  limit = 20L,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

dataset A numerical dataset identifier or a dataset short name
offset The offset of the first retrieved result.
limit Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with offset and the totalElements attribute in the output to compile all data if needed.
raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
memoised Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.
file The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
overwrite Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the differential expression analysis of the queried dataset. Note that this function does not return differential expression values themselves. Use get_differential_expression_values to get differential expression values (see examples).

The fields of the output data.table are:
• result.ID: Result set ID of the differential expression analysis. May represent multiple factors in a single model.
• contrast.ID: Id of the specific contrast factor. Together with the result.ID they uniquely represent a given contrast.
• experiment.ID: Id of the source experiment
• baseline.category: Category for the contrast
• baseline.categoryURI: URI for the baseline category
• baseline.factors: Characteristics of the baseline. This field is a data.table
• experimental.factors: Characteristics of the experimental group. This field is a data.table
• subsetFactor.subset: TRUE if the result set belong to a subset, FALSE if not. Subsets are created when performing differential expression to avoid unhelpful comparisons.
• subsetFactor.category: Category of the subset
• subsetFactor: Characteristics of the subset. This field is a data.table
• probes.Analyzed: Number of probesets represented in the contrast
• genes.Analyzed: Number of genes represented in the contrast

Examples

```r
result <- get_dataset_differential_expression_analyses("GSE2872")
get_differential_expression_values(resultSet = result$result.ID[1])
```

---

**get_dataset_expression**

*Retrieve processed expression data of a dataset*

**Description**

This function is deprecated in favor of **get_dataset_processed_expression**

**Usage**

```r
get_dataset_expression(
  dataset,
  filter = FALSE,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```
get_dataset_expression_for_genes

Arguments

- **dataset**
  A numerical dataset identifier or a dataset short name
- **filter**
  This argument is ignored due to deprecation of the function
- **raw**
  TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**
  Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- **file**
  The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
- **overwrite**
  Whether or not to overwrite if a file exists at the specified filename.

Value

If raw is FALSE (default), a data table of the expression matrix for the queried dataset. If raw is TRUE, returns the binary file in raw form.

Examples

```r
get_dataset_expression("GSE2018")
```

```
get_dataset_expression_for_genes

Retrieve the expression data matrix of a set of datasets and genes

Description

Retrieve the expression data matrix of a set of datasets and genes

Usage

```r
generate_dataset_expression_for_genes(  datasets,  genes,  keepNonSpecific = FALSE,  consolidate = NA_character_,  raw =getOption("gemma.raw", FALSE),  memoised =getOption("gemma.memoised", FALSE),  file =getOption("gemma.file", NA_character_),  overwrite =getOption("gemma.overwrite", FALSE) )
```
```
get_dataset_object

Arguments

- **datasets**: A numerical dataset identifier or a dataset short name
- **genes**: An ensembl gene identifier which typically starts with ensg or an ncbi gene identifier or an official gene symbol approved by hgnc
- **keepNonSpecific**: logical. FALSE by default. If TRUE, results from probesets that are not specific to the gene will also be returned.
- **consolidate**: An option for gene expression level consolidation. If empty, will return every probe for the genes. "pickmax" to pick the probe with the highest expression, "pickvar" to pick the probe with the highest variance and "average" for returning the average expression
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- **file**: The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
- **overwrite**: Whether or not to overwrite if a file exists at the specified filename.

Value

A list of data frames

Examples

```r
get_dataset_expression_for_genes("GSE2018", genes = c(10225, 2841))
```

Description

Return an annotated Bioconductor-compatible data structure or a long form tibble of the queried dataset, including expression data and the experimental design.
Usage

get_dataset_object(
    datasets,
    genes = NULL,
    keepNonSpecific = FALSE,
    consolidate = NA_character_,
    resultSets = NULL,
    contrasts = NULL,
    metaType = "text",
    type = "se",
    memoised = getOption("gemma.memoised", FALSE)
)

Arguments

datasets A numerical dataset identifier or a dataset short name

genes An ensembl gene identifier which typically starts with ensg or an ncbi gene
identifier or an official gene symbol approved by hgnc

keepNonSpecific logical. FALSE by default. If TRUE, results from probesets that are not specific to
the gene will also be returned.

consolidate An option for gene expression level consolidation. If empty, will return every
probe for the genes. "pickmax" to pick the probe with the highest expression,
"pickvar" to pick the prove with the highest variance and "average" for returning
the average expression

resultSets Result set IDs of the a differential expression analysis. Optional. If provided,
the output will only include the samples from the subset used in the result set
ID. Must be the same length as datasets.

contrasts Contrast IDs of a differential expression contrast. Optional. Need resultSets to
be defined to work. If provided, the output will only include samples relevant to
the specific contrats.

metaType How should the metadata information should be included. Can be "text", "uri"
or "both". "text" and "uri" options

type "se"for a SummarizedExperiment or "eset" for Expression Set. We recommend
using SummarizedExperiments which are more recent. See the Summarized
experiment vignette or the ExpressionSet vignette for more details.

memoised Whether or not to save to cache for future calls with the same inputs and use the
result saved in cache if a result is already saved. Doing options(gemma.memoised
= TRUE) will ensure that the cache is always used. Use forget_gemma_memoised
to clear the cache.

Value

A list of SummarizedExperiments, ExpressionSets or a tibble containing metadata and expression
data for the queried datasets and genes. Metadata will be expanded to include a variable number of
factors that annotates samples from a dataset but will always include single "factorValues" column
that houses data.tables that include all annotations for a given sample.
get_dataset_platforms

Examples

get_dataset_object("GSE2018")

get_dataset_platforms  Retrieve the platforms of a dataset

Description

Retrieve the platforms of a dataset

Usage

get_dataset_platforms(
  dataset,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

dataset  A numerical dataset identifier or a dataset short name
raw  TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
memoised  Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.
file  The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
overwrite  Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the platform(s). A list if raw = TRUE. A 404 error if the given identifier does not map to any object

The fields of the output data.table are:

- platform.ID: Internal identifier of the platform
- platform.ShortName: Shortname of the platform.
- platform.Name: Full name of the platform.
- platform.Description: Free text description of the platform
get_dataset_processed_expression

Retrieve processed expression data of a dataset

Description

Retrieve processed expression data of a dataset

Usage

get_dataset_processed_expression(
  dataset,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

dataset A numerical dataset identifier or a dataset short name
raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
memoised Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.
file The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
overwrite Whether or not to overwrite if a file exists at the specified filename.
get_dataset_quantitation_types

Value

If `raw` is FALSE (default), a data table of the expression matrix for the queried dataset. If `raw` is TRUE, returns the binary file in raw form.

Examples

```r
get_dataset_processed_expression("GSE2018")
```

Description

Retrieve quantitation types of a dataset

Usage

```r
get_dataset_quantitation_types(
  dataset,
  raw =getOption("gemma.raw", FALSE),
  memoised =getOption("gemma.memoised", FALSE),
  file =getOption("gemma.file", NA_character_),
  overwrite =getOption("gemma.overwrite", FALSE)
)
```

Arguments

- **dataset**: A numerical dataset identifier or a dataset short name
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- **file**: The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
- **overwrite**: Whether or not to overwrite if a file exists at the specified filename.
Value

A data.table containing the quantitation types

The fields of the output data.table are:

• id: If of the quantitation type. Any raw quantitation type can be accessed by `get_dataset_raw_expression` function using this id.
• name: Name of the quantitation type
• description: Description of the quantitation type
• type: Type of the quantitation type. Either raw or processed. Each dataset will have one processed quantitation type which is the data returned using `get_dataset_processed_expression`.
• preferred: The preferred raw quantitation type. This version is used in generation of the processed data within gemma.
• recomputed: If TRUE this quantitation type is generated by recomputing raw data files Gemma had access to.

Examples

```r
get_dataset_quantitation_types("GSE59918")
```

---

### get_dataset_raw_expression

`get_dataset_raw_expression` _Retrieve raw expression data of a dataset_

**Description**

Retrieve raw expression data of a dataset

**Usage**

```r
get_dataset_raw_expression(
  dataset,
  quantitationType,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

**Arguments**

- **dataset**  
  A numerical dataset identifier or a dataset short name
- **quantitationType**  
  Quantitation type id. These can be acquired using `get_dataset_quantitation_types` function. This endpoint can only return non-processed quantitation types.
**get_dataset_samples**

**Description**

Retrieve the samples of a dataset

**Usage**

```r
get_dataset_samples(
  dataset,
  raw =getOption("gemma.raw", FALSE),
  memoised =getOption("gemma.memoised", FALSE),
  file =getOption("gemma.file", NA_character_),
  overwrite =getOption("gemma.overwrite", FALSE)
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dataset</td>
<td>A numerical dataset identifier or a dataset short name</td>
</tr>
<tr>
<td>raw</td>
<td>TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.</td>
</tr>
</tbody>
</table>

**Value**

If raw is FALSE (default), a data table of the expression matrix for the queried dataset. If raw is TRUE, returns the binary file in raw form.

**Examples**

```r
q_types <- get_dataset_quantitation_types("GSE59918")
get_dataset_raw_expression("GSE59918", q_types$id[q_types$name == "Counts"])
```

---

**get_dataset_samples**

Retrieve the samples of a dataset

**Description**

Retrieve the samples of a dataset

**Usage**

```r
get_dataset_samples(
  dataset,
  raw =getOption("gemma.raw", FALSE),
  memoised =getOption("gemma.memoised", FALSE),
  file =getOption("gemma.file", NA_character_),
  overwrite =getOption("gemma.overwrite", FALSE)
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dataset</td>
<td>A numerical dataset identifier or a dataset short name</td>
</tr>
<tr>
<td>raw</td>
<td>TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.</td>
</tr>
</tbody>
</table>

---

**Value**

If raw is FALSE (default), a data table of the expression matrix for the queried dataset. If raw is TRUE, returns the binary file in raw form.

**Examples**

```r
q_types <- get_dataset_quantitation_types("GSE59918")
get_dataset_raw_expression("GSE59918", q_types$id[q_types$name == "Counts"])
```
get_differential_expression_values

memoised  Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

file  The name of a file to save the results to, or `NULL` to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

overwrite  Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the samples of the queried dataset. A list if `raw = TRUE`. A 404 error if the given identifier does not map to any object.

The fields of the output data.table are:

- `sample.Name`: Internal name given to the sample.
- `sample.ID`: Internal ID of the sample
- `sample.Description`: Free text description of the sample
- `sample.Outlier`: Whether or not the sample is marked as an outlier
- `sample.Accession`: Accession ID of the sample in its original database
- `sample.Database`: Database of origin for the sample
- `sample.Characteristics`: Characteristics of the sample. This field is a data table
- `sample.FactorValues`: Experimental factor values of the sample. This field is a data table

Examples

```r
head(get_dataset_samples("GSE2018"))
```

get_differential_expression_values

 Retrieve differential expression results

Description

Retrieves the differential expression result set(s) associated with the dataset. To get more information about the contrasts in individual resultSets and annotation terms associated them, use `get_dataset_differential_expression_analyses()`

Usage

```r
get_differential_expression_values(
  dataset = NA_character_,
  resultSet = NA_integer_,
  readableContrasts = FALSE,
  memoised = getOption("gemma.memoised", FALSE)
)
```
**get_genes**

**Arguments**

- **dataset**: A dataset identifier.
- **resultSet**: A resultSet identifier.
- **readableContrasts**: If **FALSE** (default), the returned columns will use internal contrasts IDs as names. Details about the contrasts can be accessed using `get_dataset_differential_expression_analyses`. If **TRUE** IDs will be replaced with human readable contrast information.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

**Details**

In Gemma each result set corresponds to the estimated effects associated with a single factor in the design, and each can have multiple contrasts (for each level compared to baseline). Thus a dataset with a 2x3 factorial design will have two result sets, one of which will have one contrast, and one having two contrasts.

The methodology for differential expression is explained in *Curation of over 10000 transcriptomic studies to enable data reuse*. Briefly, differential expression analysis is performed on the dataset based on the annotated experimental design with up two three potentially nested factors. Gemma attempts to automatically assign baseline conditions for each factor. In the absence of a clear control condition, a baseline is arbitrarily selected. A generalized linear model with empirical Bayes shrinkage of t-statistics is fit to the data for each platform element (probe/gene) using an implementation of the limma algorithm. For RNA-seq data, we use weighted regression, applying the voom algorithm to compute weights from the mean–variance relationship of the data. Contrasts of each condition are then computed compared to the selected baseline. In some situations, Gemma will split the data into subsets for analysis. A typical such situation is when a ‘batch’ factor is present and confounded with another factor, the subsets being determined by the levels of the confounding factor.

**Value**

A list of data tables with differential expression values per result set.

**Examples**

```r
get_differential_expression_values("GSE2018")
```

---

**get_genes**

*Retrieve genes matching gene identifiers*

**Description**

Retrieve genes matching gene identifiers
Usage

get_genes(
  genes,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

genes An ensembl gene identifier which typically starts with ensg or an ncbi gene identifier or an official gene symbol approved by hgnc

raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

memoised Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.

file The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

overwrite Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the queried gene(s) A list if raw = TRUE.

The fields of the output data.table are:

- gene.Symbol: Symbol for the gene
- gene.Ensembl: Ensembl ID for the gene
- gene.NCBI: NCBI id for the gene
- gene.Name: Name of the gene
- gene.MFX.Rank: Multifunctionality rank for the gene
- taxon.Name: Name of the species
- taxon.Scientific: Scientific name for the taxon
- taxon.ID: Internal identifier given to the species by Gemma
- taxon.NCBI: NCBI ID of the taxon
- taxon.Database.Name: Underlying database used in Gemma for the taxon
- taxon.Database.ID: ID of the underlying database used in Gemma for the taxon

Examples

get_genes("DYRK1A")
get_genes(c("DYRK1A", "PTEN"))
get_gene_go_terms

Retrieve the GO terms associated to a gene

Description
Retrieve the GO terms associated to a gene

Usage
get_gene_go_terms(
gene,
raw = getOption("gemma.raw", FALSE),
memoised = getOption("gemma.memoised", FALSE),
file = getOption("gemma.file", NA_character_),
overwrite = getOption("gemma.overwrite", FALSE)
)

Arguments

gene An ensembl gene identifier which typically starts with ensg or an ncbi gene identifier or an official gene symbol approved by hgnc

raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

memoised Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.

file The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

overwrite Whether or not to overwrite if a file exists at the specified filename.

Value
A data table with information about the GO terms assigned to the queried gene. A list if raw = TRUE. A 404 error if the given identifier does not map to any object.

The fields of the output data.table are:

• term.Name: Name of the term
• term.ID: ID of the term
• term.URI: URI of the term

Examples
get_gene_go_terms("DYRK1A")
get_gene_locations  

Retrieve the physical locations of a given gene

Description

Retrieve the physical locations of a given gene

Usage

```r
get_gene_locations(
  gene,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

Arguments

- **gene**: An ensembl gene identifier which typically starts with ensg or an ncbi gene identifier or an official gene symbol approved by hgnc
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- **file**: The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
- **overwrite**: Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the physical location of the queried gene. A list if `raw = TRUE`. A 404 error if the given identifier does not map to any object.

The fields of the output data.table are:

- **chromosome**: Name of the chromosome the gene is located
- **strand**: Which strand the gene is located
- **nucleotide**: Nucleotide number for the gene
- **length**: Gene length
- **taxon.name**: Name of the taxon
get_gene_probes

- `taxon.Scientific`: Scientific name for the taxon
- `taxon.ID`: Internal ID for the taxon given by Gemma
- `taxon.NCBI`: NCBI ID for the taxon
- `taxon.Database.Name`: Name of the database used in Gemma for the taxon

Examples

```r
get_gene_locations("DYRK1A")
```

---

**Description**

Retrieve the probes associated to a gene across all platforms

**Usage**

```r
get_gene_probes(
  gene,
  offset = 0L,
  limit = 20L,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

**Arguments**

- **gene**: An ensembl gene identifier which typically starts with ensg or an ncbi gene identifier or an official gene symbol approved by hgnc.
- **offset**: The offset of the first retrieved result.
- **limit**: Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with `offset` and the `totalElements` attribute in the output to compile all data if needed.
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- **file**: The name of a file to save the results to, or NULL to not write results to a file. If `raw` == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
- **overwrite**: Whether or not to overwrite if a file exists at the specified filename.
Value
A data table with information about the probes representing a gene across all platforms. A list if `raw = TRUE`. A 404 error if the given identifier does not map to any genes.

The fields of the output data table are:

- `mapping.name`: Name of the mapping. Typically the probeset name
- `mapping.description`: A free text field providing optional information about the mapping
- `platform.ShortName`: Shortname of the platform given by Gemma. Typically the GPL identifier.
- `platform.Name`: Full name of the platform
- `platform.ID`: Id number of the platform given by Gemma
- `platform.Taxon`: Species the platform was designed for
- `platform.TaxonID`: Id number of the species given by Gemma
- `platform.Type`: Type of the platform.
- `platform.Description`: Free text field describing the platform.
- `platform.Troubled`: Whether the platform is marked as troubled by a Gemma curator.

Examples

```
get_gene_probes("DYRK1A")
```

---

**get_platforms_by_ids**

Retrieve all platforms matching a set of platform identifiers

Description
Retrieve all platforms matching a set of platform identifiers

Usage
```
get_platforms_by_ids(
   platforms = NA_character_,
   filter = NA_character_,
   taxa = NA_character_,
   offset = 0L,
   limit = 20L,
   sort = "+id",
   raw = getOption("gemma.raw", FALSE),
   memoised = getOption("gemma.memoised", FALSE),
   file = getOption("gemma.file", NA_character_),
   overwrite = getOption("gemma.overwrite", FALSE)
)
```
get_platforms_by_ids

Arguments

platforms Platform numerical identifiers or platform short names. If not specified, all platforms will be returned instead.

filter Filter results by matching expression. Use filter_properties function to get a list of all available parameters. These properties can be combined using "and" "or" clauses and may contain common operators such as ":=","<" or "in". (e.g. "taxon.commonName = human", "taxon.commonName in (human,mouse), "id < 1000")

taxa A vector of taxon common names (e.g. human, mouse, rat). Providing multiple species will return results for all species. These are appended to the filter and equivalent to filtering for taxon.commonName property.

offset The offset of the first retrieved result.

limit Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with offset and the totalElements attribute in the output to compile all data if needed.

sort Order results by the given property and direction. The '+' sign indicate ascending order whereas the '-' indicate descending.

raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

memoised Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.

file The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

overwrite Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with information about the platform(s). A list if raw = TRUE. A 404 error if the given identifier does not map to any object.

The fields of the output data.table are:

- platform.ID: Internal identifier of the platform.
- platform.ShortName: Shortname of the platform.
- platform.Name: Full name of the platform.
- platform.Description: Free text description of the platform.
- platform.Troubled: Whether or not the platform was marked "troubled" by a Gemma process or a curator.
- platform.ExperimentCount: Number of experiments using the platform within Gemma.
- platform.Type: Technology type for the platform.
get_platform_annotations

Retrieve Platform Annotations by Gemma

Description

Gets Gemma’s platform annotations including mappings of microarray probes to genes.

Usage

```r
get_platform_annotations(
  platform,  
  annotType = c("noParents", "allParents", "bioProcess"), 
  file = getOption("gemma.file", NA_character_), 
  overwrite = getOption("gemma.overwrite", FALSE), 
  memoised = getOption("gemma.memoise", FALSE), 
  unzip = FALSE
)
```

Arguments

- `platform`: A platform identifier \seealso{getPlatforms}
- `annotType`: Which GO terms should the output include
- `file`: Where to save the annotation file to, or empty to just load into memory
- `overwrite`: Whether or not to overwrite an existing file
- `memoised`: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
- `unzip`: Whether or not to unzip the file (if \param file is not empty)
Value

A table of annotations

- **ProbeName**: Probeset names provided by the platform. Gene symbols for generic annotations
- **GeneSymbols**: Genes that were found to be aligned to the probe sequence. Note that it is possible for probes to be non-specific. Alignment to multiple genes are indicated with gene symbols separated by "|"s
- **GeneNames**: Name of the gene
- **GOTerms**: GO Terms associated with the genes. annotType argument can be used to choose which terms should be included.
- **GemmaIDs** and **NCBIids**: respective IDs for the genes.

Examples

```r
tab <- get_platform_annotations("GPL96")
tab <- get_platform_annotations("Generic_human")
```

---

**get_platform_datasets**  Retrieve all experiments using a given platform

Description

Retrieve all experiments using a given platform

Usage

```r
get_platform_datasets(
  platform,  
  offset = 0L, 
  limit = 20L, 
  raw = getOption("gemma.raw", FALSE), 
  memoised = getOption("gemma.memoised", FALSE), 
  file = getOption("gemma.file", NA_character_), 
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

Arguments

- **platform**: A platform numerical identifier or a platform short name
- **offset**: The offset of the first retrieved result.
- **limit**: Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with offset and the totalElements attribute in the output to compile all data if needed.
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
get_platform_datasets

**memoised**
Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

**file**
The name of a file to save the results to, or `NULL` to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

**overwrite**
Whether or not to overwrite if a file exists at the specified filename.

**Value**
A data table with information about the queried dataset(s). A list if `raw == TRUE`. Returns an empty list if no datasets matched. A successful response may contain ‘Geeq’ information, which aims to provide a unified metric to measure experiments by the quality of their data, and their suitability for use in Gemma. You can read more about the geeq properties [here](#).

The fields of the output data.table are:

- **experiment.ShortName**: Shortname given to the dataset within Gemma. Often corresponds to accession ID
- **experiment.Name**: Full title of the dataset
- **experiment.ID**: Internal ID of the dataset.
- **experiment.Description**: Description of the dataset
- **experiment.Troubled**: Did an automatic process within gemma or a curator mark the dataset as "troubled"
- **experiment.Accession**: Accession ID of the dataset in the external database it was taken from
- **experiment.Database**: The name of the database where the dataset was taken from
- **experiment.URI**: URI of the original database
- **experiment.SampleCount**: Number of samples in the dataset
- **experiment.batchEffect**: A text field describing whether the dataset has batch effects
- **geeq.batchCorrected**: Whether batch correction has been performed on the dataset.
- **geeq.batchConfound**: 0 if batch info isn’t available, -1 if batch confound is detected, 1 if batch information is available and no batch confound found
- **geeq.batchEffect**: -1 if batch p value < 0.0001, 1 if batch p value > 0.1, 0 if otherwise and when there is no batch information is available or when the data is confounded with batches.
- **geeq.rawData**: -1 if no raw data available, 1 if raw data was available. When available, Gemma reprocesses raw data to get expression values and batches
- **geeq.qScore**: Data quality score given to the dataset by Gemma.
- **geeq.sScore**: Suitability score given to the dataset by Gemma. Refers to factors like batches, platforms and other aspects of experimental design
- **taxon.Name**: Name of the species
- **taxon.Scienitic**: Scientific name for the taxon
get_platform_element_genes

- **taxon.ID**: Internal identifier given to the species by Gemma
- **taxon.NCBI**: NCBI ID of the taxon
- **taxon.Database.Name**: Underlying database used in Gemma for the taxon
- **taxon.Database.ID**: ID of the underlying database used in Gemma for the taxon

Examples

```r
head(get_platform_datasets("GPL1355"))
```

---

get_platform_element_genes

*Retrieve the genes associated to a probe in a given platform*

Description

Retrieve the genes associated to a probe in a given platform

Usage

```r
get_platform_element_genes(
  platform,
  probe,
  offset = 0L,
  limit = 20L,
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

Arguments

- **platform**: A platform numerical identifier or a platform short name
- **probe**: A probe name or its numerical identifier
- **offset**: The offset of the first retrieved result.
- **limit**: Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with `offset` and the `totalElements` attribute in the output to compile all data if needed.
- **raw**: TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
- **memoised**: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
get_taxa

Description

Returns taxa and their versions used in Gemma

Usage

get_taxa(memoised = getOption("gemma.memoised", FALSE))

Arguments

- memoised: Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.
get_taxa_by_ids

Value
A data frame including the names, IDs and database information about the taxons

Examples
get_taxa()

get_taxa_by_ids (taxa, raw = getOption("gemma.raw", FALSE), memoised = getOption("gemma.memoised", FALSE), file = getOption("gemma.file", NA_character_), overwrite = getOption("gemma.overwrite", FALSE))

Arguments
taxa Limits the result to entities with given identifiers. A vector of identifiers. Identifiers can be any of the following:
• taxon ID
• scientific name
• common name Retrieval by ID is more efficient. Do not combine different identifiers in one query. For convenience, below is a list of officially supported taxa

<table>
<thead>
<tr>
<th>ID</th>
<th>Common name</th>
<th>Scientific name</th>
<th>NCBIID</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>human</td>
<td>Homo sapiens</td>
<td>9606</td>
</tr>
<tr>
<td>2</td>
<td>mouse</td>
<td>Mus musculus</td>
<td>10090</td>
</tr>
<tr>
<td>3</td>
<td>rat</td>
<td>Rattus norvegicus</td>
<td>10116</td>
</tr>
<tr>
<td>11</td>
<td>yeast</td>
<td>Saccharomyces cerevisiae</td>
<td>4932</td>
</tr>
<tr>
<td>12</td>
<td>zebrafish</td>
<td>Danio rerio</td>
<td>7955</td>
</tr>
<tr>
<td>13</td>
<td>fly</td>
<td>Drosophila melanogaster</td>
<td>7227</td>
</tr>
<tr>
<td>14</td>
<td>worm</td>
<td>Caenorhabditis elegans</td>
<td>6239</td>
</tr>
</tbody>
</table>

raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
memoised  Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

file  The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

overwrite  Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with the queried taxa’s details.

Examples

```r
get_taxa_by_ids(c("mouse", "human"))
```

---

get_taxon_datasets  Retrieve the datasets for a given taxon

Description

This function is deprecated in favor of `get_datasets`

Usage

```r
get_taxon_datasets(
  taxon,
  offset = 0L,
  limit = 20,
  sort = "+id",
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE),
  ...
)
```

Arguments

taxon  can either be Taxon ID, Taxon NCBI ID, or one of its string identifiers: scientific name, common name. It is recommended to use Taxon ID for efficiency. Please note, that not all taxa have all the possible identifiers available. Use the `get_taxa_by_ids` function to retrieve the necessary information. For convenience, below is a list of officially supported taxa:
ID  | Comm.name | Scient.name          | NcbiID |
---  |-----------|----------------------|--------|
1    | human     | Homo sapiens         | 9606   |
2    | mouse     | Mus musculus         | 10090  |
3    | rat       | Rattus norvegicus    | 10116  |
11   | yeast     | Saccharomyces cerevisiae | 4932 |
12   | zebrafish | Danio rerio          | 7955   |
13   | fly       | Drosophila melanogaster | 7227 |
14   | worm      | Caenorhabditis elegans | 6239 |

offset  | The offset of the first retrieved result.
limit   | Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with offset and the totalElements attribute in the output to compile all data if needed.
sort    | Order results by the given property and direction. The '+' sign indicate ascending order whereas the '-' indicate descending.
raw     | TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.
memoised| Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.
file    | The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be a JSON file. Otherwise, it will be a RDS file.
overwrite| Whether or not to overwrite if a file exists at the specified filename.
...     | Kept for compatibility. Ignored

Value

A data table with information about the queried dataset(s). A list if raw = TRUE. Returns an empty list if no datasets matched. A successful response may contain 'Geeq' information, which aims to provide a unified metric to measure experiments by the quality of their data, and their suitability for use in Gemma. You can read more about the geeq properties here.

The fields of the output data.table are:

- experiment.ShortName: Shortname given to the dataset within Gemma. Often corresponds to accession ID
- experiment.Name: Full title of the dataset
- experiment.ID: Internal ID of the dataset.
- experiment.Description: Description of the dataset
- experiment.Troubled: Did an automatic process within gemma or a curator mark the dataset as "troubled"
- experiment.Accession: Accession ID of the dataset in the external database it was taken from
• **experiment.Database**: The name of the database where the dataset was taken from
• **experiment.URI**: URI of the original database
• **experiment.SampleCount**: Number of samples in the dataset
• **experiment.batchEffect**: A text field describing whether the dataset has batch effects
• **geeq.batchCorrected**: Whether batch correction has been performed on the dataset.
• **geeq.batchConfound**: 0 if batch info isn’t available, -1 if batch confound is detected, 1 if batch information is available and no batch confound found
• **geeq.batchEffect**: -1 if batch p value < 0.0001, 1 if batch p value > 0.1, 0 if otherwise and when there is no batch information is available or when the data is confounded with batches.
• **geeq.rawData**: -1 if no raw data available, 1 if raw data was available. When available, Gemma reprocesses raw data to get expression values and batches
• **geeq.qScore**: Data quality score given to the dataset by Gemma.
• **geeq.sScore**: Suitability score given to the dataset by Gemma. Refers to factors like batches, platforms and other aspects of experimental design
• **taxon.Name**: Name of the species
• **taxon.Scientific**: Scientific name for the taxon
• **taxon.ID**: Internal identifier given to the species by Gemma
• **taxon.NCBI**: NCBI ID of the taxon
• **taxon.Database.Name**: Underlying database used in Gemma for the taxon
• **taxon.Database.ID**: ID of the underlying database used in Gemma for the taxon

**Examples**

get_taxon_datasets("human")

**Description**

Using on the output of `get_dataset_samples`, this function creates a simplified design table, granting one column to each experimental variable.

**Usage**

make_design(samples, metaType = "text")

**Arguments**

- **samples**: An output from `get_dataset_samples`. The output should not be raw
- **metaType**: Type of metadata to include in the output. "text", "uri" or "both"
**nullCheck**

**Value**

A data.frame including the design table for the dataset

**Examples**

```r
samples <- get_dataset_samples('GSE46416')
make_design(samples)
```

---

**nullCheck**

_Avoid NULLS as data.table columns_

**Description**

_Avoid NULLS as data.table columns_

**Usage**

```r
nullCheck(x, natype = NA)
```

**Arguments**

- **x**: A value that might be null
- **natype**: What to fill in when data is unavailable

**Value**

*x* as is or natype

---

**processAnnotations**

_Processes JSON as annotations_

**Description**

_Processes JSON as annotations_

**Usage**

```r
processAnnotations(d)
```

**Arguments**

- **d**: The JSON to process
**Value**

A data table with information about the annotations of the queried dataset. A list if `raw = TRUE`. A 404 error if the given identifier does not map to any object.

The fields of the output data.table are:

- **class.Type**: Type of the annotation class
- **class.Name**: Name of the annotation class (e.g. organism part)
- **class.URI**: URI for the annotation class
- **term.Name**: Name of the annotation term (e.g. lung)
- **term.URI**: URI for the annotation term

---

**processCharacteristicBasicValueObject**

*Processes JSON as a factor*

---

**Description**

Processes JSON as a factor

**Usage**

`processCharacteristicBasicValueObject(d)`

**Arguments**

- **d**: The JSON to process

**Value**

A processed data.table

---

**processDatasetResultSets**

*Processes JSON as a datasets result set*

---

**Description**

Processes JSON as a datasets result set

**Usage**

`processDatasetResultSets(d)`
processDatasets

Arguments

d The JSON to process

Value

A data table with the queried datasets’ resultSet ID(s). A list if raw = TRUE. Use get_differential_expression_values to get differential expression values (see examples). Use get_dataset_differential_expression_analyses to get more detailed information about a result set.

The fields of the output data table are:

• resultSet.id: Internal ID given to the result set. Can be used to access the results using get_differential_expression_values
• factor.category: What is the category splitting the experimental groups in the result set (e.g. disease)
• factor.levels: What are the conditions that are compared in the result set (e.g. control, bipolar disorder)

processDatasets Processes JSON as a vector of datasets

Description

Processes JSON as a vector of datasets

Usage

processDatasets(d)

Arguments

d The JSON to process

Value

A data table with information about the queried dataset(s). A list if raw = TRUE. Returns an empty list if no datasets matched. A successful response may contain ‘Geeq’ information, which aims to provide a unified metric to measure experiments by the quality of their data, and their suitability for use in Gemma. You can read more about the geeq properties here.

The fields of the output data table are:

• experiment.ShortName: Shortname given to the dataset within Gemma. Often corresponds to accession ID
• experiment.Name: Full title of the dataset
• experiment.ID: Internal ID of the dataset
• experiment.Description: Description of the dataset
processDEA

Processes JSON as a differential expression analysis

Description

Processes JSON as a differential expression analysis

Usage

processDEA(d)

Arguments

d The JSON to process
Value

A data table with information about the differential expression analysis of the queried dataset. Note
that this function does not return differential expression values themselves. Use `get_differential_expression_values`
to get differential expression values (see examples).

The fields of the output data.table are:

- **result.ID**: Result set ID of the differential expression analysis. May represent multiple fac-
tors in a single model.
- **contrast.ID**: Id of the specific contrast factor. Together with the result.ID they uniquely
represent a given contrast.
- **experiment.ID**: Id of the source experiment
- **baseline.category**: Category for the contrast
- **baseline.categoryURI**: URI for the baseline category
- **baseline.factors**: Characteristics of the baseline. This field is a data.table
- **experimental.factors**: Characteristics of the experimental group. This field is a data.table
- **subsetFactor.subset**: TRUE if the result set belong to a subset, FALSE if not. Subsets are
created when performing differential expression to avoid unhelpful comparisons.
- **subsetFactor.category**: Category of the subset
- **subsetFactor**: Characteristics of the subset. This field is a data.table
- **probes.Analyzed**: Number of probesets represented in the contrast
- **genes.Analyzed**: Number of genes represented in the contrast

---

**processDEcontrasts**  
*Replaces factor ids by the factors strings in DE table columns*

Description

Replaces factor ids by the factors strings in DE table columns

Usage

```r
processDEcontrasts(rs, rsID)
```

Arguments

- `rs`  
The resultSet matrix to process

Value

A processed matrix
**processDEMatrix**  
Processes differential expression matrix

**Description**  
Processes differential expression matrix

**Usage**  
processDEMatrix(m)

**Arguments**  
- **m**  
The differential expression matrix to process

**Value**  
A processed matrix

**processDesignMatrix**  
Processes design matrix

**Description**  
Processes design matrix

**Usage**  
processDesignMatrix(m)

**Arguments**  
- **m**  
The design matrix to process

**Value**  
A processed matrix
processElements

Description

Processes JSON as a vector of elements

Usage

processElements(d)

Arguments

d The JSON to process

Value

A data table with information about the probes representing a gene across all platforms. A list if raw = TRUE. A 404 error if the given identifier does not map to any genes.

The fields of the output data.table are:

- mapping.name: Name of the mapping. Typically the probeset name
- mapping.description: A free text field providing optional information about the mapping
- platform.ShortName: Shortname of the platform given by Gemma. Typically the GPL identifier.
- platform.Name: Full name of the platform
- platform.ID: Id number of the platform given by Gemma
- platform.Taxon: Species the platform was designed for
- platform.TaxonID: Id number of the species given by Gemma
- platform.Type: Type of the platform.
- platform.Description: Free text field describing the platform.
- platform.Troubled: Whether the platform is marked as troubled by a Gemma curator.
### processExpressionMatrix

*Processes expression matrix*

**Description**

Processes expression matrix

**Usage**

`processExpressionMatrix(m)`

**Arguments**

- `m` The expression matrix to process

**Value**

A processed matrix

---

### processFile

*Processes a response as a gzip file*

**Description**

Processes a response as a gzip file

**Usage**

`processFile(content)`

**Arguments**

- `content` The content from an `http_get` request

**Value**

A processed data.table
processGemmaArray

Processes JSON as an array

Description
Processes JSON as an array

Usage
processGemmaArray(d)

Arguments

| d       | The JSON to process |

Value
A data table with information about the probes representing the gene across different platforms.

processGemmaFactor

Processes JSON as a factor

Description
Processes JSON as a factor

Usage
processGemmaFactor(d)

Arguments

| d       | The JSON to process |

Value
A processed data.table
processGeneLocation  
*Processes JSON as a vector of gene locations*

**Description**

Processes JSON as a vector of gene locations

**Usage**

```r
processGeneLocation(d)
```

**Arguments**

- `d` The JSON to process

**Value**

A data table with information about the physical location of the queried gene. A list if `raw = TRUE`. A 404 error if the given identifier does not map to any object.

The fields of the output data table are:

- `chromosome`: Name of the chromosome the gene is located
- `strand`: Which strand the gene is located
- `nucleotide`: Nucleotide number for the gene
- `length`: Gene length
- `taxon.name`: Name of the taxon
- `taxonScientific`: Scientific name for the taxon
- `taxon.ID`: Internal ID for the taxon given by Gemma
- `taxon.NCBI`: NCBI ID for the taxon
- `taxon.Database.Name`: Name of the database used in Gemma for the taxon

---

processGenes  
*Processes JSON as a vector of genes*

**Description**

Processes JSON as a vector of genes

**Usage**

```r
processGenes(d)
```
**processGO**

**Arguments**

- **d**
  - The JSON to process

**Value**

A data table with information about the queried gene(s). A list if `raw = TRUE`.

The fields of the output data.table are:

- `gene.Symbol`: Symbol for the gene
- `gene.Ensembl`: Ensembl ID for the gene
- `gene.NCBI`: NCBI id for the gene
- `gene.Name`: Name of the gene
- `gene.MFX.Rank`: Multifunctionality rank for the gene
- `taxon.Name`: Name of the species
- `taxon.Scientific`: Scientific name for the taxon
- `taxon.ID`: Internal identifier given to the species by Gemma
- `taxon.NCBI`: NCBI ID of the taxon
- `taxon.Database.Name`: Underlying database used in Gemma for the taxon
- `taxon.Database.ID`: ID of the underlying database used in Gemma for the taxon

---

**processGO**

*Processes JSON as GO terms*

**Description**

Processes JSON as GO terms

**Usage**

`processGO(d)`

**Arguments**

- **d**
  - The JSON to process

**Value**

A data table with information about the GO terms assigned to the queried gene. A list if `raw = TRUE`. A 404 error if the given identifier does not map to any object.

The fields of the output data.table are:

- `term.Name`: Name of the term
- `term.ID`: ID of the term
- `term.URI`: URI of the term
processPlatforms

Processes JSON as a vector of platforms

Description

Processes JSON as a vector of platforms

Usage

processPlatforms(d)

Arguments

d       The JSON to process

Value

A data table with information about the platform(s). A list if raw = TRUE. A 404 error if the given identifier does not map to any object

The fields of the output data.table are:

• platform.ID: Internal identifier of the platform
• platform.ShortName: Shortname of the platform.
• platform.Name: Full name of the platform.
• platform.Description: Free text description of the platform
• platform.Troubled: Whether or not the platform was marked "troubled" by a Gemma process or a curator
• platform.ExperimentCount: Number of experiments using the platform within Gemma
• platform.Type: Technology type for the platform.
• taxon.Name: Name of the species platform was made for
• taxon.Scientific: Scientific name for the taxon
• taxon.ID: Internal identifier given to the species by Gemma
• taxon.NCBI: NCBI ID of the taxon
• taxon.Database.Name: Underlying database used in Gemma for the taxon
• taxon.Database.ID: ID of the underlying database used in Gemma for the taxon
**processQuantitationTypeValueObject**

**Description**

processQuantitationTypeValueObject

**Usage**

processQuantitationTypeValueObject(d)

**Arguments**

d The JSON to process

**Value**

A data.table containing the quantitation types

The fields of the output data.table are:

- id: If of the quantitation type. Any raw quantitation type can be accessed by `get_dataset_raw_expression` function using this id.
- name: Name of the quantitation type
- description: Description of the quantitation type
- type: Type of the quantitation type. Either raw or processed. Each dataset will have one processed quantitation type which is the data returned using `get_dataset_processed_expression`
- preferred: The preferred raw quantitation type. This version is used in generation of the processed data within gemma.
- recomputed: If TRUE this quantitation type is generated by recomputing raw data files Gemma had access to.

**processResultSetFactors**

*Processes JSON as a result set*

**Description**

Processes JSON as a result set

**Usage**

processResultSetFactors(d)
processSamples

Arguments

d The JSON to process

Value

A processed data.table

processSamples Processes JSON as a vector of samples

Description

Processes JSON as a vector of samples

Usage

processSamples(d)

Arguments

d The JSON to process

Value

A data table with information about the samples of the queried dataset. A list if raw = TRUE. A 404 error if the given identifier does not map to any object.

The fields of the output data.table are:

- `sample.Name`: Internal name given to the sample.
- `sample.ID`: Internal ID of the sample
- `sample.Description`: Free text description of the sample
- `sample.Outlier`: Whether or not the sample is marked as an outlier
- `sample.Accession`: Accession ID of the sample in its original database
- `sample.Database`: Database of origin for the sample
- `sample.Characteristics`: Characteristics of the sample. This field is a data table
- `sample.FactorValues`: Experimental factor values of the sample. This field is a data table
processSearchAnnotations

Processes JSON as an annotation

Description

Processes JSON as an annotation

Usage

processSearchAnnotations(d)

Arguments

d The JSON to process

Value

A data table with annotations (annotation search result value objects) matching the given identifiers. A list if raw = TRUE. A 400 error if required parameters are missing.

The fields of the output data.table are:

- category.Name: Category that the annotation belongs to
- category.URI: URI for the category.Name
- value.Name: Annotation term
- value.URI: URI for the value.Name

processTaxon Processes JSON as a vector of taxa

Description

Processes JSON as a vector of taxa

Usage

processTaxon(d)

Arguments

d The JSON to process
Value

A processed data.table

- taxon.Name: Name of the species
- taxon.Scientific: Scientific name for the taxon
- taxon.ID: Internal identifier given to the species by Gemma
- taxon.NCBI: NCBI ID of the taxon
- taxon.Database.Name: Underlying database used in Gemma for the taxon
- taxon.Database.ID: ID of the underlying database used in Gemma for the taxon

---

process_search  

*Returns the ids of the found results*

---

Description

Returns the ids of the found results

Usage

process_search(d)

Value

A data.table or a list of resultObjects

---

search_annotations  

*Search for annotation tags*

---

Description

Search for annotation tags

Usage

search_annotations(
    query,
    raw = getOption("gemma.raw", FALSE),
    memoised = getOption("gemma.memoised", FALSE),
    file = getOption("gemma.file", NA_character_),
    overwrite = getOption("gemma.overwrite", FALSE)
)
search_datasets

Arguments

query
The search query

raw
TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

memoised
Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

file
The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.

overwrite
Whether or not to overwrite if a file exists at the specified filename.

Value

A data table with annotations (annotation search result value objects) matching the given identifiers. A list if raw = TRUE. A 400 error if required parameters are missing.

The fields of the output data.table are:

- category.Name: Category that the annotation belongs to
- category.URI: URI for the category.Name
- value.Name: Annotation term
- value.URI: URI for the value.Name

Examples

search_annotations("traumatic")

search_datasets Retrieve datasets associated to an annotation tags search

Description

This function is deprecated in favor of `get_datasets`

Usage

search_datasets(
  query,
  taxon = NA_character_,
  offset = 0L,
  limit = 20L,
  sort = "+id",
  raw = getOption("gemma.raw", FALSE),
)
Arguments

query The search query. Either plain text (‘traumatic’), or an ontology term URI (‘http://purl.obolibrary.org/obo/UBERON_0002048’). Datasets that contain the given string in their short or full name will also be matched. Can be multiple identifiers separated by commas.

taxon Can either be Taxon ID, Taxon NCBI ID, or one of its string identifiers: scientific name, common name. It is recommended to use Taxon ID for efficiency. Please note, that not all taxa have all the possible identifiers available. Use the get_taxa_by_ids function to retrieve the necessary information. For convenience, below is a list of officially supported taxa:

<table>
<thead>
<tr>
<th>ID</th>
<th>Comm.name</th>
<th>Scient.name</th>
<th>NcbiID</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>human</td>
<td>Homo sapiens</td>
<td>9606</td>
</tr>
<tr>
<td>2</td>
<td>mouse</td>
<td>Mus musculus</td>
<td>10090</td>
</tr>
<tr>
<td>3</td>
<td>rat</td>
<td>Rattus norvegicus</td>
<td>10116</td>
</tr>
<tr>
<td>11</td>
<td>yeast</td>
<td>Saccharomyces cerevisiae</td>
<td>4932</td>
</tr>
<tr>
<td>12</td>
<td>zebrafish</td>
<td>Danio rerio</td>
<td>7955</td>
</tr>
<tr>
<td>13</td>
<td>fly</td>
<td>Drosophila melanogaster</td>
<td>7227</td>
</tr>
<tr>
<td>14</td>
<td>worm</td>
<td>Caenorhabditis elegans</td>
<td>6239</td>
</tr>
</tbody>
</table>

offset The offset of the first retrieved result.

limit Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with offset and the totalElements attribute in the output to compile all data if needed.

sort Order results by the given property and direction. The ‘+’ sign indicate ascending order whereas the ‘-’ indicate descending.

raw TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

memoised Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing options(gemma.memoised = TRUE) will ensure that the cache is always used. Use forget_gemma_memoised to clear the cache.

file The name of a file to save the results to, or NULL to not write results to a file. If raw == TRUE, the output will be a JSON file. Otherwise, it will be a RDS file.

overwrite Whether or not to overwrite if a file exists at the specified filename.

attributes If TRUE additional information from the call will be added into the output object’s attributes such as offset and available elements.

... Kept for compatibility, ignored.
search_datasets

Value

A data table with information about the queried dataset(s). A list if raw = TRUE. Returns an empty list if no datasets matched. A successful response may contain 'Geeq' information, which aims to provide a unified metric to measure experiments by the quality of their data, and their suitability for use in Gemma. You can read more about the geeq properties here.

The fields of the output data.table are:

- `experiment.ShortName`: Shortname given to the dataset within Gemma. Often corresponds to accession ID
- `experiment.Name`: Full title of the dataset
- `experiment.ID`: Internal ID of the dataset.
- `experiment.Description`: Description of the dataset
- `experiment.Troubled`: Did an automatic process within gemma or a curator mark the dataset as "troubled"
- `experiment.Accession`: Accession ID of the dataset in the external database it was taken from
- `experiment.Database`: The name of the database where the dataset was taken from
- `experiment.URI`: URI of the original database
- `experiment.SampleCount`: Number of samples in the dataset
- `experiment.batchEffect`: A text field describing whether the dataset has batch effects
- `geeq.batchCorrected`: Whether batch correction has been performed on the dataset.
- `geeq.batchConfound`: 0 if batch info isn't available, -1 if batch confound is detected, 1 if batch information is available and no batch confound found
- `geeq.batchEffect`: -1 if batch p value < 0.0001, 1 if batch p value > 0.1, 0 if otherwise and when there is no batch information is available or when the data is confounded with batches.
- `geeq.rawData`: -1 if no raw data available, 1 if raw data was available. When available, Gemma reprocesses raw data to get expression values and batches
- `geeq.qScore`: Data quality score given to the dataset by Gemma.
- `geeq.sScore`: Suitability score given to the dataset by Gemma. Refers to factors like batches, platforms and other aspects of experimental design
- `taxon.Name`: Name of the species
- `taxon.Scientific`: Scientific name for the taxon
- `taxon.ID`: Internal identifier given to the species by Gemma
- `taxon.NCBI`: NCBI ID of the taxon
- `taxon.Database.Name`: Underlying database used in Gemma for the taxon
- `taxon.Database.ID`: ID of the underlying database used in Gemma for the taxon

Examples

search_datasets("bipolar", taxon = "human")
search_gemma  
Search everything in Gemma

**Description**

Search everything in Gemma

**Usage**

```r
search_gemma(
  query,
  taxon = NA_character_,
  platform = NA_character_,
  limit = 20,
  resultType = "experiment",
  raw = getOption("gemma.raw", FALSE),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE)
)
```

**Arguments**

- **query**
  The search query. Either plain text ('traumatic'), or an ontology term URI ('http://purl.obolibrary.org/obo/UBERON_0002048'). Datasets that contain the given string in their short or full name will also be matched. Can be multiple identifiers separated by commas.

- **taxon**
  A numerical taxon identifier or an ncbi taxon identifier or a taxon identifier that matches either its scientific or common name

- **platform**
  A platform numerical identifier or a platform short name

- **limit**
  Optional, defaults to 20. Limits the result to specified amount of objects. Has a maximum value of 100. Use together with `offset` and the `totalElements` attribute in the output to compile all data if needed.

- **resultType**
  The kind of results that should be included in the output. Can be experiment, gene, platform or a long object type name, documented in the API documentation.

- **raw**
  TRUE to receive results as-is from Gemma, or FALSE to enable parsing. Raw results usually contain additional fields and flags that are omitted in the parsed results.

- **memoised**
  Whether or not to save to cache for future calls with the same inputs and use the result saved in cache if a result is already saved. Doing `options(gemma.memoised = TRUE)` will ensure that the cache is always used. Use `forget_gemma_memoised` to clear the cache.

- **file**
  The name of a file to save the results to, or NULL to not write results to a file. If `raw == TRUE`, the output will be the raw endpoint from the API, likely a JSON or a gzip file. Otherwise, it will be a RDS file.
**set_gemma_user**

Whether or not to overwrite if a file exists at the specified filename.

**Value**

If `raw = FALSE` and `resultType` is experiment, gene or platform, a data.table containing the search results. If it is any other type, a list of results. A list with additional details about the search if `raw = TRUE`

**Examples**

```r
search_gemma("bipolar")
```

---

**set_gemma_user**

**Authentication by user name**

**Description**

Allows the user to access information that requires logging in to Gemma. To log out, run `set_gemma_user` without specifying the username or password.

**Usage**

```r
set_gemma_user(username = NULL, password = NULL)
```

**Arguments**

- **username**: Your username (or empty, if logging out)
- **password**: Your password (or empty, if logging out)

**Value**

TRUE if authentication is successful, FALSE if not

---

**validateBoolean**

**Validate a boolean value**

**Description**

Validate a boolean value

**Usage**

```r
validateBoolean(name, ...)
```
validateLimit

**Arguments**

- **name**: The variable name
- ... Any boolean types

**Value**

The validated boolean as a character string (true or false), or stop with an error message

---

validateID

**Description**

Validate identifiers (ie. gene ID, platform ID, etc.) that are homogeneous (either all numerics or all not)

**Usage**

validateID(name, ...)

**Arguments**

- **name**: The variable name
- ... Any identifiers

**Value**

The validated identifiers, or stop with an error message

---

validateLimit

**Description**

Validate a limit value

**Usage**

validateLimit(name, ...)

**Arguments**

- **name**: The variable name
- ... Any possible integers
validateOptionalID

Value

The validated integers, or stop with an error message

validateOptionalID Validate identifiers (ie. gene ID, platform ID, etc.) that are homogeneous (either all numerics or all not)

Description

Validate identifiers (ie. gene ID, platform ID, etc.) that are homogeneous (either all numerics or all not)

Usage

validateOptionalID(name, ...)

Arguments

name The variable name
... Any identifiers

Value

The validated identifiers, or stop with an error message

validateOptionalQuery Validate am optional query

Description

Validate am optional query

Usage

validateOptionalQuery(name, ...)

Arguments

name The variable name
... Any queries

Value

The validated queries
validateOptionalTaxon  Validate a taxon using the acceptable taxa entries

Description
Validate a taxon using the acceptable taxa entries

Usage
validateOptionalTaxon(name, ...)

Arguments
name  The variable name
...  Any taxa to validate

Value
The validated taxon, or stop with an error message

validatePositiveInteger  Validate a non-negative integer value

Description
Validate a non-negative integer value

Usage
validatePositiveInteger(name, ...)

Arguments
name  The variable name
...  Any possible integers

Value
The validated integers, or stop with an error message
validateQuery | Validate a query

**Description**
Validate a query

**Usage**
```python
validateQuery(name, ...)
```

**Arguments**
- **name**
  - The variable name
- ... ( Any queries)

**Value**
The validated queries, or stop with an error message

---

validateResultType | Validate result types

**Description**
Validate result types

**Usage**
```python
validateResultType(name, ...)
```

**Arguments**
- **name**
  - The variable name
- ... (result types)

**Value**
Validated result types. Either returned as they are or they will be replaced from human readable variants
validateSingleID

*Validate a single identifier (ie. gene ID, platform ID, etc.)*

**Description**

Validate a single identifier (ie. gene ID, platform ID, etc.)

**Usage**

```
validateSingleID(name, ...)
```

**Arguments**

- `name` The variable name
- `...` An identifier

**Value**

The validated identifier, or stop with an error message

---

validateSort

*Validate a sort argument*

**Description**

Validate a sort argument

**Usage**

```
validateSort(name, ...)
```

**Arguments**

- `name` The variable name
- `...` Any sort arguments

**Value**

The validated sort arguments, or stop with an error message
**validateTaxa**

Validating taxa using the acceptable taxa entries

**Description**

Validate taxa using the acceptable taxa entries

**Usage**

```r
cvalidateTaxa(name, ...)
```

**Arguments**

- `name`: The variable name
- `...`: Any taxa to validate

**Value**

The validated taxa, or stop with an error message

---

**validateTaxon**

Validating a taxon using the acceptable taxa entries

**Description**

Validate a taxon using the acceptable taxa entries

**Usage**

```r
cvalidateTaxon(name, ...)
```

**Arguments**

- `name`: The variable name
- `...`: Any taxa to validate

**Value**

The validated taxon, or stop with an error message
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