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 2.99.3

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.

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`.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

Examples

```
# gemma.R:::.getResultSets(523099)
```

---

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

```
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

```
filter_properties()
```

Value

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

Examples

```
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

```
forget_gemma_memoised()
```

Value

TRUE to indicate cache was cleared.

Examples

```
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_valu` 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)

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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

```
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

```
# get singular value decomposition for the dataset
gemma_call('datasets/{dataset}/svd',dataset = 1)
```

gemma_kable — *Create printable tables out of gemma.R outputs*

Description

Creates a kable where certain columns are automatically shortened to better fit a document.

Usage

```
gemma_kable(table)
```

Arguments

table	A data.table or data.frame outputted by a gemma.R function

gemma_memoise — *Enable and disable memoisation of gemma.R functions*

Description

Enable and disable memoisation of gemma.R functions

Usage

```
gemma_memoise(
  memoised = FALSE,
  cache = rappdirs::user_cache_dir(appname = "gemmaR")
)
```

Arguments

memoised	boolean. If TRUE memoisation will be enabled
cache	File path or "cache_in_memory". File path will chose a location to save the cache files for memoisation. "cache_in_memory" will store the cache in the current R session

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

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

Arguments

`query`	Output from a gemma.R function with offset and limit 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. This function always saves the output as an RDS 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.

get_child_terms *Return child terms of a term*

Description

When querying for ontology terms, Gemma propagates these terms to include any datasets with their child terms in the results. This function returns these children for any number of terms, including all children and the terms itself in the output vector

Usage

```
get_child_terms(terms)
```

Arguments

terms	An array of terms

Value

An array containing descendends of the annotation terms, including the terms themselves

Examples

```
get_child_terms("http://purl.obolibrary.org/obo/MONDO_0000408")
```

get_datasets *Retrieve all datasets*

Description

Retrieve all datasets

Usage

```
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 of full name will also be matched.
`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 appended to the filter and equivalent to filtering for `allCharacteristics.valueUri`
`offset`	The offset of the first retrieved result.
`limit`	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.

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.batchEffectText`: A text field describing whether the dataset has batch effects
- `experiment.batchCorrected`: Whether batch correction has been performed on the dataset.
- `experiment.batchConfound`: 0 if batch info isn't available, -1 if batch counfoud is detected, 1 if batch information is available and no batch confound found
- `experiment.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.
- `experiment.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 underyling database used in Gemma for the taxon

Examples

```
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 *Retrieve datasets by their identifiers*

Description

Retrieve datasets by their identifiers

Usage

```
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
`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 appended to the filter and equivalent to filtering for `allCharacteristics.valueUri`
`offset`	The offset of the first retrieved result.
`limit`	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.

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.batchEffectText`: A text field describing whether the dataset has batch effects
- `experiment.batchCorrected`: Whether batch correction has been performed on the dataset.
- `experiment.batchConfound`: 0 if batch info isn't available, -1 if batch counfoud is detected, 1 if batch information is available and no batch confound found
- `experiment.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.
- `experiment.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 underyling database used in Gemma for the taxon

Examples

```
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.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
- object.class: Class of object that the term originated from.

Examples

```
get_dataset_annotations("GSE2018")
```

---

get_dataset_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,
  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 differential expression analysis of the queried dataset. Note that this funciton 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
- `factor.category`: Category for the contrast
- `factor.category.URI`: URI for the contrast category
- `factor.ID`: ID of the factor
- `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
- `isSubset`: TRUE if the result set belong to a subset, FALSE if not. Subsets are created when performing differential expression to avoid unhelpful comparisons.
- `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

```
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

```
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)
)
```

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

```
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

```
get_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)
)
```

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
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

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

---

get_dataset_object *Compile gene expression data and metadata*

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. "tidy" for a long form data frame compatible with tidyverse functions. 'list' to return a list containing individual data frames containing expression values, design and the experiment.

`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 `SummarizedExperiment`s, `ExpressionSet`s 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.

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
- `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 underyling database used in Gemma for the taxon

Examples

```
get_dataset_platforms("GSE2018")
```

---

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.

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

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

---

get_dataset_quantitation_types

Retrieve quantitation types of a dataset

Description

Retrieve quantitation types of a dataset

Usage

```
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`
- `ratio`: Whether or not the quanitation type is a ratio of multiple quantitation types. Typically TRUE for processed TWOCOLOR quantitation type.
- `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

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

---

get_dataset_raw_expression

Retrieve raw expression data of a dataset

Description

Retrieve raw expression data of a dataset

Usage

```
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.
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

```
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

```
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

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 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 it's 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

```
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

```
get_differential_expression_values(
  dataset = NA_character_,
  resultSets = NA_integer_,
  readableContrasts = FALSE,
  memoised = getOption("gemma.memoised", FALSE)
)
```

Arguments

`dataset` A dataset identifier.

`resultSets` resultSet identifiers. If a dataset is not provided, all result sets will be downloaded. If it is provided it will only be used to ensure all result sets belong to the dataset.

`readableContrasts` If `FALSE` (default), the returned columns will use internal constrasts IDs as names. Details about the contrasts can be accessed using `get_dataset_differential_expression_ana` 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

```
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 querried 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.aliases: Gene aliases. Each row includes a vector
- 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

```
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
- `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

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

---

get_gene_probes *Retrieve the probes associated to a genes across all platforms*

Description

Retrieve the probes associated to a genes across all platforms

Usage

```
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	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 platrofms. 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:

- `element.name`: Name of the element. Typically the probeset name
- `element.description`: A free text field providing optional information about the element
- `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.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.
- `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 underyling database used in Gemma for the taxon

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)
)
```

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	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.
- `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 underyling database used in Gemma for the taxon

Examples

```
get_platforms_by_ids("GPL1355")
get_platforms_by_ids(c("GPL1355", "GPL96"))
```

get_platform_annotations

Retrieve Platform Annotations by Gemma

Description

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

Usage

```
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 numerical identifiers or platform short name.
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

```
head(get_platform_annotations("GPL96"))
head(get_platform_annotations('Generic_human_ncbiIds'))
```

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

Description

Retrieve all experiments using a given platform

Usage

```
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`	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 queried dataset(s). A list if `raw = TRUE`. Returns an empty list if no datasets matched.

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.batchEffectText`: A text field describing whether the dataset has batch effects
- `experiment.batchCorrected`: Whether batch correction has been performed on the dataset.
- `experiment.batchConfound`: 0 if batch info isn't available, -1 if batch counfoud is detected, 1 if batch information is available and no batch confound found
- `experiment.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.
- `experiment.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 underyling database used in Gemma for the taxon

Examples

```
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

```
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 it's numerical identifier
`offset`	The offset of the first retrieved result.
`limit`	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 querried 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.aliases`: Gene aliases. Each row includes a vector
- `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_platform_element_genes("GPL1355", "AFFX_Rat_beta-actin_M_at")
```

---

get_result_sets *Retrieve all result sets matching the provided criteria*

Description

Returns queried result set

Usage

```
get_result_sets(
  datasets = NA_character_,
  resultSets = NA_character_,
  filter = NA_character_,
  offset = 0,
  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

datasets	A numerical dataset identifier or a dataset short name
resultSets	A resultSet identifier. Note that result set identifiers are not static and can change when Gemma re-runs analyses internally. Whem using these as inputs, try to make sure you access a currently existing result set ID by basing them on result sets returned for a particular dataset or filter used in get_result_sets
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")
offset	The offset of the first retrieved result.
limit	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.

Details

Output and usage of this function is mostly identical to get_dataset_differential_expression_analyses. The principal difference being the ability to restrict your result sets, being able to query across multiple datasets and being able to use the filter argument to search based on result set properties.

Value

A data table with information about the queried result sets. Note that this function does not return differential expression values themselves. Use get_differential_expression_values to get differential expression values

- 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
- factor.category: Category for the contrast
- factor.category.URI: URI for the contrast category
- factor.ID: ID of the factor
- 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
- isSubset: TRUE if the result set belong to a subset, FALSE if not. Subsets are created when performing differential expression to avoid unhelpful comparisons.
- subsetFactor: Characteristics of the subset. This field is a data.table

Examples

```
get_result_sets(dataset = 1)
# get all contrasts comparing disease states. use filter_properties to see avaialble options
get_result_sets(filter = "baselineGroup.characteristics.value = disease")
```

---

get_taxa *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.

Value

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

Examples

```
get_taxa()
```

get_taxa_by_ids *Retrieve taxa by their identifiers*

Description

Retrieve taxa by their identifiers

Usage

```
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 the 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

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

`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

```
gemma.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

```
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.

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.batchEffectText: A text field describing whether the dataset has batch effects
- experiment.batchCorrected: Whether batch correction has been performed on the dataset.
- experiment.batchConfound: 0 if batch info isn't available, -1 if batch counfoud is detected, 1 if batch information is available and no batch confound found
- experiment.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.

- `experiment.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 underyling database used in Gemma for the taxon

Examples

```
get_taxon_datasets("human")
```

`isEmpty` *Check for empty arguments*

Description

Gemma functions accept typed NAs instead of simple NULLS. I believe this was done as a non-standard-in-R way of specifying data types for the users. Usually this is fine but it makes checking for emptyness a bit annoying since a user can still provide NULLs to make them empty

Usage

```
isEmpty(x)
```

Arguments

`x`	A parameter that can be NA or NULL when empty

make_design — *Make simplified design frames*

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"

Value

A data.frame including the design table for the dataset

Examples

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

memoise — *Memoise doc*

Description

Memoise doc

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.

nullCheck *Avoid NULLS as data.table columns*

Description

Avoid NULLS as data.table columns

Usage

```
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 natypee

processAnnotations *Processes JSON as annotations*

Description

Processes JSON as annotations

Usage

```
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.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
- `object.class`: Class of object that the term originated from.

processCharacteristicValueObject

Processes JSON as a factor

Description

Processes JSON as a factor

Usage

```
processCharacteristicValueObject(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)
```

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.

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.batchEffectText`: A text field describing whether the dataset has batch effects
- `experiment.batchCorrected`: Whether batch correction has been performed on the dataset.
- `experiment.batchConfound`: 0 if batch info isn't available, -1 if batch counfoud is detected, 1 if batch information is available and no batch confound found

- `experiment.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.
- `experiment.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 underyling database used in Gemma for the taxon

---

`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 funciton 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
- `factor.category`: Category for the contrast

- `factor.category.URI`: URI for the contrast category
- `factor.ID`: ID of the factor
- `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
- `isSubset`: TRUE if the result set belong to a subset, FALSE if not. Subsets are created when performing differential expression to avoid unhelpful comparisons.
- `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

```
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

processDifferentialExpressionAnalysisResultSetValueObject *Process JSON of a result set*

Description

Process JSON of a result set

Usage

```
processDifferentialExpressionAnalysisResultSetValueObject(d)
```

Value

A data table with information about the queried result sets. Note that this function does not return differential expression values themselves. Use `get_differential_expression_values` to get differential expression values

- `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
- `factor.category`: Category for the contrast
- `factor.category.URI`: URI for the contrast category

- factor.ID: ID of the factor
- 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
- isSubset: TRUE if the result set belong to a subset, FALSE if not. Subsets are created when performing differential expression to avoid unhelpful comparisons.
- subsetFactor: Characteristics of the subset. This field is a data.table

---

processElements *Processes JSON as a vector of elements*

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 platrofms. 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:

- element.name: Name of the element. Typically the probeset name
- element.description: A free text field providing optional information about the element
- 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.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.
- 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 underyling database used in Gemma for the taxon

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.

processGeneLocation *Processes JSON as a vector of gene locations*

Description

Processes JSON as a vector of gene locations

Usage

```
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

- `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

`processGenes` *Processes JSON as a vector of genes*

Description

Processes JSON as a vector of genes

Usage

```
processGenes(d)
```

Arguments

`d`	The JSON to process

Value

A data table with information about the querried 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.aliases`: Gene aliases. Each row includes a vector
- `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 underyling database used in Gemma for the taxon

---

`processQuantitationTypeValueObject` *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`
- `ratio`: Whether or not the quanitation type is a ratio of multiple quantitation types. Typically TRUE for processed TWOCOLOR quantitation type.
- `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)
```

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 it's 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 underyling 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)
)
```

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),
  memoised = getOption("gemma.memoised", FALSE),
  file = getOption("gemma.file", NA_character_),
  overwrite = getOption("gemma.overwrite", FALSE),
  attributes = getOption("gemma.attributes", TRUE),
  ...
)
```

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:

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.

`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.

Value

A data table with information about the queried dataset(s). A list if `raw = TRUE`. Returns an empty list if no datasets matched.

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.batchEffectText`: A text field describing whether the dataset has batch effects
- `experiment.batchCorrected`: Whether batch correction has been performed on the dataset.
- `experiment.batchConfound`: 0 if batch info isn't available, -1 if batch counfoud is detected, 1 if batch information is available and no batch confound found
- `experiment.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.
- `experiment.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 underyling 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

```
search_gemma(
  query,
  taxon = NA_character_,
  platform = NA_character_,
  limit = 100,
  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 of 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	Defaults to 100 with a maximum value of 2000. Limits the number of returned results. Note that this function does not support pagination.
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.
overwrite	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

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

---

setGemmaPath *Set gemma path*

Description

Set gemma path

Usage

```
setGemmaPath(path)
```

Arguments

path	"dev", "prod" or a link to use to access gemma API

Value

Link to Gemma API

---

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

```
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

subset_factorValues *Get a subset of an array of factorValues*

Description

Get a subset of an array of factorValues

Usage

```
subset_factorValues(
  factorValues,
  factorValue = NULL,
  differential_expressions = NULL,
  resultSet = NULL,
  contrast = NULL
)
```

Arguments

factorValue	unimplemented
differential_expressions	

Value

a boolean vector, samples representing the resultSet and/or the contrast are set to TRUE

update_result *Update result*

Description

Re-runs the function used to create a gemma.R output to update the data at hand. Useful if you have a reason to believe parts of the data has changed since your last accession and you wish to update while decoupling the update process from your original code used to generate the data.

Usage

```
update_result(query)
```

Arguments

query	Output from a gemma.R function

Details

Note that if you have used the file and overwrite arguments with the original call, this will also repeat to regenarete the file based on your initial preference

Examples

```
annots <- get_dataset_annotations(1)
# wait for a couple of years..
# wonder if the results are the same
updated_annots <- update_result(annots)

# also works with outputs of get_all_pages
platforms <- get_all_pages(get_platforms_by_ids())
updated_platforms <- update_result(platforms)
```

---

validateBoolean *Validate a boolean value*

Description

Validate a boolean value

Usage

```
validateBoolean(name, ...)
```

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 — *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

```
validateID(name, ...)
```

Arguments

`name`	The variable name
`...`	Any identifiers

Value

The validated identifiers, or stop with an error message

validateLimit — *Validate a limit value*

Description

Validate a limit value

Usage

```
validateLimit(name, ...)
```

Arguments

`name`	The variable name
`...`	Any possible integers

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

```
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

```
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 — *Validate taxa using the acceptable taxa entries*

Description

Validate taxa using the acceptable taxa entries

Usage

```
validateTaxa(name, ...)
```

Arguments

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

Value

The validated taxa, or stop with an error message

validateTaxon — *Validate a taxon using the acceptable taxa entries*

Description

Validate a taxon using the acceptable taxa entries

Usage

```
validateTaxon(name, ...)
```

Arguments

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

Value

The validated taxon, or stop with an error message

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