Package ‘Rga4gh’

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Type Package

Title An Interface to the GA4GH API

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Description
An Interface to the GA4GH API that allows users to easily GET responses and POST requests to GA4GH Servers. See <http://ga4gh.org> for more information about the GA4GH project.

Depends R (>= 3.1.0), httr

Imports jsonlite

Suggests magrittr

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LazyData TRUE

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R topics documented:

`ga4gh_client` *GA4GH Client*

Description

‘ga4gh_client‘ creates an object with class ga4gh_client that you can use to call the API specified by the arguments in the function. This is so you can query an API multiple times without having to worry about where it is every time. You can also set some defaults for the client to determine how responses from the client typically behave. Creating these objects also makes it easier to query multiple servers with similar requests.

Usage

```
ga4gh_client(server, port = NULL, api_location = "/ga4gh", log_level = 0,
  authentication_key = "", page_size = 10)
```

Arguments

`server`	The URL of the GA4GH server
`port`	The port number the GA4GH server is running on
`api_location`	A string to suffix to the server giving the location of the API on the server. By default this is "/ga4gh" i.e. the API is at http(s)://IP_ADDRESS/ga4gh
`log_level`	The amount of debugging information to log
`authentication_key`	The authentication key provided by the server after logging in
`page_size`	The default number of results for the client to return for paged responses

Value

An object with class ga4ghClient

Examples

```
## Create a client for the reference server at http://1kgenomes.ga4gh.org
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
## Use this client as the first argument in the high-level API functions

## Search for datasets in this server
library(magrittr)
datasets <- ref_client %>% search_datasets() %>% content()

## or specify the api location in the search function
search_datasets("http://1kgenomes.ga4gh.org")

## End(Not run)
```

`get_bio_sample` *GET a Bio Sample*

Description

GET a Bio Sample

Usage

```
get_bio_sample(client, bio_sample_id)
```

Arguments

`client`	A ga4gh_client object
`bio_sample_id`	The ID of the BioSample

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
bio_sample <- ref_client %>% get_bio_sample("id")

## End(Not run)
```

`get_call_set` *GET a Call Set*

Description

GET a Call Set

Usage

```
get_call_set(client, call_set_id)
```

Arguments

`client`	A ga4gh_client object
`call_set_id`	The ID of the Call Set

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
call_set <- ref_client %>% get_call_set("id")

## End(Not run)
```

`get_dataset` *GET a Dataset*

Description

GET a Dataset

Usage

```
get_dataset(client, dataset_id)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
dataset <- ref_client %>% get_dataset("id")

## End(Not run)
```

`get_expression_level` *GET an Expression Level*

Description

GET an Expression Level

Usage

```
get_expression_level(client, expression_level_id)
```

Arguments

`client`	A ga4gh_client object
`expression_level_id`	The ID of the Expression Level

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
exp_level <- ref_client %>% get_expression_level("id")

## End(Not run)
```

`get_feature` *GET a Feature*

Description

GET a Feature

Usage

```
get_feature(client, feature_id)
```

Arguments

`client`	A ga4gh_client object
`feature_id`	The ID of the Feature

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
feature <- ref_client %>% get_feature("id")

## End(Not run)
```

`get_feature_set` *GET a Feature Set*

Description

GET a Feature Set

Usage

```
get_feature_set(client, feature_set_id)
```

Arguments

`client`	A ga4gh_client object
`feature_set_id`	The ID of the Feature Set

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
feature_set <- ref_client %>% get_feature_set("id")

## End(Not run)
```

`get_ga4gh` *GET an Object*

Description

GET an object from the GA4GH API

Usage

```
get_ga4gh(object, ...)

## S3 method for class 'ga4ghClient'
get_ga4gh(object, operation, id, ...)

## Default S3 method:
get_ga4gh(object, operation, id, port = NULL, ...)

## S3 method for class 'list'
get_ga4gh(object, operation, id, ...)
```

Arguments

`object`	An object to GET from. I.e. A ga4ghClient object, a url for the server or a list of either.
`...`	Arguments to pass to other methods
`operation`	The name of the operation. Eg "datasets"
`id`	The ID of the Object
`port`	The port number

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:

## Use the client and get an object from the api
ref_client %>% get_ga4gh("datasets", "id")

## Or provide the API location as a string
get_ga4gh("http://1kgenomes.ga4gh.org", "datasets", "id")

## End(Not run)
```

`get_individual` *GET an Individual*

Description

GET an Individual

Usage

```
get_individual(client, individual_id)
```

Arguments

`client`	A ga4gh_client object
`individual_id`	The ID of the Individual

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
individual <- ref_client %>% get_individual("id")

## End(Not run)
```

`get_read_group` *GET a Read Group*

Description

GET a Read Group

Usage

```
get_read_group(client, read_group_id)
```

Arguments

`client`	A ga4gh_client object
`read_group_id`	The ID of the Read Group

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
read_group <- ref_client %>% get_read_group("id")

## End(Not run)
```

`get_read_group_set` *GET a Read Group Set*

Description

GET a Read Group Set

Usage

```
get_read_group_set(client, read_group_set_id)
```

Arguments

`client`	A ga4gh_client object
`read_group_set_id`	The ID of the Read Group Set

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
read_group_set <- ref_client %>% get_read_group_set("id")

## End(Not run)
```

`get_reference_id` *GET a Reference*

Description

GET a Reference

Usage

```
get_reference(client, reference_id)
```

Arguments

`client`	A ga4gh_client object
`reference_id`	The ID of the Reference

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
reference <- ref_client %>% get_reference("id")

## End(Not run)
```

`get_reference_set` *GET a Reference Set*

Description

GET a Reference Set

Usage

```
get_reference_set(client, reference_set_id)
```

Arguments

`client`	A ga4gh_client object
`reference_set_id`	The ID of the Reference Set

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
reference_set <- ref_client %>% get_reference_set("id")

## End(Not run)
```

`get_rna_quantification`

GET an RNA Quantification

Description

GET an RNA Quantification

Usage

```
get_rna_quantification(client, rna_quantification_id)
```

Arguments

`client`	A ga4gh_client object
`rna_quantification_id`	The ID of the RNA Quantification

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
rna_quantification <- ref_client %>% get_rna_quantification("id")

## End(Not run)
```

`get_rna_quantification_set`

GET an RNA Quantification Set

Description

GET an RNA Quantification Set

Usage

```
get_rna_quantification_set(client, rna_quantification_set_id)
```

Arguments

`client`	A ga4gh_client object
`rna_quantification_set_id`	The ID of the RNA Quantification Set

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
rna_quantification_set <- ref_client %>% get_rna_quantification_set("id")

## End(Not run)
```

`get_variant` *GET a Variant*

Description

GET a Variant

Usage

```
get_variant(client, variant_id)
```

Arguments

`client`	A ga4gh_client object
`variant_id`	The ID of the Variant

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
variant <- ref_client %>% get_variant("id")

## End(Not run)
```

`get_variant_annotation_set` *GET a Variant Annotation Set*

Description

GET a Variant Annotation Set

Usage

```
get_variant_annotation_set(client, variant_annotation_set_id)
```

Arguments

`client`	A ga4gh_client object
`variant_annotation_set_id`	The ID of the Variant Annotation Set

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
variant_annotation_set <- ref_client %>% get_variant_annotation_set("id")

## End(Not run)
```

`get_variant_set` *GET a Variant Set*

Description

GET a Variant Set

Usage

```
get_variant_set(client, variant_set_id)
```

Arguments

`client`	A ga4gh_client object
`variant_set_id`	The ID of the Variant Set

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")
## Not run:
library(magrittr)
## Retrieve the object with id 'id'
variant_set <- ref_client %>% get_variant_set("id")

## End(Not run)
```

---

post_ga4gh *POST to a GA4GH Server*

Description

Use this to POST a request to an operation. The operations should simply be specified as a path in the API i.e. "/datasets/search" to search datasets. The body can be json or an R list. Use the search_* functions for a simpler interface.

Usage

```
post_ga4gh(client, operation, body)
```

Arguments

`client`	A ga4gh_client object
`operation`	The API operation to POST to as a string. Eg "/datasets/search"
`body`	The body of the POST either as JSON or a list (which will be converted to json by httr)

Examples

```
## Create a client
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "", log_level = 1)

## A request body as a list
body_list <- list(pageSize = 2)

## Not run:
## Post to the /datasets/search operation
datasets_list <- ref_client %>% post_ga4gh("/datasets/search", body_list) %>% content
datasets_list


## End(Not run)
```

`search_bio_samples` *Search for Bio Samples*

Description

Search for Bio Samples

Usage

```
search_bio_samples(client, dataset_id, individual_id = NULL, name = NULL,
  page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset to search within
`individual_id`	Return BioSamples for the provided Individual ID
`name`	Return BioSamples with the given name found by case-sensitive string matching.
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Search for bio samples in the dataset
bio_samples <- ref_client %>% search_bio_samples(d_id) %>% content()
bio_samples


## End(Not run)
```

`search_call_sets` *Search for Call Sets*

Description

Search for Call Sets

Usage

```
search_call_sets(client, variant_set_id = NULL, bio_sample_id = NULL,
  name = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`variant_set_id`	The ID of the Variant Set to search within
`bio_sample_id`	Return only call sets generated from the provided BioSample ID.
`name`	Only return call sets with this name (case-sensitive, exact match).
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Find a variant set to search in
variant_sets <- ref_client %>% search_variant_sets(d_id) %>% content()
vs_id <- variant_sets$variantSets[[1]]$id

## Search for call sets in the variant set
call_sets <- ref_client %>% search_call_sets(vs_id) %>% content()
call_sets


## End(Not run)
```

`search_datasets` *Search for Datasets*

Description

Search for Datasets

Usage

```
search_datasets(client, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```

ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
## Use the client to search for datasets
library(magrittr)
datasets <- ref_client %>% search_datasets() %>% content()
datasets

## Or specify the API location within search_datasets
search_datasets("http://1kgenomes.ga4gh.org")



## End(Not run)
```

`search_expression_levels` *Search for Expression Levels*

Description

Search for Expression Levels

Usage

```
search_expression_levels(client, rna_quantification_id = NULL,
  feature_ids = NULL, threshold = NULL, page_size = NULL,
  page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`rna_quantification_id`	The ID of the RNA Quantification to search within
`feature_ids`	A list of Feature IDs. Only return expressions with any of the specified feature_ids.
`threshold`	Number
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:

library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Find an rna quantification set to search in
rna_quantification_sets <- ref_client %>%
 search_rna_quantification_sets(d_id) %>% content()
rqs_id <- rna_quantification_sets$rnaQuantificationSets[[1]]$id

## Find an rna quantification to search in
rna_quantifications <- ref_client %>%
 search_rna_quantifications(rqs_id) %>% content()
rq_id <- rna_quantifications$rnaQuantifications[[1]]$id

## Search for expression levels in the rna quantification
expression_levels <- ref_client %>%
 search_expression_levels(rq_id) %>% content()
expression_levels


## End(Not run)
```

`search_features` *Search for Features*

Description

Search for Features

Usage

```
search_features(client, feature_set_id = NULL, parent_id = NULL,
  feature_types = NULL, reference_name = NULL, gene_symbol = NULL,
  name = NULL, start = NULL, end = NULL, page_size = NULL,
  page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`feature_set_id`	The ID of the Feature Set to search within. Either feature_set_id or parent_id must be non-null.
`parent_id`	Restricts the search to direct children of the given parent feature ID. Either feature_set_id or parent_id must be non-null.
`feature_types`	A list of feature types. If specified, this query matches only annotations whose feature_type matches one of the provided ontology terms.
`reference_name`	Only return features on the reference with this name
`gene_symbol`	Only return features with matching the provided gene symbol (case-sensitive, exact match).
`name`	Only returns features with this name (case-sensitive, exact match).
`start`	The beginning of the window (0-based, inclusive) for which overlapping features should be returned. Genomic positions are non-negative integers less than reference length.
`end`	The end of the window (0-based, exclusive) for which overlapping features should be returned.
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
```

```
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Find a feature set to search in
feature_sets <- ref_client %>% search_feature_sets(d_id) %>% content()
fs_id <- feature_sets$featureSets[[1]]$id

## Search the for features in the feature set
features <- ref_client %>% search_features(fs_id) %>% content()
features$features[[1]]


## End(Not run)
```

`search_feature_phenotype_associations` *Search for Feature Phenotype Associations*

Description

Search for Feature Phenotype Associations

Usage

```
search_feature_phenotype_associations(client, ...)
```

Arguments

`client`	A ga4gh_client object
`...`	Other named arguments for the body of the POST request

`search_feature_sets` *Search for Feature Sets*

Description

Search for Feature Sets

Usage

```
search_feature_sets(client, dataset_id = NULL, page_size = NULL,
  page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset to search within
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Search for feature sets in the dataset
feature_sets <- ref_client %>% search_feature_sets(d_id) %>% content()
feature_sets


## End(Not run)
```

`search_ga4gh` *Search*

Description

Search the GA4GH API

Usage

```
search_ga4gh(object, ...)

## S3 method for class 'ga4ghClient'
search_ga4gh(object, operation, ...)

## Default S3 method:
search_ga4gh(object, port = NULL, operation, ...)

## S3 method for class 'list'
search_ga4gh(object, operation, ...)
```

Arguments

`object`	An object to POST to. I.e. A ga4ghClient object, a url for the server or a list of either.
`...`	Named fields for the JSON body
`operation`	The name of an operation. Eg "variantsets"
`port`	The port number

`search_individuals` *Search for Individuals*

Description

Search for Individuals

Usage

```
search_individuals(client, dataset_id = NULL, name = NULL,
  page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset to search within
`name`	Return Individuals with the given name found by case-sensitive string matching.
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Search for individuals in the dataset
individuals <- ref_client %>% search_individuals(d_id) %>% content()
individuals


## End(Not run)
```

`search_phenotypes` *Search for Phenotypes*

Description

Search for Phenotypes

Usage

```
search_phenotypes(client, phenotype_association_set_id = NULL,
  description = NULL, id = NULL, qualifiers = NULL, type = NULL,
  age_of_onset = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`phenotype_association_set_id`	The ID of Phenotype Association Set to search within
`description`	String
`id`	String
`qualifiers`	A data.frame with columns id, sourceName, sourceVersion, term.
`type`	A named list with names id, sourceName, sourceVersion, term. Only return results that match this type
`age_of_onset`	A named list with names id, sourceName, sourceVersion, term. Only return results that match this age_of_onset
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Find a phenotype association set to search in
phenotype_association_sets <- ref_client %>%
 search_phenotype_association_sets(d_id) %>% content()
pas_id <- phenotype_association_sets$phenotypeAssociationSets[[1]]$id
```

```
## Search for pheotypes in the phenotype association set
phenotypes <- ref_client %>% search_phenotypes(pas_id) %>% content()
phenotypes$phenotypes[[1]]


## End(Not run)
```

---

search_phenotype_association_sets

Search for Phenotype Association Sets

Description

Search for Phenotype Association Sets

Usage

```
search_phenotype_association_sets(client, dataset_id = NULL,
  page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset to search within
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Search for phenotype association sets in the dataset
phenotype_association_sets <- ref_client %>%
 search_phenotype_association_sets(d_id) %>% content()
phenotype_association_sets
```

```
## End(Not run)
```

`search_reads` *Search for Reads*

Description

Search for Reads

Usage

```
search_reads(client, read_group_ids, reference_id = NULL, start = NULL,
  end = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`read_group_ids`	A list of Read Group IDs. The Read Groups to search. At least one id must be specified.
`reference_id`	The reference to query. Leaving blank returns results from all references, including unmapped reads - this could be very large.
`start`	The start position (0-based) of this query. If a reference is specified, this defaults to 0. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 0).
`end`	The end position (0-based, exclusive) of this query. If a reference is specified, this defaults to the reference's length.
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id
```

```
## Find a read group to search in
read_group_sets <- ref_client %>% search_read_group_sets(d_id) %>% content()
rg_id <- read_group_sets$readGroupSets[[1]]$readGroups[[1]]$id

## Find a reference_id to map reads (unmapped reads not supported yet)
rs_id <- ref_client %>% search_reference_sets %>% content() %>%
 `$`("referenceSets") %>% `[[`(1) %>% `$`("id")
ref_id <- ref_client %>% search_references(rs_id) %>% content() %>%
 `$`("references") %>% `[[`(1) %>% `$`("id")

## Search for reads in the read group set
reads <- ref_client %>% search_reads(rg_id, reference_id = ref_id) %>% content()
reads


## End(Not run)
```

---

search_read_group_sets

Search for Read Group Sets

Description

Search for Read Group Sets

Usage

```
search_read_group_sets(client, dataset_id = NULL, bio_sample_id = NULL,
  name = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset to search within
`bio_sample_id`	Specifying the id of a BioSample record will return only readgroups with the given bio_sample_id.
`name`	Only return read group sets with this name (case-sensitive, exact match).
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Search for read group sets in the dataset
read_group_sets <- ref_client %>% search_read_group_sets(d_id) %>% content()
read_group_sets

## End(Not run)
```

`search_references` *Search for References*

Description

Search for References

Usage

```
search_references(client, reference_set_id = NULL, accession = NULL,
  md5checksum = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`reference_set_id`	The ID of the Reference Set to search within
`accession`	Return the References for which the accession matches this string (case-sensitive, exact match).
`md5checksum`	Return the References for which the md5checksum matches this string (case-sensitive, exact match).
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a reference set to search in
reference_sets <- ref_client %>% search_reference_sets() %>% content()
rs_id <- reference_sets$referenceSets[[1]]$id

## Search for references in the reference set
references <- ref_client %>% search_references(rs_id) %>% content()
references

## End(Not run)
```

`search_reference_bases` *Search for Reference Bases*

Description

Search for Reference Bases

Usage

```
search_reference_bases(client, reference_id = NULL, start = NULL,
  end = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`reference_id`	The ID of the Reference to search within
`start`	The start position (0-based) of this query. Defaults to 0. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 0).
`end`	The end position (0-based, exclusive) of this query. Defaults to the length of this Reference
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a reference set to search in
reference_sets <- ref_client %>% search_reference_sets() %>% content()
rs_id <- reference_sets$referenceSets[[1]]$id

## Find a reference to search in
references <- ref_client %>% search_references(rs_id) %>% content()
ref_id <- references$references[[1]]$id

## Find a string of bases from 10000 -> 11000
reference_bases <- ref_client %>%
 search_reference_bases(ref_id, start = 10000, end = 11000) %>% content()
reference_bases

## End(Not run)
```

`search_reference_sets` *Search for Reference Sets*

Description

Search for Reference Sets

Usage

```
search_reference_sets(client, assembly_id = NULL, accession = NULL,
  md5checksum = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`assembly_id`	Return the Reference Sets for which the assembly_id matches this string (case-sensitive, exact match).
`accession`	Return the Reference Sets for which the accession matches this string (case-sensitive, exact match).
`md5checksum`	Return the Reference Sets for which the md5checksum matches this string (case-sensitive, exact match).
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Search for reference sets
reference_sets <- ref_client %>% search_reference_sets() %>% content()
reference_sets

## End(Not run)
```

---

search_rna_quantifications

Search for RNA Quantifications

Description

Search for RNA Quantifications

Usage

```
search_rna_quantifications(client, rna_quantification_set_id,
  page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`rna_quantification_set_id`	The ID of the RNA Quantification Set to search within
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:

library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id
```

```
## Find an rna quantification set to search in
rna_quantification_sets <- ref_client %>%
 search_rna_quantification_sets(d_id) %>% content()
rqs_id <- rna_quantification_sets$rnaQuantificationSets[[1]]$id

## Search for rna quantifications in the rna quantification set
rna_quantifications <- ref_client %>%
 search_rna_quantifications(rqs_id) %>% content()
rna_quantifications

## End(Not run)
```

`search_rna_quantification_sets` *Search for RNA Quantification Sets*

Description

Search for RNA Quantification Sets

Usage

```
search_rna_quantification_sets(client, dataset_id = NULL, page_size = NULL,
  page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset to search within
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:

library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id
```

```
## Search for rna quantification sets in the dataset
rna_quantification_sets <- ref_client %>%
 search_rna_quantification_sets(d_id) %>% content()
rna_quantification_sets


## End(Not run)
```

`search_variants` *Search for Variants*

Description

Search for Variants

Usage

```
search_variants(client, variant_set_id, call_set_ids = NULL,
  reference_name = NULL, start = NULL, end = NULL, page_size = NULL,
  page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`variant_set_id`	The ID of the Variant Set to search within
`call_set_ids`	A list of Call Set IDs. Only return variant calls which belong to call sets with these IDs. If unspecified, return all variants and no variant call objects.
`reference_name`	Only return variants on this reference.
`start`	The beginning of the window (0-based, inclusive) for which overlapping variants should be returned. Genomic positions are non-negative integers less than reference length.
`end`	The end of the window (0-based, exclusive) for which overlapping variants should be returned.
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Find a variant set to search in
variant_sets <- ref_client %>% search_variant_sets(d_id) %>% content()
vs_id <- variant_sets$variantSets[[1]]$id

## Search for variants in the variant set
variants <- ref_client %>% search_variants(vs_id, reference_name = "1") %>%
 content()
variants$variants[[1]]

## End(Not run)
```

`search_variant_annotations`

Search for Variant Annotations

Description

Search for Variant Annotations

Usage

```
search_variant_annotations(client, variant_annotation_set_id,
  reference_id = NULL, reference_name = NULL, start = NULL, end = NULL,
  effects = NULL, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`variant_annotation_set_id`	The ID of the Variant Annoation Set to search within.
`reference_id`	Only return variants with reference alleles on th reference with this ID. One of this field or referenceName is required.
`reference_name`	Only return variants with reference alleles on the reference with this name. One of this field or referenceId is required.

`start`	The beginning of the window (0-based, inclusive) for which variants with overlapping reference alleles should be returned. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 0).
`end`	The end of the window (0-based, exclusive) for which variants with overlapping reference alleles should be returned.
`effects`	A data.frame with columns id, sourceName, sourceVersion, term. This filter allows variant, transcript combinations to be extracted by effect type(s). Only return variant annotations including any of these effects and only return transcript effects including any of these effects. Exact matching across all fields of the Sequence Ontology OntologyTerm is required. (A transcript effect may have multiple SO effects which will all be reported.) If empty, return all variant annotations.
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content
d_id <- datasets$datasets[[1]]$id

## Find a variant set to search in
variant_sets <- ref_client %>% search_variant_sets(d_id) %>% content()
vs_id <- variant_sets$variantSets[[2]]$id

## Find a variant annotation set to search in
variant_annotation_sets <- ref_client %>%
 search_variant_annotation_sets(vs_id) %>% content()
vas_id <- variant_annotation_sets$variantAnnotationSets[[1]]$id

## Search for variant annotations in the variant annotation set
variant_annotations <- ref_client %>%
 search_variant_annotations(vas_id, reference_name = "1") %>% content
variant_annotations$variantAnnotations[[1]]

## End(Not run)
```

`search_variant_annotation_sets`

Search for Variant Annotation Sets

Description

Search for Variant Annotation Sets

Usage

```
search_variant_annotation_sets(client, variant_set_id, page_size = NULL,
  page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`variant_set_id`	The ID of the Variant Set to Search
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content
d_id <- datasets$datasets[[1]]$id

## Find a variant set to search in
variant_sets <- ref_client %>% search_variant_sets(d_id) %>% content()
vs_id <- variant_sets$variantSets[[2]]$id

## Search for variant annotation sets in the variant set
variant_annotation_sets <- ref_client %>%
 search_variant_annotation_sets(vs_id) %>% content()
variant_annotation_sets

## End(Not run)
```

`search_variant_sets` *Search for Variant Sets*

Description

Search for Variant Sets

Usage

```
search_variant_sets(client, dataset_id, page_size = NULL, page_token = NULL)
```

Arguments

`client`	A ga4gh_client object
`dataset_id`	The ID of the Dataset to search within
`page_size`	Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
`page_token`	The continuation token, which is used to page through large result sets. To get the next page of results, set this parameter to the value of nextPageToken from the previous response.

Examples

```
ref_client <- ga4gh_client("http://1kgenomes.ga4gh.org", api_location = "")

## Not run:
library(magrittr)
## Find a dataset to search in
datasets <- ref_client %>% search_datasets() %>% content()
d_id <- datasets$datasets[[1]]$id

## Search for variantsets in the dataset
variant_sets <- ref_client %>% search_variant_sets(d_id) %>% content()
variant_sets


## End(Not run)
```

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