Package ‘Rga4gh’

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.

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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

```r
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

```r
## 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**

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

**arguments**

- **client**: A ga4gh_client object
- **bio_sample_id**: The ID of the BioSample
get_call_set

## Examples

```r
## 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

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

### Arguments

- **client** | A ga4gh_client object
- **call_set_id** | The ID of the Call Set

### Examples

```r
## 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  

**Description**

GET a Dataset

**Usage**

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

**Arguments**

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

**Examples**

```r
## 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  

**Description**

GET an Expression Level

**Usage**

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

**Arguments**

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

## 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)

---

### 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, ...)

get_individual

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

```r
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
get_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'
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**
```r
## 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

```r
## 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

```r
## 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**

```r
## 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
get_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

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_set**

**get_variant_annotation_set**

---

**Description**

GET a Variant Annotation Set

**Usage**

```r
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**

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

---

**Description**

GET a Variant Set

**Usage**

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

**Arguments**

- **client**: A `ga4gh_client` object
- **variant_set_id**: The ID of the Variant Set
Examples

```r
## 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**

```r
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**

```r
## 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  

**Description**

Search for Bio Samples

**Usage**

```r
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**

```r
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

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
search_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

```r
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)
```

Description

Search the GA4GH API

Usage

```r
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, ...)
```
search_individuals

Arguments

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

Description

Search for Individuals

Usage

```r
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

```r
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  

**Description**

Search for Phenotypes

**Usage**

```r
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**

```r
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 phenotypes in the phenotype association set

```r
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**

```r
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**

```r
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
```
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

```r
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)

```r
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

```r
reads <- ref_client %>% search_reads(rg_id, reference_id = ref_id) %>% content()
``` 

## End(Not run)

---

### search_read_group_sets

**Search for Read Group Sets**

#### Description

Search for Read Group Sets

#### Usage

```r
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

```r
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

```r
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.
```
**search_reference_bases**

**Search for Reference Bases**

**Description**

Search for Reference Bases

**Usage**

```r
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 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**

```r
define reference_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)
```
Examples

```r
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

```r
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

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
page_size Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.
page_token

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

```r
rna_quantification_sets <- ref_client %>%
  search_rna_quantification_sets(d_id) %>% content()
```

```r
rqs_id <- rna_quantification_sets$rnaQuantificationSets[[1]]$id
```

## Search for rna quantifications in the rna quantification set

```r
rna_quantifications <- ref_client %>%
  search_rna_quantifications(rqs_id) %>% content()
```

```r
rna_quantifications
```

## End(Not run)

---

**search_rna_quantification_sets**

*Search for RNA Quantification Sets*

### Description

Search for RNA Quantification Sets

### Usage

```r
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

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

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

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

## End(Not run)

---

search_variants | Search for Variants

### Description

Search for Variants

### Usage

```r
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

```r
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**

```r
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 Annotation Set to search within.
- `reference_id` Only return variants with reference alleles on the 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.
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).

The end of the window (0-based, exclusive) for which variants with overlapping reference alleles should be returned.

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.

Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.

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

```r
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

## 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**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>client</td>
<td>A ga4gh_client object</td>
</tr>
<tr>
<td>dataset_id</td>
<td>The ID of the Dataset to search within</td>
</tr>
</tbody>
</table>
| page_size  | Specifies the maximum number of results to return in a single page. If unspe-
|            | cified, 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**

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

```r
## 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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