Package ‘Rga4gh’

November 7, 2016

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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## ga4gh_client

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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

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

get_bio_sample

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>server</td>
<td>The URL of the GA4GH server</td>
</tr>
<tr>
<td>port</td>
<td>The port number the GA4GH server is running on</td>
</tr>
<tr>
<td>api_location</td>
<td>A string to suffix to the server giving the location of the API on the server. By default this is &quot;/ga4gh&quot; i.e. the API is at http(s)://IP_ADDRESS/ga4gh</td>
</tr>
<tr>
<td>log_level</td>
<td>The amount of debugging information to log</td>
</tr>
<tr>
<td>auth_key</td>
<td>The authentication key provided by the server after logging in</td>
</tr>
<tr>
<td>page_size</td>
<td>The default number of results for the client to return for paged responses</td>
</tr>
</tbody>
</table>

**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  

**Description**

GET a Bio Sample

**Usage**

get_bio_sample(client, bio_sample_id)

**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>bio_sample_id</td>
<td>The ID of the BioSample</td>
</tr>
</tbody>
</table>
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

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

```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

**GET a 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

**GET an 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

get_feature 

Description

GET a Feature

Usage

get_feature(client, feature_id)

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>feature_id</td>
<td>The ID of the Feature</td>
</tr>
</tbody>
</table>

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'
exp_level <- ref_client %>% get_expression_level("id")
## End(Not run)
```
**get_feature_set**  
*GET a Feature Set*

**Description**  
GET a Feature Set

**Usage**  
```r  
get_feature_set(client, feature_set_id)  
```

**Arguments**  
- **client**: A ga4gh_client object  
- **feature_set_id**: The ID of the Feature 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'  
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**  
```r  
get_ga4gh(object, ...)  
```

**Arguments**  
- **object**: The object to be retrieved

**Examples**  
```r  
## 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

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

```r
## 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

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

Arguments

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

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 <- 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
get_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 <- 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
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'
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

**Description**

GET a Variant Annotation Set

**Usage**

```r
going {client, variant_annotation_set_id}
```

**Arguments**

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

**Examples**

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

get_variant_set

**Description**

GET a Variant Set

**Usage**

```r
going {client, variant_set_id}
```

**Arguments**

- `client`: A ga4gh_client object
- `variant_set_id`: The ID of the Variant Set
post_ga4gh

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

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
search_expression_levels

Usage

```r
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

```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 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

```r
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

<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>feature_set_id</td>
<td>The ID of the Feature Set to search within. Either feature_set_id or parent_id must be non-null.</td>
</tr>
<tr>
<td>parent_id</td>
<td>Restricts the search to direct children of the given parent feature ID. Either feature_set_id or parent_id must be non-null.</td>
</tr>
<tr>
<td>feature_types</td>
<td>A list of feature types. If specified, this query matches only annotations whose feature_type matches one of the provided ontology terms.</td>
</tr>
<tr>
<td>reference_name</td>
<td>Only return features on the reference with this name</td>
</tr>
<tr>
<td>gene_symbol</td>
<td>Only return features with matching the provided gene symbol (case-sensitive, exact match).</td>
</tr>
<tr>
<td>name</td>
<td>Only returns features with this name (case-sensitive, exact match).</td>
</tr>
<tr>
<td>start</td>
<td>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.</td>
</tr>
<tr>
<td>end</td>
<td>The end of the window (0-based, exclusive) for which overlapping features should be returned.</td>
</tr>
<tr>
<td>page_size</td>
<td>Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.</td>
</tr>
<tr>
<td>page_token</td>
<td>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.</td>
</tr>
</tbody>
</table>

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

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

## End (Not run)
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

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, ...)
search_individuals

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

```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  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_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://ikgenomes.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
```

```r
phenotypes <- ref_client %>% search_phenotypes(pas_id)
phenotypes$phenotypes[[1]]
```
search_reads

Description

Search for Reads

Usage

search_reads(clientL read_group_idsL 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
## 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.
search_references

Examples

```r
ref_client <- ga4gh_client("http://ekgenomes.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

<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>reference_set_id</td>
<td>The ID of the Reference Set to search within</td>
</tr>
<tr>
<td>accession</td>
<td>Return the References for which the accession matches this string (case-sensitive, exact match).</td>
</tr>
<tr>
<td>md5checksum</td>
<td>Return the References for which the md5checksum matches this string (case-sensitive, exact match).</td>
</tr>
<tr>
<td>page_size</td>
<td>Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.</td>
</tr>
<tr>
<td>page_token</td>
<td>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.</td>
</tr>
</tbody>
</table>
search_reference_bases

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.
search_reference_sets

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.
search_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)
## Search for reference sets
reference_sets <- ref_client %>% search_reference_sets() %>% search_rna_quantifications()

datasets <- ref_client %>% search_datasets() %>% search_rna_quantifications("dataset_id")
d_id <- datasets$datasets[[1]]$id
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_variants

## Search for rna quantification sets in the dataset

```r
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

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

#### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>client</td>
<td>A ga4gh_client object</td>
</tr>
<tr>
<td>variant_set_id</td>
<td>The ID of the Variant Set to search within</td>
</tr>
<tr>
<td>call_set_ids</td>
<td>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.</td>
</tr>
<tr>
<td>reference_name</td>
<td>Only return variants on this reference.</td>
</tr>
<tr>
<td>start</td>
<td>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.</td>
</tr>
<tr>
<td>end</td>
<td>The end of the window (0-based, exclusive) for which overlapping variants should be returned.</td>
</tr>
<tr>
<td>page_size</td>
<td>Specifies the maximum number of results to return in a single page. If unspecified, the client default will be used.</td>
</tr>
<tr>
<td>page_token</td>
<td>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.</td>
</tr>
</tbody>
</table>
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 = "chr1") %>%
           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 = "") %>% 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  

### 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 variant sets in the dataset
variant_sets <- ref_client %>% search_variant_sets(d_id) %>% content()

## End(Not run)
```
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