Package 'variantUser'

March 24, 2021

Title variantUser

Version 1.36.0-1

API version v0.1

Description This is the API for layer 3 of the Roche pRed project. This swagger page describes the variantUser API endpoints for ODM. These are typically used to find and retrieve variant data and metadata. Before carrying out any API calls you will need an API token. API tokens can be obtained under your profile within the Genestack software. Further instructions can be found [here](https://odm-user-guide.readthedocs.io/en/latest/doc-odm-user-guide/getting-a-genestack-api-token.html). To try out calls in this swagger page: 1. Click the 'Authorize' button below to enter your API token 2. Scroll to the 'Parameters' section for the method you wish to try out and click the 'Try it out' button 3. Enter parameter values that you wish to try 4. Scroll to the bottom of the Parameters section and click the 'Execute' bar that appears   The server response will be in the section that follows.

Depends R (>= 3.3.2)

License Proprietary

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

R topics documented:

VariantSPoTApi_get_all_variants
                    Retrieve multiple variant data and metadata objects

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Description

Retrieve multiple variant data and metadata objects

Usage

```
VariantSPoTApi_get_all_variants(
  filter,
  query,
  search_specific_terms,
  run_filter,
  info_filter,
  genes,
  interval,
  variation_id,
  reference,
  alteration,
  alleles,
  quality,
  use_versions,
  returned_metadata_fields,
  page_limit,
  cursor,
  ...
)
```

Arguments

filter	Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP
query	Search for variant objects via a full text query over all variant metadata. E.g. dbSNP
search_specific_terms	
	If the full-text query term is present in an ODM dictionary, enabling this parameter will modify the query to include child terms of the full-text query. For example, the search query "Body fluid" can be expanded to include the term "Blood" (a child term of "Body fluid") so files containing either "Body fluid" or "Blood" in their metadata will be returned in the search results. The parent-child relationship is defined by the key "broaders" in the dictionary. If the full query term is not present in a dictionary then this parameter has no effect.
run_filter	Genestack accession that corresponds to the vcf column used to link variants from the same run to a sample

info_filter	Filter by vcf INFO field key=value(or range) pairs. Multiple filters can be separated with semicolons. E.g. 'AF=(0.8:0.95);VT=SNP'
genes	Specify a chromosome interval related with the genes list. Use commas to specify multiple genes.
interval	Specify a chromosome interval to find genes between these positions. E.g. 2:233364596-233385916. Use commas to specify multiple intervals.
variation_id	One or more specific variation IDs can be specified. E.g. rs838705 use | characters to specify mutliple IDs.
reference	Reference bases, with multiple characters seperated by |. E.g. CA|G.
alteration	Alternate bases, with multiple characters seperated by |. E.g. CA|G.
alleles	The response can be filtered by number of affected alleles. All objects which have a number of mutations that is equal or greater than the supplied value will match the search criteria. For example, if you provide '1', all variant objects which have mutations in 1, 2, or more, alleles will be displayed in the response.
quality	The objects can be filtered by quality value. Quality should be entered as an interval in parentheses with the starting and ending values are separated by a colon. For example, if you enter (100:200), variant objects with quality values greater than 100 and less than 200 will be shown in the response.
use_versions	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: * or v<version number> or <CHAIN_ID>:v<version number> or <CHAIN_ID>:<accession1,accession2,..>
returned_metadata_fields	
	The parameter defines amount of metadata attributes to return: 1. template - return metadata attributes according to applied template, if object doesn't have applied template default template will be used. This is the default for User endpoints. 2. all - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.
page_limit	Maximum number of results to return per page (see Paging above). This value must be between 0 and 2000 (inclusive). The default is 2000.
cursor	The page tag to resume results from (see paging above).

VariantSPoTApi_get_group

Retrieve a single group object by ID (accession)

Description

Retrieve a single group object by ID (accession)

Usage

```
VariantSPoTApi_get_group(id, returned_metadata_fields, ...)
```

Arguments

`id`   Unique identifier (accession) of the object.

`returned_metadata_fields`

The parameter defines amount of metadata attributes to return: 1. `template` - return metadata attributes according to applied template, if object doesn't have applied template default template will be used. This is the default for User endpoints. 2. `all` - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

`VariantSPoTApi_get_group_by_run`

Retrieve a single group object by run ID (accession)

Description

Retrieve a single group object by run ID (accession)

Usage

```
VariantSPoTApi_get_group_by_run(id, returned_metadata_fields, ...)
```

Arguments

`id`   Unique identifier (accession) of the object.

`returned_metadata_fields`

The parameter defines amount of metadata attributes to return: 1. `template` - return metadata attributes according to applied template, if object doesn't have applied template default template will be used. This is the default for User endpoints. 2. `all` - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

`VariantSPoTApi_get_variant`

Retrieve a single variant object by ID (accession)

Description

Retrieve a single variant object by ID (accession)

Usage

```
VariantSPoTApi_get_variant(id, returned_metadata_fields, ...)
```

Arguments

id   Unique identifier (accession) of the object.

returned_metadata_fields

> The parameter defines amount of metadata attributes to return: 1. `template` -
> return metadata attributes according to applied template, if object doesn't have
> applied template default template will be used. This is the default for User end-
> points. 2. `all` - return all metadata attributes with values and null attributes,
> if they are present in the applied template. This is the default for Curator end-
> points.

VariantSPoTApi_get_variant_by_version

Retrieve a single variant object by ID (accession)

Description

Retrieve a single variant object by ID (accession)

Usage

```
VariantSPoTApi_get_variant_by_version(
  id,
  version,
  returned_metadata_fields,
  ...
)
```

Arguments

id   Unique identifier (accession) of the object.

version   Unique version of the object.

returned_metadata_fields

> The parameter defines amount of metadata attributes to return: 1. `template` -
> return metadata attributes according to applied template, if object doesn't have
> applied template default template will be used. This is the default for User end-
> points. 2. `all` - return all metadata attributes with values and null attributes,
> if they are present in the applied template. This is the default for Curator end-
> points.

VariantSPoTApi_get_variant_versions

Retrieve a list of object versions by ID

Description

Retrieve a list of object versions by ID

Usage

```
VariantSPoTApi_get_variant_versions(id, ...)
```

Arguments

id   Unique identifier (accession) of the object.

VariantSPoTApi_search_groups

Retrieve groups that match a query

Description

Retrieve groups that match a query

Usage

```
VariantSPoTApi_search_groups(
  filter,
  query,
  search_specific_terms,
  returned_metadata_fields,
  use_versions,
  page_offset,
  page_limit,
  ...
)
```

Arguments

filter   Filter by variant metadata (key-value metadata pair(s)). E.g. `"Variant Source"`=dbSNP

query   Search for variant objects via a full text query over all variant metadata. E.g. dbSNP

search_specific_terms

> If the full-text query term is present in an ODM dictionary, enabling this parameter will modify the query to include child terms of the full-text query. For example, the search query "Body fluid" can be expanded to include the term "Blood" (a child term of "Body fluid") so files containing either "Body fluid" or "Blood" in their metadata will be returned in the search results. The parent-child relationship is defined by the key "broaders" in the dictionary. If the full query term is not present in a dictionary then this parameter has no effect.

returned_metadata_fields

> The parameter defines amount of metadata attributes to return: 1. `template` - return metadata attributes according to applied template, if object doesn't have applied template default template will be used. This is the default for User endpoints. 2. `all` - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

use_versions

> Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: * or v<version number> or <CHAIN_ID>:v<version number> or <CHAIN_ID>:<accession1,accession2,..>

page_offset

> Show the page pageOffset+1 results from the start of the results. E.g. 100 will show a page of results starting from the 101st result. The default value is 0.

page_limit

> Maximum number of results to return per page (see Paging above). This value must be between 0 and 2000 (inclusive). The default is 2000.

VariantSPoTApi_search_runs

Retrieve run objects related to the given group

Description

Retrieve run objects related to the given group

Usage

```
VariantSPoTApi_search_runs(id, page_offset, page_limit, ...)
```

Arguments

id

> Unique identifier (accession) of the object.

page_offset

> Show the page pageOffset+1 results from the start of the results. E.g. 100 will show a page of results starting from the 101st result. The default value is 0.

page_limit

> Maximum number of results to return per page (see Paging above). This value must be between 0 and 2000 (inclusive). The default is 2000.