
ga4gh-client Documentation

Release 0.0.1

GA4GH

Mar 16, 2017

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Global Alliance for Genomics & Health

`ga4gh-client` is a package that contains the client functionality of the `ga4gh` package.

See the documentation for the `ga4gh` package on its [readthedocs](#) page.

Contents:

CHAPTER 1

Python Client Library

This is the GA4GH client API library. This is a convenient wrapper for the low-level HTTP GA4GH API, and abstracts away network centric details such as paging. The methods and types used by the client library are defined by the [GA4GH schema](#).

Warning: This client API should be considered early alpha quality, and may change in arbitrary ways.

Todo

A full description of this API and links to a tutorial on how to use it, as well as a quickstart showing the basic usage.

Types

Todo

Add links to the upstream documentation for the GA4GH types.

Client API

Todo

Add overview documentation for the client API.

0.6.0a10

Features:

- Added **support for BigWig files** in a new Continuous Data object (#63) New endpoints and message types include:
 - *POST /continuoussets/search*
 - *GET /continuoussets/{id}*
 - *POST /continuous/search*
 - Continuous (new)
 - ContinuousSet (new)
- Add **ability to list and join peer server networks** (#60) New endpoints and message types include:
 - *POST /peers/list*
 - *POST /peers/announce*
 - *GET /info*
 - ListPeersResponse (new)
 - Peer (new)
 - AnnouncePeerResponse (new)
 - GetInfoResponse (new)
- Remove feature_id from ExpressionLevel and add ability to search by the Name field (#67) Impacts
 - *POST /expressionlevels/search*
 - *GET /expressionlevels/{id}*
- Replaced info fields with rich type Attributes fields (#46) Impacts the following message types:

- TranscriptEffect
- VariantAnnotation
- Individual
- Biosample
- Experiment (new)
- Analysis (new)
- Dataset
- ReadGroup
- ReadGroupSet
- ReadAlignment
- Reference
- ReferenceSet
- RnaQuantificationSet
- RnaQuantification
- ExpressionLevel
- Feature
- VariantSetMetadata
- CallSet
- Call
- Variant
- Replace NCBI taxon ID integer with ontology term. Impacts the following message types:
- Reference
- ReferenceSet
- Changed ontology term “id” to “term_id” (#48) Impacts the following message types:
- OntologyTerm

Documentation:

- Created a basic Info page for the Pypi repository (#68)

0.6.0a9.post2

Bugfix release which uses the new release process.

0.6.0a9.post1

Bugfix release which fixes the following issues:

- wrong attributes on RnaQuantification (#53)
- wrong attributes on ExpressionLevels (#51)

0.6.0a9

A new versioning scheme has been introduced that will make it easy to tell which version of the client to use against a protocol version!

- **Calls are now returned as ListValues and can be int32, empty, or strings** to cover the case when a VCF call states no call was made.
- Refactor “BioSample” to “Biosample”.
- Switch to stable protobuf version (3.1).
- Improve generated documentation.
- Add authorization via headers.

0.0.4

0.0.3

Add hierarchical namespace

0.0.2

Release using new ga4gh packages, ga4gh-common and ga4gh-schemas

0.0.1

Initial release