Python

Overview

OpenCGA implements a Python REST client library called **PyOpenCGA** to execute any query or operation through the REST web services API. **PyOpenCGA** provides programmatic access to **all the implemented** REST web services, providing an easy, lightweight, fast and intuitive solution to access OpenCGA data. The library offers the convenience of an object-oriented scripting language and provides the ability to integrate the obtained results into other Python applications.

Some of the main features include:

- full RESTful web service API implemented, all endpoints are supported including new alignment or clinical functionality.
- data is returned in a new *RestResponse* object which contains metadata and the results, some handy methods and iterators implemented.
- it uses the OpenCGA *client-configuration.yml* file.
- several Jupyter Notebooks implemented.

PyOpenCGA has been implemented by Daniel Perez, Pablo Marin and David Gomez and it is based on a previous library called *pyCGA* implemented by Antonio Rueda and Daniel Perez from Genomics England. The code is open-source and can be found at https://github.com/opencb/opencga/tree/develop/opencga-client/src/main/python/pyOpenCGA. It can be installed using PyPI and . Please, find more details on how to use the python library at Using the Python client.

Installation

Python client requires at least **Python 3.x,** although most of the code is fully compatible with Python 2.7. You can install PyOpenCGA either from PyPI repository or from source code.

PyPI

PyOpenCGA client is available at PyPI repository at https://pypi.org/project/pyopencga/. Installation is as simple as running the following command line:

```
## Latest stable version
pip install pyopencga
```

Source Code

From OpenCGA v2.0.0 the Python client source code can be found at GitHub Release at https://github.com/opencb/opencga/releases. You can easily install *pyOpenCGA* using the *setup.py* file.

```
## Get latest stable version from https://github.com/opencb/opencga
/releases. You can use wget from the terminal
wget https://github.com/opencb/opencga/releases/download/v2.0.0/opencga-
2.0.0.tar.gz

## Decompress
tar -zxvf opencga-2.0.0.tar.gz

## Move to the pyOpenCGA client folder
cd opencga-2.0.0/clients/python

## Install the library
python setup.py install
```

Getting started

Client Configuration

Configuration is handled by the *ClientConfiguration* class. You can create a *ClientConfiguration* using either the *conf/client-configuration.yml* file or by passing a dictionary.

Table of Contents:

Useful Links

- PyPI PyOpenCGA
- PyOpenCGA notebooks

```
## Import ClientConfiguration class
from pyopencga.opencga_config import ClientConfiguration

## You can create a ClientConfiguration by using the path to the client-
configuration.yml file (it can also accept a JSON file)
config = ClientConfiguration('opencga-2.0.0/conf/client-configuration.yml')

## Additionally, you can pass a dictionary using the same structure as the
client-configuration.yml (the only required parameter is REST host)
config = ClientConfiguration({"rest": {"host": "http://bioinfo.hpc.cam.ac.
uk/opencga-prod"}})
```

OpenCGA Client

OpencgaClient is the main class in *pyOpenCGA*. It manages login/logout authentication, REST clients initialisation and provides a set of other utilities.

To create an *OpencgaClient* instance, a *ClientConfiguration* instance must be passed as an argument. You can authenticate in two different ways. First, you can login by providing the user and optionally the password. Second, you can provide a valid token when creating *OpencgaClient*. Remember that tokens are only valid for a period of time.

```
## Import ClientConfiguration and OpencgaClient class
from pyopencga.opencga_config import ClientConfiguration
from pyopencga.opencga_client import OpencgaClient

## Create an instance of OpencgaClient passing the configuration
config = ClientConfiguration('opencga-2.0.0/conf/client-configuration.yml')
oc = OpencgaClient(config)

## Two authentication options:
## Option 1. If the user has a valid token, it can be passed to start
doing calls as an authenticated user
oc = OpencgaClient(config, token='TOKEN')

## Option 2. If no token is provided, the user must login with valid
credentials. Password is optional (if it is not passed to the login
method, it will be prompted to the user)
oc.login(user='USER')        ## The password will be asked
# or
oc.login(user='USER', password='PASSWORD')

## You can logout by executing the following command, the token will be
deleted.
oc.logout()
```

The *OpencgaClient* class works as a *client factory* containing all the different *clie nts,* one per REST resource, that are necessary to call any REST web service. Below is a list of available clients:

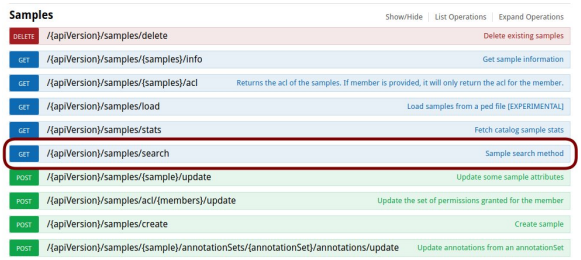
```
## Create main clients
users = oc.users
projects = oc.projects
studies = oc.studies
files = oc.files
jobs = oc.jobs
families = oc.families
individuals = oc.individuals
samples = oc.samples
cohorts = oc.cohorts
panels = oc.panels

## Create analysis clients
alignments = oc.alignment
variants = oc.variant
clinical = oc.clinical
ga4gh = oc.ga4gh

## Create administrative clients
admin = oc.admin
meta = oc.meta
variant_operations = oc.variant_operations
```

Client API

Clients implements **all** available REST API endpoints, one method has been implemented for each REST web service. The list of available actions that can be performed with all those clients can be checked in Swagger as explained in RESTful Web Services#Swagger. Each particular client has a method defined for each available web service implemented for the resource. For instance, the whole list of actions available for the **Sample** resource are shown below.



For all those actions, there is a method available in the sample client. For instance, to search for samples using the */search* web service, you need to execute:

```
## Look for the first 5 sample IDs of the study "study"
sample_result = oc.samples.search(study='study', limit=5, include='id')
```

Working with the *RestResponse*

As described in RESTful Web Services#RESTResponse, all REST web services return a *RestResponse* object containing some metadata and a list of *OpenCGAResults*. Each of these *OpenCGAResults* contain some other metadata and the actual data results.

To work with these REST responses in an easier way, *RestResponse* class has been implemented to wrap the web service *RetResponse* object and to offer some useful methods to process the results. For instance, the *sample_result* variable from the example above is a *RestResponse* instance. This object defines several methods to navigate through the data.

The implemented *RestResponse* methods are:

```
## Returns the list of results for the response in position "response_pos"
(response_pos=0 by default)
sample_response.get_results(response_pos)

## Returns the result in position "result_pos" for the response in
position "response_pos" (response_pos=0 by default)
sample_response.get_result(result_pos, response_pos)

## Returns the list of responses
sample_response.get_responses()

## Returns the response in position "response_pos" (response_pos=0 by
default)
sample_response.get_response(response_pos)

## Returns all results from the response in position "response_pos" as an
iterator (response_pos=None returns all results for all QueryResponses)
sample_response.result_iterator(response_pos)

## Returns all response events by type "event_type" ('INFO', 'WARNING' or
'ERROR') (event_type=None returns all types of event)
sample_response.get_response_events(event_type)

## Returns all response events by type "event_type" ('INFO', 'WARNING or
'ERROR') for the response in position "response_pos" (event_type=None
returns all types of event; response_pos=0 by default)
sample_response.get_result_events(event_type, response_pos)

## Return number of matches for the response in position "response_pos"
(response_pos=None returns the number for all QueryResponses)
sample_response.get_num_matches(response_pos)

## Return number of results for the response in position "response_pos"
(response_pos=None returns the number for all QueryResponses)
sample_response.get_num_results(response_pos)

## Return number of insertions for the response in position "response_pos"
(response_pos=None returns the number for all QueryResponses)
sample_response.get_num_inserted(response_pos)

## Return number of updates for the response in position "response_pos"
(response_pos=None returns the number for all QueryResponses)
sample_response.get_num_updated(response_pos)

## Return number of deletions for the response in position "response_pos"
(response_pos=None returns the number for all QueryResponses)
sample_response.get_num_deleted(response_pos)
```

To explore the data in an easier way, a method named ***print_results*** has also been implemented to show the response in a more human-readable format.

```
## Print results of the query for the response in position "response_pos"
(response_pos=None returns the results for all QueryResponses)
sample_response.print_results(fields='id', response_pos=0, limit=5,
separator='\t', metadata=True, outfile='path/to/output.tsv')
```

Examples and tutorials

Setting up OpencgaClient and logging in

```
# First, we need to import both the ClientConfiguration and the
OpencgaClient
from pyopencga.opencga_config import ClientConfiguration
from pyopencga.opencga_client import OpencgaClient

# Second, we need to set up the configuration
# The main client-configuration.yml file has a "host" section to point to
the REST OpenCGA endpoints
# We need to either pass the path to the configuration file or a
dictionary with the same structure of the file
config = ClientConfiguration({'rest': {'host': 'http://bioinfo.hpc.cam.ac.
uk/opencga-prod'}})

# Third, we create an instance of the OpencgaClient passing the
configuration
oc = OpencgaClient(config)

# Finally, we need to authenticate.
oc.login(user='demouser', password='demouser')

# Additionally, we can check that we've logged in successfully by printing
the obtained token
print(oc.token)
```

Getting ID's for available projects, studies, families and samples

```
# We can get the ID of all the available projects in this OpenCGA
installation
for project in oc.projects.search().get_results():
    print(project['id'])

# We can get the ID of all the available studies in the project
for study in oc.studies.search(project='family').get_results():
    print(study['id'])

# We can get the ID for all the available families in the study
for family in oc.families.search(study='corpasome').get_results():
    print(family['id'])

# We can get the ID for all the available samples in the study
for sample in oc.samples.search(study='corpasome').get_results():
    print(sample['id'])
```

Getting gene variants for individuals with a particular disorder

```
# We are interested in looking for all the individuals containing a
particular disorder: "OMIM:611597"
individuals_query_response = oc.individuals.search(
    study='corpasome',  # name of the study where the families are stored
    disorders='OMIM:611597',  # id of the disorders of interest
    include='id'  # retrieve only these fields from the results
)

# If we want to know exactly the number of individuals obtained, we can
run:
print(individuals_query_response.get_num_results())

# Now we fetch all the variants falling in the "BFSP2" gene for those
individuals
# In this case, we will limit the variant query to a maximum of 10 results
# We also exclude sample information (includeSample='none') as it can be
huge and would make this query much slower
for individual in individuals_query_response.get_results():
    print('Individual: ' + individual['id'])
    samples = ','.join([sample['id'] for sample in individual['samples']])
    variant_response = oc.variants.query(study='corpasome',
sample=samples, gene='BFSP2', includeSample='none', limit=10)
    if variant_response.get_num_results() > 0:
        for variant in variant_response.get_results():
            print('{}:{}-{}\t{}'.format(variant['chromosome'], str(variant
['start']), str(variant['end']), variant['type']))
    else:
        print('No variant results found')
```

Getting sample variant ID's

```
# Now we are interested in getting the rs IDs for the first 10 variants
for a particular sample
for variant in oc.variants.query(sample='ISDBM322015', study='corpasome',
limit=10).get_results():
    print(variant['names'])

# We can also get rs IDs for multiple samples
for variant in oc.variants.query(sample='ISDBM322015,ISDBM322016,
ISDBM322017,ISDBM322018', study='corpasome', limit=10).get_results():
    print(variant['names'])
```

Getting all samples containing a variant

```
# If we have an ID for a variant, we can obtain its ID in OpenCGA
(chromosome:position:reference:alternate)
variant_id = oc.variants.query(study='corpasome', xref='rs1851943').
get_result(0)['id']

# Now we are interested in getting all the samples that have that
particular ID
for variant in oc.variants.query_sample(study='corpasome',
variant=variant_id, debug=True).get_results():
    for study in variant['studies']:
        for sample in study['samples']:
            print(sample['sampleId'])
```

Additionally, there are several notebooks defined in https://github.com/opencb/opencga/tree/develop/opencga-client/src/main/python/notebooks with more real examples.