
mg-rest-dm Documentation

Release 0.0.1

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Oct 31, 2017

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Requirements and Installation

Requirements

Software

- Python 2.7.10+
- pyenv
- pyenv virtualenv
- pip

Python Modules

- DMP
- Flask
- Flask-Restful
- pytest
- Waitress
- Sphinx
- sphinx-autobuild

Installation

Basics

Directly from GitHub:

```
1 git clone https://github.com/Multiscale-Genomics/mg-rest-dm.git
2 cd mg-rest-dm/
3 pip install -e .
4 pip install -r requirements.txt
```

Using pip:

```
1 pip install git+https://github.com/Multiscale-Genomics/mg-rest-dm.git
```

Setting up a server

```
1 git clone https://github.com/Multiscale-Genomics/mg-rest-dm.git
2
3 cd mg-rest-dm
4 pyenv virtualenv 2.7.12 mg-rest-dm
5 pyenv activate mg-rest-dm
6 pip install git+https://github.com/Multiscale-Genomics/mg-dm-api.git
7 pip install -e .
8 pyenv deactivate
```

Requires a file with the name *mongodb.cnf* with the following parameters to define the MongoDB server:

```
1 [dmp]
2 host = localhost
3 port = 27017
4 user = testuser
5 pass = test123
6 db = dmp
```

Customise the *rest/auth_meta.json* file to locate the authentication server

Starting the service:

```
1 nohup ${PATH_2_PYENV}/versions/2.7.12/envs/mg-rest-dm/bin/waitress-serve --listen=127.
  ↳0.0.1:5002 rest.app:APP &
```

Testing

Test scripts are located in the *test/* directory. Run *pytest* from the root repository directory to ensure that the API is working correctly.

The scripts require a valid hdf5 file generated using the scripts from *mg-dm-api* and a matching *datasets.json* file located in the *rest/* directory

Documentation

To build the documentation:

```
1 pip install Sphinx
2 pip install sphinx-autobuild
3 cd docs
4 make html
```

Methods

class `rest.app.EndPoints`

Class to handle the http requests for returning information about the end points

get ()

GET list all end points

List of all of the end points for the current service.

Example

```
1 curl -X GET http://localhost:5002/mug/api/dmp
```

class `rest.app.FileMeta`

Class to handle the http requests for retrieving the data from a file. This class is able to handle big[Bed|Wig] file and serve back the matching region in the relevant format. It is also possible to stream back the whole file of any type for use in other tools.

delete (*args, **kwargs)

DELETE Remove a file from the DM API

Function to remove the file from teh DM API. This will result in the file being removed from the records and therefore not available within the VRE or from the RESTful interface

Parameters

- **should be passed as the data block with the HTTP request**
(*This*) –
- **json** (*dict*) –
file_id [str] ID of the stored file

Example

```
1 echo '{
2   "file_id": "<file_id>"
3 }' > data.json
4
5 curl -X DELETE
6   -H "Content-Type: application/json"
7   -H "Authorization: Bearer teststring"
8   -d @data.json http://localhost:5002/mug/api/dmp/file
```

get (*args, **kwargs)

GET List values from the file

Call to obtain regions from the compressed index files for Bed, Wig and TSV based file formats that contain genomic information.

Other files can be streamed.

Parameters **file_id** (*str*) – Identifier of the file to retrieve data from

Returns Returns a formatted in the relevant file type with any genomic features matching the format of the file.

Return type file

Examples

```
1 curl -X GET http://localhost:5002/mug/api/dmp/track?file_id=test_file
```

post (*args, **kwargs)

POST Add a new file to the DM API

Parameters

- **should be passed as the data block with the HTTP request** (*This*) –

- **json** (*dict*) –

user_id [str] User identifier

file_path [str] Location of the file

file_type [str] Tag for the file extension. The valid parameters are defined within the DM API documentation (mg-dm-api)

data_type [str]

What type of experiment is this data from. Options include RNA-seq ChIP-seq
MNase-seq WGBS HiC

taxon_id [int] Taxonomic identifier for a species (Human = 9606)

compressed Options of the compression level of the file. If file is not compressed then do not include this parameter

source_id [list] List of file_ids that were used for generating this file. If this is the root file then do not include this parameter.

meta_data [dict] Hash array describing the relevant metadata for the file, including the assembly if relevant

Returns Returns the id of the stored file

Return type file_id

Example

```

1 echo '{
2   "data_type": "RNA-seq",
3   "file_type": "fastq",
4   "meta_data": {
5     "assembly" : "GRCh38"
6   }, "taxon_id": 9606,
7   "file_path": "/tmp/test/path/RNA-seq/testing_123.fastq",
8   "parent_dir" "/tmp/test/path/RNA-seq/",
9   "size": 64000,
10  }' > data.json
11
12 curl -X POST
13   -H "Content-Type: application/json"
14   -H "Authorization: Bearer teststring"
15   -d @data.json http://localhost:5002/mug/api/dmp/file

```

put (*args, **kwargs)

PUT Update meta data

Request to update the meta data for a given file. This allows for the adding or removal of key-value pairs from the meta data.

Parameters

- **should be passed as the data block with the HTTP request** (*This*)–

- **json** (*dict*)–

user_id [str] User identifier

file_id [str] ID of the stored file

type [str] Options are ‘add_meta’ or ‘remove_meta’ to modify they key-value pairs for the file entry. Minimum sets of pairs are defined within the DM API (mg-dm-api)

meta_data [dict] Hash array describing the relevant metadata key-value pairs that are to be added

Returns Returns the id of the stored file

Return type file_id

Example

To add a new key value pair:

```
1 echo '{
2   "type": "add_meta",
3   "file_id": "<file_id>",
4   "meta_data": {"citation": "PMID:1234567890"}
5 }' > data.json
6
7 curl -X PUT
8   -H "Content-Type: application/json"
9   -H "Authorization: Bearer teststring"
10  -d @data.json http://localhost:5002/mug/api/dmp/file
```

To remove a key value pair:

```
1 echo '{
2   "type": "remove_meta",
3   "file_id": "<file_id>",
4   "meta_data": ["citation"]
5 }' > data.json
6
7 curl -X PUT
8   -H "Content-Type: application/json"
9   -H "Authorization: Bearer teststring"
10  -d @data.json http://localhost:5002/mug/api/dmp/file
```

To modify a column value (file size):

```
1 echo '{
2   "type": "modify_column",
3   "file_id": "<file_id>",
4   "key": "<column_key>"
5   "value": "<new_value>"
6 }' > data.json
7
8 curl -X PUT
9   -H "Content-Type: application/json"
10  -H "Authorization: Bearer teststring"
11  -d @data.json http://localhost:5002/mug/api/dmp/file
```

class `rest.app.Files`

Class to handle the http requests for retrieving the list of files for a given user handle

get (**args*, ***kwargs*)

GET List user tracks

Function to list the files that are owned by a single user. It is possible to filter by assembly, file or data type, or to find track files that contain data for a given region

Parameters

- **assembly** (*str*) – Genome assembly accession
- **region** (*str*) – <chromosome>:<start_pos>:<end_pos>
- **file_type** (*str*) –
- **data_type** (*str*) –

Example

```
1 curl -X GET http://localhost:5002/mug/api/dmp/Files?>
```

class rest.app.**FileHistory**

Class to handle the http requests for retrieving the list of file history of a given file for a given user handle

get (*args, **kwargs)

GET the list of files that were used for generating the defined file

Example

```
1 curl -X GET http://localhost:5002/mug/api/dmp/file_history?file_id=<file_id>
```

class rest.app.**Ping**

Class to handle the http requests to ping a service

get ()

GET Status

List the current status of the service along with the relevant information about the version.

Example

```
1 curl -X GET http://localhost:5002/mug/api/dmp/ping
```


CHAPTER 3

Architectural Decision Record (ADR)

This file is a record of the choices that have been made about the choice of software, packages, pipelines and data structures that have been made in this repository. This document should serve the help future developers (including the original authors) understand what certain choices were made.

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