mg-rest-adjacency Documentation

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Requirements and Installation

1.1 Requirements

1.1.1 Software

- Python 2.7.10+
- pyenv
- pyenv virtualenv
- pip

1.1.2 Python Modules

- h5py
- NumPy
- Flask
- Flask-Restful
- json
- pytest
- Waitress
- Sphinx
- sphinx-autobuild

1.2 Installation

1.2.1 Basics

Directly from GitHub:

```
git clone https://github.com/Multiscale-Genomics/mg-rest-adjacency.git
cd mg-rest-adjacency/
pip install -e .
pip install -r requirements.txt
```

Using pip:

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

1.2.2 Setting up a server

```
git clone https://github.com/Multiscale-Genomics/mg-rest-adjacency.git

cd mg-rest-adjacency
pyenv virtualenv 2.7.12 mg-rest-adjacency
pyenv activate mg-rest-service
pip install git+https://github.com/Multiscale-Genomics/mg-dm-api.git
pip install -e .

pyenv deactivate
```

Starting the service:

```
nohup ${PATH_2_PYENV}/versions/2.7.12/envs/mg-rest-adjacency/bin/waitress-serve --

→listen=127.0.0.1:5002 rest.app:app &
```

1.3 Testing

Test scripts are located in the *test/* directory. Run *pytest* to 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-storage-hdf5 and a matching datasets.json file located in the *rest/* directory

1.4 Documentation

To build the documentation:

```
pip install Sphinx
pip install sphinx-autobuild
cd docs
make html
```

mg-rest-adjacency server

2.1 Methods

class rest.app.GetEndPoints

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

```
curl -X GET http://localhost:5001/mug/api/adjacency
```

class rest.app.GetDetails

Class to handle the http requests for the size of the chromosome, the number of bins and available resolutions

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

GET List details from the file

Call to list the available chromosomes and resolutions within a dataset

Parameters

- user_id(str) User ID
- **file_id** (str) Identifier of the file to retrieve data from

Returns

chromosomes [list] List of the available chromosomes and their length

resolutions [list] List of the resolutions for the dataset

Return type dict

Examples

```
curl -X GET

-H "Authorization: Bearer teststring"

http://localhost:5001/mug/api/adjacency/details?file_id=test_file
```

class rest.app.GetInteractions

Class to handle the http requests for retrieving ranges of interactions from a given dataset

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

GET List details from the file

Call to list the available chromosomes and resolutions within a dataset

Parameters

- user id(str) User ID
- **file_id** (str) Identifier of the file to retrieve data from
- **chrom** (str) Chromosome identifier (1, 2, 3, chr1, chr2, chr3, I, II, III, etc) for the chromosome of interest
- **start** (*int*) Start position for a selected region
- end (int) End position for a selected region
- res (int) Resolution of the dataset requested
- limit chr (str) Limit the interactions returned to those between chr and
- limit_start (int) Start position for a specific interacting chromosomal region. This is to be used in conjunction with the limit_chr parameter
- **limit_end** (*int*) End position for a specific interacting chromosomal region This is to be used in conjunction with the limit chr parameter

Returns

chr [str] Chromosome ID

resolutions [list] List of the resolutions for the dataset

start [int] Start position for a selected region

end [int] End position for a selected region

res [int] Resolution of the dataset requested

limit_chr [str] Limit the interactions returned to those between chr and

limit_start [int] Start position for a specific interacting chromosomal region. This is to be used in conjunction with the limit_chr parameter

limit_end [int] End position for a specific interacting chromosomal region This is to be used in conjunction with the limit_chr parameter

values [list] List of values for each window of the region of a given resolution

log [list] List of errors that have occurred

Return type dict

Examples

```
curl -X GET

-H "Authorization: Bearer teststring"

http://localhost:5001/mug/api/adjacency/getInteractions?file_id=test_file&
-chr=<chr_id>&res=<res>
```

Notes

By default this is in JSON format. If the output is required in a tab separated format then the following needs to be specified in the header of the request:

```
curl -X GET

-H "Accept: application/tsv"

-H "Authorization: Bearer teststring"

http://localhost:5001/mug/api/adjacency/getInteractions?file_id=test_file&
-chr=<chr_id>&res=<res>
```

This will return the values from the JSON format in the following order

- 1. Chromosome 1
- 2. Starting position for chromosome 1
- 3. Chromosome 2
- 4. Starting position for chromosome 2
- 5. Value

class rest.app.GetValue

Class to handle the http requests for retrieving a single value from a given dataset

```
get (*args, **kwargs)
GET single value
```

Call to get a single value for a spcific bin x bin location

Parameters

```
• user_id(str) - User ID
```

- **file_id** (str) Identifier of the file to retrieve data from
- pos_x (int) Location of the window on the first region of interest
- pos_y (int) Location of the window on the second region of interest
- res (int) Resolution of the dataset requested

Returns

```
chrA [str] Chromosome ID 1
chrB [str] Chromosome ID 2
resolution [int] Resolution of the bin of interest
pos_x [int] Location of the window on the first region of interest
pos_y [int] Location of the window on the second region of interest is to be used in conjunction with the limit_chr parameter
```

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values [list] List of values for each window of the region of a given resolutionReturn type dict

Examples

class rest.app.Ping

Class to handle the http requests to ping a service

```
static get()
GET Status
```

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

Examples

```
curl -X GET http://localhost:5001/mug/api/adjacency/ping
```

$\mathsf{CHAPTER}\,3$

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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