

User Manual for MeganServer

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1 Introduction

MeganServer [1] is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details.

You should have received a copy of the GNU General Public License along with this program. If not, see <http://www.gnu.org/licenses>.

A paper describing the MeganServer is published in *Bioinformatics* journal [1], and source code files can be downloaded from <http://github.com/husonlab/megan-ce/tree/master/src/megan/ms>.

MeganServer is provided as a standalone program in MEGAN6 [2], both with the Community- and Ultimate-Edition.

The Community Edition of this program is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation, either version 3 of the License, or (at your option) any later version.

The Ultimate Edition of this program is licensed by Computomics GmbH for a fee. The Ultimate Edition is based on the Community Edition and includes additional, proprietary code, which is not open source.

The DIAMOND+MEGAN pipeline [3, 4, 5] is a popular approach to metagenomic data analysis [6]. In it, the user first aligns metagenomic sequenced reads against protein databases such as NCBI-nr [7] or AnnoTree [8, 9], using by the DIAMOND high-throughput DNA-to-protein alignment tool. They then use MEGAN or the associated commandline tool `daa-meganizer` to perform taxonomic and functional binning of the reads, based on the alignments. One main advantage of this approach is that MEGAN provides a graphical user interface and the program can be run on a laptop or desktop. MEGAN supports the visualization of charts, alignment inspection, comparison between different sample group, gene-centric assembly and several other features. The tool is useful for users both with and without programming skills.

As sequencing costs decrease, the number of metagenomic projects, involved samples and amount of sequenced DNA increase. Processing the resulting huge datasets can be a problem. Previous versions of MEGAN required that the files to be analyzed must be present on the local machine that is running MEGAN, requiring that large files be downloaded to personal computers.

To address this issue, we present `megan-server`, a program that can serve files that are hosted on a server to instances of MEGAN running on personal computers, over the web. This uses a lightweight Representational State Transfer-Application Programming Interface (REST-API)-based framework [10] written in Java.

This allows researchers to analyze files produced by the DIAMOND+MEGAN pipeline on their local computer, without any need to download data from a server directory.

Data is sent and received via REST which makes reuse of HTTP technology. While users can access the files using a web browser, they will usually access the files via the MEGAN, which acts as a client and communicates with instances of MeganServer.

2 Support for MeganServer

If you have any queries/questions regarding installation, usage, or want us to include new features, etc of MeganServer, please use the [MEGAN community](#) website to post them.

3 MeganServer public instance

For teaching and testing purposes we maintain a public instance of MeganServer. Anyone can access it at <http://maira.cs.uni-tuebingen.de:8001/megan6server/help> (username:guest and password:guest). It currently servers about 20 short-read metagenomic datasets and more than 80 long-reads published datasets. See Figure 1.

4 Installation

Megan Server is provided as a standalone program `tools/megan-server` in the Megan6 software suite. MEGAN6 can be downloaded from the [MEGAN6 Download Page](#).

4.1 Installers for the Community Edition

There are three different installers for the Community Edition, targeting different operating systems:

- `MEGAN_COMMUNITY_windows-64x_6.24.11.exe` provides an installer for a 64-bit version of MEGAN for Windows.
- `MEGAN_COMMUNITY_macos_6.24.11.dmg` provides an installer for MacOS X.
- `MEGAN_COMMUNITY_unix_6.24.11.sh` provides an installer for Linux and Unix.

4.2 Installers for the Ultimate Edition

There are three different installers for the Community Edition, targeting different operating systems:

- `MEGAN_Ultimate_windows-64x_6.24.11.exe` provides an installer for a 64-bit version of MEGAN for Windows.
- `MEGAN_Ultimate_macos_6.24.11.dmg` provides an installer for MacOS X.
- `MEGAN_Ultimate_unix_6.24.11.sh` provides an installer for Linux and Unix.

Once MEGAN6 is installed, MeganServer will be present as `tools/megan-server` in your MEGAN installation directory. Note that only the MacOS X and Linux versions provide the tools directory.

5 Configuration

Once MEGAN6 is installed, the user can run MeganServer.

The command `tools/megan-server -h` will list all available commandline options:

```
tools/megan-server -h
SYNOPSIS
    MeganServer [options]
DESCRIPTION
    Serves MEGAN files over the web via HTTP
OPTIONS
    Input
        -i, --input [string]      Input directory. Mandatory option.
        -r, --recurse             Recursively visit all input subdirectories.
                                Default value: true.
        -x, --extensions [string(s)] Input file extensions. Default value(s):
                                '.daa' '.rma' '.rma6' '.megan' '.megan.gz'.

    Server
        -e, --endpoint [string]   Endpoint name. Default value: megan6server
        -p, --port [number]       Server port. Default value: 8001.
        -g, --allowGuest          Allow guest login (name: guest, pwd: guest).
                                Default value: false.

    Other:
        -u, --usersFile [string]  File containing list of users.
                                Default value: MeganServerUsers.def
        -bl, --backlog [number]   Set the socket backlog. Default value: 100.
        -pt, --pageTimeout [number] Number of seconds to keep pending pages alive.
                                Default value: 10000.
        -rpp, --readsPerPage [number] Number of reads per page to serve.
                                Default value: 100.
        -t, --threads [number]   Number of threads. Default value: 8.
        -d, --debug              Debug mode. Default value: false.
        -v, --verbose            Echo commandline options and be verbose.
                                Default value: false.
        -h, --help              Show program usage and quit.

AUTHOR(s)
    Daniel H. Huson.
VERSION
    MEGAN Community Edition (version 6.24.11, built 01 Dec 2022).
Copyright (C) 2022 Daniel H. Huson. This program comes with ABSOLUTELY NO WARRANTY..
```

To serve a directory `dir` containing your meganized DAA file, you need to run the following basic command:

```
megan-server -g -i <dir> -e <name> -p <port>
```

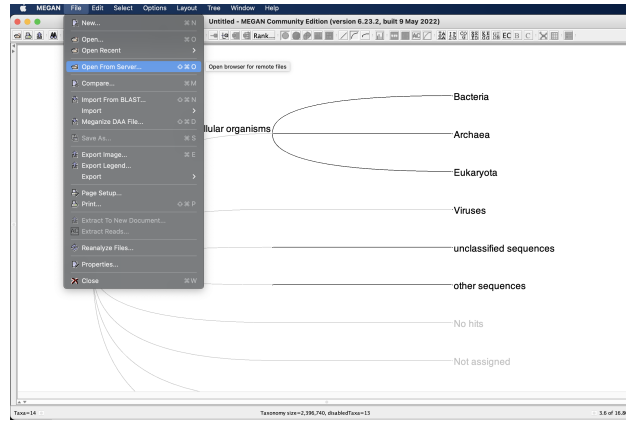
The flag `-g` enables guest login, `<dir>` is the directory to be served, `<name>` is the endpoint name, e.g. `megan6server`, and `<port>` is the port you want to use, (default is 8001). During startup, MeganServer will list the HTTP address (for e.g. <http://maira.cs.uni-tuebingen.de:8001/megan6server/help>, <http://maira.cs.uni-tuebingen.de:8001/megan6server>), which can be used to access and analyze data.

6 MEGAN Client

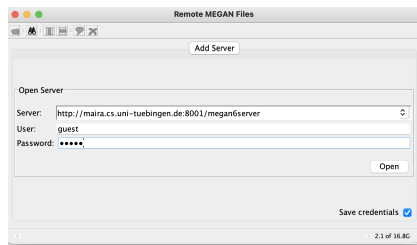
You can access files using the program MEGAN, which acts as a client for a MeganServer instance. To access a server, select the `File` → `Open From Server...` menu item (Figure 1a). In the dialog window (Figure 1b), enter the server endpoint and user credentials (for example, user `guest` and password `guest`) for the public server running at <http://maira.cs.uni-tuebingen.de:8001/megan6server>.

Users have been provided with many features to carry out analysis of their interests like comparative analysis (Figure 1e), different types of clustering, inspect reads (Figure 2d), alignments (Figure 2e), gene-centric assembly [11], etc.

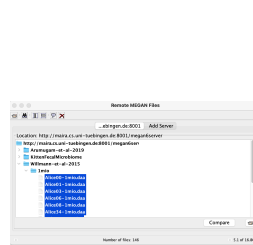
a



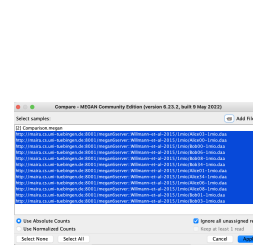
b



c



d



e

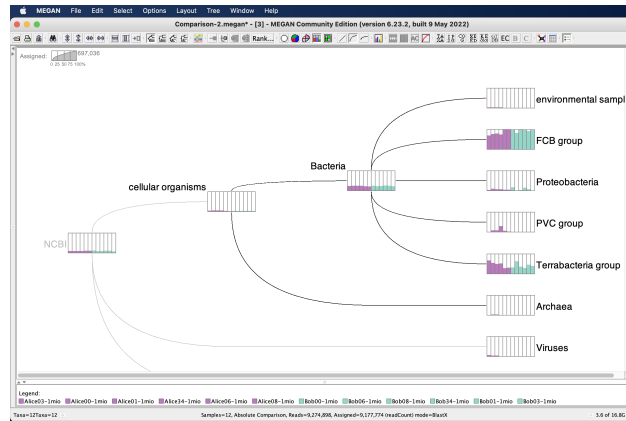


Figure 1: **Accessing and interacting via MEGAN-GUI:** (a) To access an instance of MeganServer, select the File → Open From Server... menu item and then (b) enter the server endpoint and user credentials. (c) After successfully contacting the service, an overview of all available remote files is displayed. (d) If more than one file is selected, then one can use the Compare dialog to combine multiple files into a single document. (e) Pressing Apply will open the files in the default NCBI taxonomy viewer.

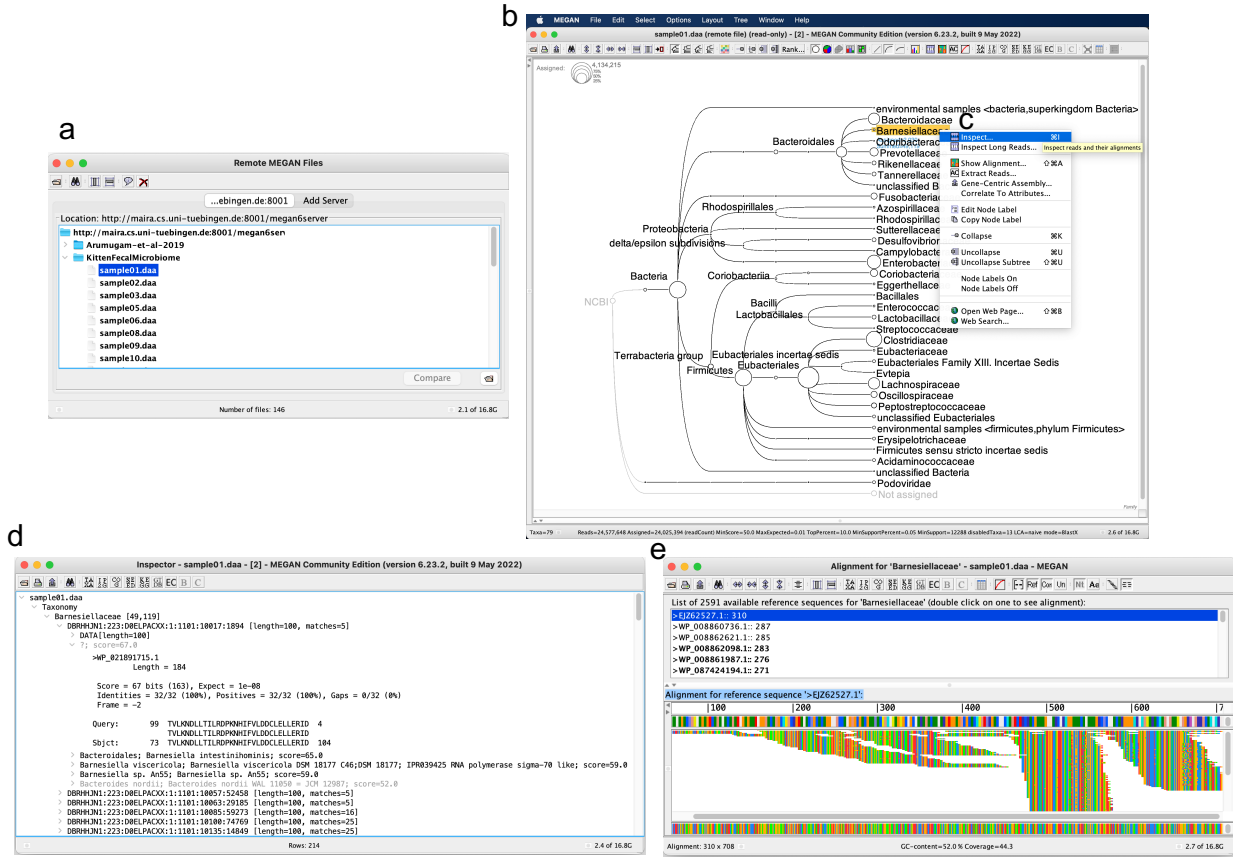


Figure 2: **Accessing and interacting via MEGAN-GUI continued:** (a) Double-click a sample of interest from the list of available remote files. (b) This will open the file in the default NCBI taxonomy viewer. (c) Select a node or leaf of interest. This will display the number of reads assigned and summed to that node or leaf. Right-click on a node to obtain a context menu, showing various analysis options. (d) The Inspect... menu item opens the inspector window for the corresponding node. (e) The Show Alignment... menu item opens the Alignment dialog for the corresponding node.

More details on using MEGAN and performing various kinds of analysis can be found in the MEGAN manual <https://software-ab.cs.uni-tuebingen.de/download/megan6/manual.pdf>.

7 MeganServer RESTful API

MeganServer uses a RESTful API to publish its services and to transfer data. MEGAN6 communicates with MeganServer using this API. However, the API also be accessed using a web browser. This section describes all API commands in detail with examples.

Note that some of the API commands can provide a response either in text format (parameter `binary=true`) or binary format (parameter `binary=false`).

7.1 General

7.1.1 help

- **Name:** help
- **Description:** Get a list of all accessible commands of MeganServer
- **Parameters:**
 - No Parameters
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/help>
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/help`

7.1.2 about

- **Name:** about
- **Description:** Get a version number, Hostname, IP address, Port, Known users, Total requests, Server start date and time of MeganServer.
- **Parameters:**
 - No Parameters
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/about>
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/about`

7.1.3 isReadOnly

- **Name:** isReadOnly
- **Description:** Determines if user has read/write permissions. At present, datasets are readOnly, no matter if a user is admin or not, hence always true
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** –
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/isReadOnly?file=KittenFecalMicrobiome/sample01.daa>
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/isReadOnly?file=KittenFecalMicrobiome/sample01.daa`

7.2 Files

7.2.1 list

- **Name:** List all datasets served by active MeganServer instance.
- **Description:** At present, always true.
- **Parameters:**
 - **readCount**
 - * **Name:** readCount
 - * **Description:** Include read count to the result (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** -
 - **matchCount**
 - * **Name:** matchCount
 - * **Description:** Include match count to the result (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** -
 - **metadata**
 - * **Name:** metadata
 - * **Description:** Include metadata to the result (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** -
- **Examples:**
 - `http://maira.cs.uni-tuebingen.de:8001/megan6server/list`
 - `http://maira.cs.uni-tuebingen.de:8001/megan6server/list?readCount=true`
 - `http://maira.cs.uni-tuebingen.de:8001/megan6server/list?matchCount=true`
 - `http://maira.cs.uni-tuebingen.de:8001/megan6server/list?metadata=true`
 - `http://maira.cs.uni-tuebingen.de:8001/megan6server/list?readCount=true&matchCount=true&metadata=true`
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/list`
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/list?readCount=true`
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/list?matchCount=true`
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/list?metadata=true`
 - `curl -u guest:guest "http://maira.cs.uni-tuebingen.de:8001/megan6server/list?readCount=true&matchCount=true&metadata=true"`

7.2.2 getAuxiliary

- **Name:** getAuxiliary
- **Description:** Get auxiliary data for the dataset. For e.g, metadata, USE_STATE, SAMPLE_ATTRIBUTES, etc.
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -
 - **binary**
 - * **Name:** file
 - * **Description:** Download result in binary format (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** false
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getAuxiliary?file=KittenFecalMicrobiome/sample01.daa>
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getAuxiliary?file=KittenFecalMicrobiome/sample01.daa&binary=true>
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getAuxiliary?file=KittenFecalMicrobiome/sample01.daa`
 - `curl -u guest:guest "http://maira.cs.uni-tuebingen.de:8001/megan6server/getAuxiliary?file=KittenFecalMicrobiome/sample01.daa&binary=true" -o output.binary`

7.2.3 getNumberOfReads

- **Name:** getNumberOfReads
- **Description:** Get number of reads for one or more than one dataset (separated by comma).
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfReads?file=KittenFecalMicrobiome/sample01.daa>

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfReads?file=KittenFecalMicrobiome/sample01.daa,KittenFecalMicrobiome/sample02.daa>
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfReads?file=KittenFecalMicrobiome/sample01.daa`
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfReads?file=KittenFecalMicrobiome/sample01.daa,KittenFecalMicrobiome/sample02.daa`

7.2.4 getNumberOfMatches

- **Name:** getNumberOfMatches
- **Description:** Get number of matches for one or more than one dataset (separated by comma).
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -

- **Examples:**

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfMatches?file=KittenFecalMicrobiome/sample01.daa>
- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfMatches?file=KittenFecalMicrobiome/sample01.daa,KittenFecalMicrobiome/sample02.daa>
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfMatches?file=KittenFecalMicrobiome/sample01.daa`
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getNumberOfMatches?file=KittenFecalMicrobiome/sample01.daa,KittenFecalMicrobiome/sample02.daa`

7.2.5 getClassificationNames

- **Name:** getClassificationNames
- **Description:** Get list of all classifications for one or more than one dataset (separated by comma).
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -

- **Examples:**

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationNames?file=KittenFecalMicrobiome/sample01.daa>

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationNames?file=KittenFecalMicrosample01.daa,KittenFecalMicrobiome/sample02.daa>
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationNames?file=KittenFecalMicrobiome/sample01.daa`
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationNames?file=KittenFecalMicrobiome/sample01.daa,KittenFecalMicrobiome/sample02.daa`

7.2.6 getDescription

- **Name:** getDescription
- **Description:** Get a description of a file, if available.
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getDescription?file=KittenFecalMicrobiome/sample01.daa>
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getDescription?file=KittenFecalMicrobiome/sample01.daa`

7.2.7 download

- **Name:** download
- **Description:** Download a dataset.
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/download?file=KittenFecalMicrobiome/sample01.daa>
 - `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/download?file=KittenFecalMicrobiome/sample01.daa -o sample01.daa`

7.3 Reads and matches

7.3.1 getRead

- **Name:** getRead
- **Description:** Get read and optionally all matches for given dataset and readId.
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -
 - **readId**
 - * **Name:** readId
 - * **Description:** readId of your interest.
 - * **Required:** true
 - * **Default Value:** -
 - **headers**
 - * **Name:** header
 - * **Description:** Help to view dataset header(Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
 - **sequence**
 - * **Name:** sequence
 - * **Description:** Help to view dataset sequences (reads)(Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
 - **matches**
 - * **Name:** matches
 - * **Description:** Help to view alignment (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
 - **binary**
 - * **Name:** binary
 - * **Description:** Download result in binary format (Boolean:true or false).
 - * **Required:** -

- * **Default Value:** true

- **Examples:**

- Used for MEGAN internal working.

7.3.2 getReads

- **Name:** isReadOnly

- **Description:** Get all reads for a given dataset; returns first page and page-id for next.

- **Parameters:**

- **file**

- * **Name:** file

- * **Description:** An identifier of a dataset. Either a path or a name.

- * **Required:** true

- * **Default Value:** -

- **readIds**

- * **Name:** readIds

- * **Description:** Help to view dataset readIds (Boolean:true or false).

- * **Required:** -

- * **Default Value:** true

- **headers**

- * **Name:** headers

- * **Description:** Help to view dataset headers (Boolean:true or false).

- * **Required:** -

- * **Default Value:** true

- **sequences**

- * **Name:** sequences

- * **Description:** Help to view dataset sequences (reads)(Boolean:true or false).

- * **Required:** -

- * **Default Value:** true

- **matches**

- * **Name:** matches

- * **Description:** Help to view alignment (Boolean:true or false).

- * **Required:** -

- * **Default Value:** true

- **binary**

- * **Name:** binary

- * **Description:** Download result in binary format (Boolean:true or false).
- * **Required:** -
- * **Default Value:** true

- **Examples:**

- `http://maira.cs.uni-tuebingen.de:8001/megan6server/getReads?file=KittenFecalMicrobiome/sample01.daa&binary=false`
- `http://maira.cs.uni-tuebingen.de:8001/megan6server/getReads?file=KittenFecalMicrobiome/sample01.daa&binary=false&readIds=false`
- `http://maira.cs.uni-tuebingen.de:8001/megan6server/getReads?file=KittenFecalMicrobiome/sample01.daa&binary=false&readIds=false&headers=false`
- `http://maira.cs.uni-tuebingen.de:8001/megan6server/getReads?file=KittenFecalMicrobiome/sample01.daa&binary=false&readIds=false&headers=false&sequences=false`
- `http://maira.cs.uni-tuebingen.de:8001/megan6server/getReads?file=KittenFecalMicrobiome/sample01.daa&binary=false&readIds=false&headers=false&sequences=false&matches=false`
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getReads?file=KittenFecalMicrobiome/sample01.daa&binary=false -o output.txt`

7.3.3 getReadsForClass

- **Name:** getReadsForClass
- **Description:** Get all reads for a given file, classification and one or more classes.
- **Parameters:**
 - **file**
 - * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -
 - **classification**
 - * **Name:** classification
 - * **Description:** Classification like Taxonomy, SEED, EGGNOG, GTDB, EC, INTERPRO2GO.
 - * **Required:** true
 - * **Default Value:** -
 - **classId**
 - * **Name:** classId
 - * **Description:** The id of a classification such as Taxonomy, SEED, EGGNOG, GTDB, EC, INTERPRO2GO (For e.g, Bacteria Taxonomy is 2).
 - * **Required:** true
 - * **Default Value:** -

- **readIds**
 - * **Name:** readIds
 - * **Description:** Help to view dataset readIds (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
- **headers**
 - * **Name:** headers
 - * **Description:** Help to view dataset headers (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
- **sequences**
 - * **Name:** sequences
 - * **Description:** Help to view dataset sequences (reads)(Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
- **pageSize**
 - * **Name:** pageSize
 - * **Description:** Number of dataset reads (read results) you want to see on the given page.
 - * **Required:** -
 - * **Default Value:** true
- **matches**
 - * **Name:** matches
 - * **Description:** Help to view alignment (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
- **binary**
 - * **Name:** binary
 - * **Description:** Download result in binary format (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** true
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome.sample01.daa&classification=taxonomy&classId=2&binary=false>
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome.sample01.daa&classification=taxonomy&classId=2,742742&binary=false>

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome/sample01.daa&classification=taxonomy&classId=2&binary=false&readIds=false>
- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome/sample01.daa&classification=taxonomy&classId=2&binary=false&readIds=false&headers=false>
- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome/sample01.daa&classification=taxonomy&classId=2&binary=false&readIds=false&headers=false&sequences=false>
- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome/sample01.daa&classification=taxonomy&classId=2&binary=false&readIds=false&headers=false&sequences=false&pageSize=100>
- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome/sample01.daa&classification=taxonomy&classId=2>
- `curl -u guest:guest http://maira.cs.uni-tuebingen.de:8001/megan6server/getReadsForClass?file=KittenFecalMicrobiome/sample01.daa&binary=false&classification=taxonomy&classId=2&sequences=true&matches=true&pageSize=100 -o output.txt`

7.3.4 getNext

- **Name:** getNext
- **Description:** Get the next page of reads.
- **Parameters:**
 - **pageld**
 - * **Name:** pageld
 - * **Description:** page Id numeric.
 - * **Required:** true
 - * **Default Value:** -
 - **binary**
 - * **Name:** binary
 - * **Description:** Download result in binary format (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** false
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getNext?pageId=32>
 - Used for MEGAN internal working.

7.4 Classifications

7.4.1 getClassificationBlock

- **Name:** getClassificationBlock

- **Description:** Get the classifications block for a named dataset and classification (number of reads assigned to all node in a classification).

- **Parameters:**

- **file**

- * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true
 - * **Default Value:** -

- **classification**

- * **Name:** classification
 - * **Description:** Classification like Taxonomy, SEED, EGGNOG, GTDB, EC, INTERPRO2GO.
 - * **Required:** true
 - * **Default Value:** -

- **binary**

- * **Name:** binary
 - * **Description:** Download result in binary format (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** false

- **Examples:**

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationBlock?file=KittenFecalMicrobiome/sample01.daa&classification=SEED>
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationBlock?file=KittenFecalMicrobiome/sample01.daa&classification=SEED&binary=true>
 - `curl -u guest:guest "http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationBlock?file=KittenFecalMicrobiome/sample01.daa&classification=SEED"`
 - `curl -u guest:guest "http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassificationBlock?file=KittenFecalMicrobiome/sample01.daa&classification=SEED&binary=true"`

7.4.2 getClassSize

- **Name:** getClassSize
- **Description:** Get the number of reads assigned to one node in a classification for a named dataset.

- **Parameters:**

- **file**

- * **Name:** file
 - * **Description:** An identifier of a dataset. Either a path or a name.
 - * **Required:** true

- * **Default Value:** -
- **classification**
 - * **Name:** classification
 - * **Description:** Classification like Taxonomy, SEED, EGGNOG, GTDB, EC, INTERPRO2GO.
 - * **Required:** true
 - * **Default Value:** -
- **classId**
 - * **Name:** classId
 - * **Description:** The id of a classification such as Taxonomy, SEED, EGGNOG, GTDB, EC, INTERPRO2GO (For e.g, Bacteria Taxonomy is 2).
 - * **Required:** -
 - * **Default Value:** -
- **sum**
 - * **Name:** sum
 - * **Description:** Return only read assigned to classId (Boolean:true or false).
 - * **Required:** -
 - * **Default Value:** -
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassSize?file=KittenFecalMicrobiome/sample02.daa&classification=taxonomy&classId=2>
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassSize?file=KittenFecalMicrobiome/sample02.daa&classification=taxonomy&classId=2&sum=true>
 - `curl -u guest:guest "http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassSize?file=KittenFecalMicrobiome/sample02.daa&classification=taxonomy&classId=2"`
 - `curl -u guest:guest "http://maira.cs.uni-tuebingen.de:8001/megan6server/getClassSize?file=KittenFecalMicrobiome/sample02.daa&classification=taxonomy&classId=2&sum=true"`

7.5 Admin

These commands can only be used by a user that has admin privileges.

7.5.1 admin/update

- **Name:** admin/update
- **Description:** Update server after files have been added to root directory.
- **Parameters:**
 - No Parameters
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/update>

```
- curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/update
```

7.5.2 admin/listUsers

- **Name:** admin/listUsers
- **Description:** List all defined active users.
- **Parameters:**
 - No Parameters
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/listUsers>
 - `curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/listUsers`

7.5.3 admin/addUser

- **Name:** admin/addUser
- **Description:** Add a new user
- **Parameters:**
 - **name**
 - * **Name:** name
 - * **Description:** User name for the new user.
 - * **Required:** true
 - * **Default Value:** -
 - **password**
 - * **Name:** password
 - * **Description:** Password for the new user, minimum 8 characters .
 - * **Required:** true
 - * **Default Value:** -
 - **isAdmin**
 - * **Name:** isAdmin
 - * **Description:** If the new user should be provided with admin rights.
 - * **Required:** true
 - * **Default Value:** -
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/addUser?name=ABCD&password=1234&isAdmin=true>

```
- curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/addUser?name=ABCD&password=1234&isAdmin=true
```

7.5.4 admin/removeUser

- **Name:** admin/removeUser
- **Description:** Remove/Delete user and revoke credentials.
- **Parameters:**
 - **name**
 - * **Name:** name
 - * **Description:** User name to Remove/Delete.
 - * **Required:** true
 - * **Default Value:** -
 - **Examples:**
 - * <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/removeUser?name=ABCD>
 - * `curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/removeUser?name=ABCD`

7.5.5 admin/addRole

Available in MEGAN UE only.

MeganServer UE supports multiple projects and to grant users access to individual projects that are given a “role” that matches the project name.

- **Name:** admin/addRole
- **Description:** Add a role to a user.
- **Parameters:**
 - **user**
 - * **Name:** user
 - * **Description:** User name for the user.
 - * **Required:** true
 - * **Default Value:** -
 - **role**
 - * **Name:** role
 - * **Description:** The role for the user name to add e.g. admin, guest.
 - * **Required:** true
 - * **Default Value:** -
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/addRole?user=ABCD&role=admin>

```
- curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/addRole?user=ABCD&role=admin
```

7.5.6 admin/removeRole

Available in MEGAN UE only.

- **Name:** admin/removeRole
- **Description:** Remove a role from a user.
- **Parameters:**
 - **user**
 - * **Name:** user
 - * **Description:** User name for the user.
 - * **Required:** true
 - * **Default Value:** -
 - **role**
 - * **Name:** role
 - * **Description:** The role for the user name to remove e.g.admin, guest.
 - * **Required:** true
 - * **Default Value:** -
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/isReadOnly>
 - `curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/isReadOnly`

7.5.7 admin/getLog

- **Name:** admin/getLog
- **Description:** Get log entries for MeganServer.
- **Parameters:**
 - No Parameters
- **Examples:**
 - <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/getLog>
 - `curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/getLog`

7.5.8 admin/clearLog

- **Name:** admin/clearLog
- **Description:** Clear log entries for MeganServer.

- **Parameters:**

- No Parameters

- **Examples:**

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/clearLog>
- `curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/clearLog`

7.5.9 admin/shutdown

- **Name:** admin/shutdown

- **Description:** Shutdown the MeganServer.

- **Parameters:**

- No Parameters

- **Examples:**

- <http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/shutdown>
- `curl -u YourAdminUserName:YoorAdminPassword http://maira.cs.uni-tuebingen.de:8001/megan6server/admin/shutdown`

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This program uses a number of external Java libraries. The JARs and their licenses are contained in the jars directory. MEGAN UE is obfuscated using yguard.

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