
ena_utils

Laboratory of Integrative System Physiology (LISP) at EPFL

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ena-utils is a small python package that provides a CLI to submit nucleotides sequences to the [European Nucleotide Archive \(ENA\)](#).

SUPPORTED SUBMISSION TYPES

- Non-multiplexed paired-end sequencing reads

FEATURES

- File upload
- Study registration
- Experiment registration
- Run registration
- Sample registration

REQUIREMENTS

- Python3
- Webin account

3.1 Instalation using pip

The latest release is available on PyPI and can be installed using pip:

```
$ pip install ena-utils
```

3.2 Isolated environments using pipx

Install and execute ena-utils in an isolated environment using pipx.

Install [pipx](#) and make sure that the `$PATH` is correctly configured.

```
$ python3 -m pip install --user pipx
$ pipx ensurepath
```

Once pipx is installed use following command to install ena-utils.

```
$ pipx install ena-utils
$ which ena-utils
~/.local/bin/ena-utils
```

3.3 File upload

The `ena-utils upload` command.

Uploading files to a Webin user file upload area is needed prior to files submission. See the associated [ENA documentation](#) for details.

Example

```
$ ena-utils upload --file_path <path/to/sequences/files.gz>
```

3.4 Submissions

The `ena-utils submit` command.

The `ena-utils submit` command has specific sub-commands for each type of object:

- Study (ex: `ena-utils submit study`)
- Sample (ex: `ena-utils submit sample`)
- Experiment (ex: `ena-utils submit experiment`)
- Run (ex: `ena-utils submit run`)

In addition, all these sub-commands come in two flavors:

- Unique object submission (ex: `ena-utils submit study`).
- Multiple objects submission using a submission file (ex: `ena-utils submit study-set`).

The `ena-utils submit` sub-commands allow to define some submission metadata. The possible metadata fields and values are specified in the [ENA schema](#) (also available in this documentation [here](#)). Check the sub-commands specific documentation to see which metadata fields are supported by your `ena-utils` version.

Template files for multiple objects submission can be created using the `ena-utils create-template` command, then edited to the specific needs of each submission.

By default, `ena-utils submit` sub-commands submit objects to the ENA test server (<https://wwwdev.ebi.ac.uk/ena/submit/drop-box/submit/>).

Any data submission to ENA first requires the registration of a study object. See the associated [ENA documentation](#) for details.

Example

```
$ ena-utils submit study -a <alias> test_alias -t <title> -d <description>
```

3.5 ena-utils

A simple CLI toolbox to submit sequences to the European Nucleotide Archive (ENA)

```
ena-utils [OPTIONS] COMMAND [ARGS]...
```

Options

-v, --verbose

Print various messages.

3.5.1 submit

Submit studies, experiments, runs and samples. - A study can be associated to multiple experiments. - An experiment can be associated to multiple runs. - An experiment can be associated to only one sample. - A run can be associated to only one experiment. - A sample can be associated to multiple experiments and runs.

```
ena-utils submit [OPTIONS] COMMAND [ARGS]...
```

Options

-u, --user <user>

Required Webin user ID (e.g. “Webin-12345”).

-p, --password <password>

Required Webin user password.

--type <type>

Type of submission.

Default ADD

-h, --hold <hold>

A date in YYYY-MM-DD format until which the submission will be held confidential.

-s, --server_address <server_address>

Server address (default to the development server. Change “wwwdev” to “www” to submit to the production server).

Default <https://wwwdev.ebi.ac.uk/ena/submit/drop-box/submit/>

--submission_xml <submission_xml>

Path to the XML submission file that will be created.

Default submission.xml

experiment

Submit a single experiment.

```
ena-utils submit experiment [OPTIONS]
```

Options

--study <study>

Required Associated study accession number (e.g. “PRJEB12345”).

--sample <sample>

Required Associated sample name (e.g. “sample_01”).

-a, --alias <alias>

Required Experiment alias (e.g. “my_experiment_01”).

- c, --center** <center>
 Required Name of the sequencing center (can be different from the study host institution).
- t, --title** <title>
 Required Experiment title (e.g. “A great experiment”).
- d, --design** <design>
 Required Experiment design (e.g. “Targeted sequencing of gene X with primers A/B.”).
- lib_name** <lib_name>
 Library name (e.g. “LIB_01”).
- lib_strategy** <lib_strategy>
 Required Library strategy (e.g. “AMPLICON”).
- lib_source** <lib_source>
 Required Library source (e.g. “METAGENOMIC”).
- lib_selection** <lib_selection>
 Required Library selection (e.g. “PCR”).
- lib_length** <lib_length>
 Required Library nominal length (e.g. “311”).
- lib_protocol** <lib_protocol>
 Required Library construction protocol (e.g. “As described previously in XY et al.”).
- instrument** <instrument>
 Required Instrument model (e.g. “Illumina MiSeq”).
- experiment_xml** <experiment_xml>
 Path to the XML experiment file that will be created.
 Default experiment.xml
- v, --verbose**
 Print various messages.

experiment-set

Submit multiple experiments using a tab-delimited table. The elements of the table must have the same format as the parameters used for a single experiment submission (see the “experiment” command above).

<pre>ena-utils submit experiment-set [OPTIONS]</pre>

Options

- table** <table>
 Path to a tab-delimited text file containing a list of experiments to submit and their parameters. The file must contain one row per experiment and the first row must contain columns headers for associated study accession number, associated sample name, alias, center, title, design, library name, library strategy, library source, library selection method, library nominal length, library protocol, and library sequencing instrument.

--study <study>
Name of the table column containing associated study accession numbers.
Default study

--sample <sample>
Name of the table column containing associated sample names.
Default sample

-a, --alias <alias>
Name of the table column containing aliases.
Default alias

-c, --center <center>
Name of the table column containing centers.
Default center

-t, --title <title>
Name of the table column containing titles.
Default title

-d, --design <design>
Name of the table column containing designs.
Default design

--lib_name <lib_name>
Name of the table column containing libraries names.
Default lib_name

--lib_strategy <lib_strategy>
Name of the table column containing libraries strategies.
Default lib_strategy

--lib_source <lib_source>
Name of the table column containing libraries sources.
Default lib_source

--lib_selection <lib_selection>
Name of the table column containing libraries selection methods.
Default lib_selection

--lib_length <lib_length>
Name of the table column containing libraries nominal lengths.
Default lib_length

--lib_protocol <lib_protocol>
Name of the table column containing libraries protocols.
Default lib_protocol

--instrument <instrument>

Name of the table column containing libraries sequencing instrument name.

Default instrument

--experiment_xml <experiment_xml>

Path to the XML experiment file that will be created.

Default experiment.xml

-v, --verbose

Print various messages.

run

Submit a single run. A md5 checksum of the run file must be provided for the submission. If a valid path to the file is provided with the `--filename` option, this is automatically calculated by ena-utils. However, if the path is not valid or the files are not accessible on your file system, the md5 checksum must be provided using either the `--checksum` option.

```
ena-utils submit run [OPTIONS]
```

Options

-e, --experiment <experiment>

Required Experiment reference (e.g. “my_experiment_01”).

-a, --alias <alias>

Required Run alias (e.g. “my_run_01.”).

-c, --center <center>

Required Name of the sequencing center.

--filename <filename>

Required Comma-delimited paths to the sequence files, absolute or relative to your working directory (e.g. “data/exp01_01_R1.fastq.gz,data/exp01_01_R2.fastq.gz”). If the sequence files are not on your file system: 1) Checksums for these files must be provided with the `--checksum` option. 2) File names still need to be provided here. 3) If a path is provided, only the file name (basename) will be used.

--filetype <filetype>

Required Comma-delimited type descriptions for the sequence files (e.g. “fastq.fastq”).

--checksum <checksum>

Comma-delimited md5 checksums for the sequence files (e.g. “51e00fbf45a12acd4cd4e65zgac54321,214f0fbf45a12acd4cd4e65zg”).

--run_xml <run_xml>

Path to the XML run file that will be created.

Default run.xml

-v, --verbose

Print various messages.

run-set

Submit multiple runs using a tab-delimited table. The elements of the table must have the same format as the parameters used for a single run submission (see the “run” command above).

```
ena-utils submit run-set [OPTIONS]
```

Options

--table <table>

Path to a tab-delimited text file containing a list of runs to submit and their parameters. The file must contain one row per run and the first row must contain columns headers for alias, sequencing center, files names and files types. Optionally, an additional column for md5 checksums can be provided (usefull when the files are not on your system and the checksum cannot be calculated by ena-utils). Using a parameters files allows to submit multiple runs at one time.

-e, --experiment <experiment>

Name of the table column containing references to associated experiments.

Default experiment

-a, --alias <alias>

Name of the table column containing runs aliases.

Default alias

-c, --center <center>

Name of the table column containing the name of the sequencing center.

Default center

--filename <filename>

Name of the table column containing comma-delimited paths to the associated sequence files.

Default filename

--filetype <filetype>

Name of the table column containing comma-delimited type description for the associated sequence files.

Default filetype

--checksum <checksum>

Name of the table column containing comma-delimited md5 checksums for the sequence files.

--run_xml <run_xml>

Path to the XML run file that will be created.

Default run.xml

-v, --verbose

Print various messages.

sample

Submit a single sample.

```
ena-utils submit sample [OPTIONS]
```

Options

-a, --alias <alias>

Required Sample alias (e.g. “sample_01”).

--title <title>

Required Sample title (e.g. “My great sample 01.”).

--taxon_id <taxon_id>

Required Sample taxon ID attribute (e.g. “10090”).

--scientific_name <scientific_name>

Required Sample scientific name attribute (e.g. “Mus musculus”).

--common_name <common_name>

Required Sample common name attribute (e.g. “house mouse”).

--attributes <attributes>

JSON-formatted string of sample attributes key:value pairs (e.g. {“age”:”2 weeks”,”strain”:”C57BL/6”}).

--sample_xml <sample_xml>

Path to the XML sample file that will be created.

Default sample.xml

-v, --verbose

Print various messages.

sample-set

Submit multiple samples using a tab-delimited table. The elements of the table must have the same format as the parameters used for a single sample submission (see the “sample” command above).

```
ena-utils submit sample-set [OPTIONS]
```

Options

--table <table>

Required Path to a tab-delimited text file containing a list of samples to submit and their parameters. The file must contain one row per sample and the first row must contain columns headers for at least alias, title, taxon ID, scientific name and common name. Additional columns are submitted as additional sample attributes. Taxon ID, scientific name and common name must comply with ENA standard organism taxonomic description (e.g. for *Mus musculus*, taxon ID is “10090”, scientific name is “*Mus musculus*” and common name is “house mouse”).

-a, --alias <alias>

Name of the table column containing sample alias.

Default alias

--title <title>

Name of the table column containing sample title.

Default title

--taxon_id <taxon_id>

Name of the table column containing sample taxon ID attribute.

Default taxon_id

--scientific_name <scientific_name>

Name of the table column containing sample scientific name attribute.

Default scientific_name

--common_name <common_name>

Name of the table column containing sample common name attribute.

Default common_name

--sample_xml <sample_xml>

Path to the XML sample file that will be created.

Default sample.xml

-v, --verbose

Print various messages.

study

Submit a single study.

```
ena-utils submit study [OPTIONS]
```

Options

-a, --alias <alias>

Required Study alias (e.g. “my_new_great_study”).

-t, --title <title>

Required Study title (e.g. “A great study.”).

-d, --description <description>

Required Study description (e.g. “A longer study description.”).

--center <center>

Name of the main research institution hosting the study.

--study_xml <study_xml>

Path to the XML project file that will be created.

Default project.xml

-v, --verbose

Print various messages.

study-set

Submit multiple studies using a tab-delimited table. The elements of the table must have the same format as the parameters used for a single study submission (see the “study” command above).

```
ena-utils submit study-set [OPTIONS]
```

Options

--table <table>

Path to a tab-delimited text file containing a list of studies to submit and their parameters. The file must contain one row per study and the first row must contain columns headers for alias, title and description.

-a, --alias <alias>

Name of the table column containing studies aliases.

Default alias

-t, --title <title>

Name of the table column containing studies titles.

Default title

-d, --description <description>

Name of the table column containing studies descriptions.

Default description

--study_xml <study_xml>

Path to the XML project file that will be created.

Default study.xml

-v, --verbose

Print various messages.

3.5.2 upload

Upload nucleotide sequences files.

```
ena-utils upload [OPTIONS]
```

Options

-u, --user <user>

Required Webin user ID (e.g. “Webin-12345”).

-p, --password <password>

Required Webin user password.

-f, --file_path <file_path>

Required Path to the sequence files - wildcards are supported - (e.g. “data/exp01_*.fastq.gz”).

-h, --host_address <host_address>

FTP server address.

Default webin2.ebi.ac.uk

-v, --verbose

Print various messages.

3.5.3 write-template

Write template files.

```
ena-utils write-template [OPTIONS] COMMAND [ARGS]...
```

experiment-table

Write a template table for experiment submission.

```
ena-utils write-template experiment-table [OPTIONS]
```

Options

-t, --table <table>

Path to the table file that will be created.

Default experiment.txt

-v, --verbose

Print various messages.

run-table

Write a template table for run submission.

```
ena-utils write-template run-table [OPTIONS]
```

Options

-t, --table <table>

Path to the table file that will be created.

Default run.txt

-v, --verbose

Print various messages.

sample-table

Write a template table for sample submission.

```
ena-utils write-template sample-table [OPTIONS]
```

Options

-t, --table <table>

Path to the table file that will be created.

Default sample.txt

-v, --verbose

Print various messages.

study-table

Write a template table for study submission.

```
ena-utils write-template study-table [OPTIONS]
```

Options

-t, --table <table>

Path to the table file that will be created.

Default project.txt

-v, --verbose

Print various messages.

3.6 ENA XML schema

- Study XML schema
- Experiment XML schema
- Run XML schema
- Sample XML schema

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