
genomehubs

Release 2.0.5

genomehubs

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CONTENTS

1	GenomeHubs	1
1.1	Installation	1
1.2	Documentation	1
1.3	Development	1
2	Installation	3
3	Usage	5
4	Reference	7
4.1	init	7
4.2	parse	8
4.3	index	9
4.4	fill	10
5	Contributing	13
5.1	Bug reports	13
5.2	Documentation improvements	13
5.3	Feature requests and feedback	13
5.4	Development	13
6	Authors	15
7	Changelog	17
7.1	2.0.0 (2020-07-02)	17
8	Indices and tables	19
	Python Module Index	21
	Index	23

GENOMEHUBS

1.1 Installation

```
conda install -c tolkit genomehubs
```

or

```
pip install genomehubs
```

You can also install the in-development version with:

```
pip install https://github.com/genomehubs/genomehubs/archive/main.zip
```

1.2 Documentation

<https://genomehubs.readthedocs.io/>

1.3 Development

To run all tests run:

```
tox
```


INSTALLATION

At the command line:

```
pip install genomehubs
```

CHAPTER THREE

USAGE

To use genomehubs in a project:

```
import genomehubs
```


REFERENCE

4.1 init

Initialise a GenomeHubs instance.

Usage:

```
genomehubs init [-hub-name STRING] [-hub-path PATH] [-hub-version PATH] [-config-file PATH...]
[-config-save PATH] [-es-host URL...] [-es-url URL] [-insdc-metadata] [-insdc-root INT...] [-restore-indices]
[-taxonomy-path PATH] [-taxonomy-ncbi-root INT] [-taxonomy-ncbi-url URL] [-taxon-preload] [-docker-contain STRING...]
[-docker-network STRING] [-docker-timeout INT] [-docker-es-container STRING] [-docker-es-image URL] [-reset] [-force-reset] [-hl-help] [-vl-version]
```

Options:

- hub-name STRING** GenomeHubs instance name.
- hub-path PATH** GenomeHubs instance root directory path.
- hub-version STR** GenomeHubs instance version string.
- config-file PATH** Path to YAML file containing configuration options.
- config-save PATH** Path to write configuration options to YAML file.
- es-host URL** ElasticSearch hostname/URL and port.
- es-url URL** Remote URL to fetch ElasticSearch code.
- insdc-metadata** Flag to index metadata for public INSDC assemblies.
- insdc-root INT** Root taxid when indexing public INSDC assemblies.
- restore-indices** Flag to restore taxon and assembly indices.
- taxonomy-path DIR** Path to directory containing raw taxonomies.
- taxonomy-ncbi-root INT** Root taxid for NCBI taxonomy index.
- taxonomy-ncbi-url URL** Remote URL to fetch NCBI taxonomy.
- taxon-preload** Flag to preload all taxa in taxonomy into taxon index.
- docker-contain STRING** GenomeHubs component to run in Docker.
- docker-network STRING** Docker network name.
- docker-timeout STRING** Time in seconds to wait for a component to start in Docker.
- docker-es-container STRING** ElasticSearch Docker container name.
- docker-es-image STRING** ElasticSearch Docker image name.

--reset	Flag to reset GenomeHubs instance if already exists.
--force-reset	Flag to force reset GenomeHubs instance if already exists.
-h, --help	Show this
-v, --version	Show version number

Examples

1. New GenomeHub with default settings `./genomehubs init`

2. New GenomeHub in specified directory, populated with Lepidoptera assembly # metadata from INSDC `./genomehubs init --hub-path /path/to/GenomeHub --insdc-root 7088 --insdc-meta`

```
genomehubs.lib.init.cli()
```

Entry point.

```
genomehubs.lib.init.main(args)
```

Initialise genomehubs.

4.2 parse

Parse a local or remote data source.

Usage:

```
genomehubs parse [-btk] [--btk-root STRING...] [--wikidata PATH] [--wikidata-root STRING...]
  [--wikidata-xref STRING...] [--gbif] [--gbif-root STRING...] [--gbif-xref STRING...] [--ncbi-
  datasets-genome PATH] [--outfile PATH] [--refseq-mitochondria] [--refseq-organelles] [--refseq-plastids]
  [--refseq-root NAME] [-h|--help] [-v|--version]
```

Options:

--btk	Parse assemblies in BlobToolKit
--btk-root STRING	Scientific name of root taxon
--gbif	Parse taxa in GBIF
--gbif-root STRING	GBIF taxon ID of root taxon
--gbif-xref STRING	Include link to external reference from GBIF (e.g. NBN, BOLD)
--wikidata PATH	Parse taxa in WikiData dump
--wikidata-root STRING	WikiData taxon ID of root taxon
--wikidata-xref STRING	Include link to external reference from WikiData (e.g. NBN, BOLD)
--ncbi-datasets-genome PATH	Parse NCBI Datasets genome directory
--outfile PATH	Save parsed output to file
--refseq-mitochondria	Parse mitochondrial genomes from the NCBI RefSeq organelle collection
--refseq-organelles	Parse all genomes from the NCBI RefSeq organelle collection
--refseq-plastids	Parse plastid genomes from the NCBI RefSeq organelle collection
--refseq-root NAME	Name (not taxId) of root taxon
-h, --help	Show this

-v, --version Show version number

`genomehubs.lib.parse.cli()`
Entry point.

`genomehubs.lib.parse.main(args)`
Parse data sources.

4.3 index

Index a file, directory or repository.

Usage:

genomehubs index [**--hub-name** STRING] [**--hub-path** PATH] [**--hub-version** PATH] [**--config-file** PATH...] [**--config-save** PATH] [**--es-host** URL...] [**--assembly-dir** PATH] [**--assembly-repo** URL] [**--assembly-exception** PATH] [**--taxon-dir** PATH] [**--taxon-repo** URL] [**--taxon-exception** PATH] [**--taxon-lookup** STRING] [**--file** PATH...] [**--file-dir** PATH...] [**--remote-file** URL...] [**--remote-file-dir** URL...] [**--taxon-id** STRING] [**--assembly-id** STRING] [**--analysis-id** STRING] [**--file-title** STRING] [**--file-description** STRING] [**--file-metadata** PATH] [**-hl** help] [**-v** version]

Options:

--hub-name STRING GenomeHubs instance name.

--hub-path PATH GenomeHubs instance root directory path.

--hub-version STR GenomeHubs instance version string.

--config-file PATH Path to YAML file containing configuration options.

--config-save PATH Path to write configuration options to YAML file.

--es-host URL Elasticsearch hostname/URL and port.

--assembly-dir PATH Path to directory containing assembly-level data.

--assembly-repo URL Remote git repository containing assembly-level data. Optionally include *~branch-name* suffix.

--assembly-exception PATH Path to directory to write assembly data that failed to import.

--taxon-lookup STRING Taxon name class to lookup (scientificall). [Default: scientific]

--taxon-dir PATH Path to directory containing taxon-level data.

--taxon-repo URL Remote git repository containing taxon-level data. Optionally include *~branch-name* suffix.

--taxon-exception PATH Path to directory to write taxon data that failed to import.

--file PATH Path to file for generic file import.

--file-dir PATH Path to directory containing generic files to import.

--remote-file URL Location of remote file for generic file import.

--remote-file-dir URL Location of remote directory containing generic files to import.

--taxon-id STRING Taxon ID to index files against.

--assembly-id STRING Assembly ID to index files against.

--analysis-id STRING Analysis ID to index files against.

--file-title STRING Default title for indexed files.
--file-description STRING Default description for all indexed files.
--file-metadata PATH CSV, TSV, YAML or JSON file metadata with one entry per file to be indexed.
-h, --help Show this
-v, --version Show version number

Examples

1. Index all files in a remote repository `./genomehubs index --taxon-repo https://github.com/genomehubs/goat-data`

`genomehubs.lib.index.cli()`

Entry point.

`genomehubs.lib.index.index_file(es, types, data, opts)`

Index a file.

`genomehubs.lib.index.main(args)`

Index files.

4.4 fill

Fill attribute values.

Usage:

genomehubs fill [**--hub-name STRING**] [**--hub-path PATH**] [**--hub-version PATH**] [**--config-file PATH...**]
 [**--config-save PATH**] [**--es-host URL...**] [**--traverse-infer-ancestors**] [**--traverse-infer-descendants**]
 [**--traverse-infer-both**] [**--traverse-threads INT**] [**--traverse-depth INT**] [**--traverse-root STRING**] [**--traverse-weight STRING**] [**-h|--help**] [**-v|--version**]

Options:

--hub-name STRING GenomeHubs instance name.
--hub-path PATH GenomeHubs instance root directory path.
--hub-version STR GenomeHubs instance version string.
--config-file PATH Path to YAML file containing configuration options.
--config-save PATH Path to write configuration options to YAML file.
--es-host URL Elasticsearch hostname/URL and port.
--traverse-depth INT Maximum depth for tree traversal relative to root taxon.
--traverse-infer-ancestors Flag to enable tree traversal from tips to root.
--traverse-infer-descendants Flag to enable tree traversal from root to tips.
--traverse-infer-both Flag to enable tree traversal from tips to root and back to tips.
--traverse-root ID Root taxon id for tree traversal.
--traverse-threads INT Number of threads to use for tree traversal. [Default: 1]
--traverse-weight STRING Weighting scheme for setting values during tree traversal.
-h, --help Show this

-v, --version Show version number

Examples

1. Traverse tree up to taxon_id 7088 ./genomehubs fill --traverse-root 7088

`genomehubs.lib.fill.apply_summary(summary, values, *, max_value=None, min_value=None)`
Apply summary statistic functions.

`genomehubs.lib.fill.cli()`
Entry point.

`genomehubs.lib.fill.copy_attribute_summary(source, meta)`
Copy an attribute summary, removing values.

`genomehubs.lib.fill.get_max_depth(es, *, index)`
Find max depth of root lineage.

`genomehubs.lib.fill.get_max_depth_by_lineage(es, *, index, root)`
Find max depth of specified root lineage.

`genomehubs.lib.fill.main(args)`
Initialise genomehubs.

`genomehubs.lib.fill.set_values_from_descendants(*, attributes, descendant_values, meta, parent, taxon_rank, parents)`
Set attribute summary values from descendant values.

`genomehubs.lib.fill.stream_descendant_nodes_missing_attributes(es, *, index, attributes, root, size=10)`
Get entries descended from root that lack one or more attributes.

`genomehubs.lib.fill.stream_missing_attributes_at_level(es, *, nodes, attrs, template, level=1)`
Stream all descendant nodes with missing attributes.

`genomehubs.lib.fill.stream_nodes_by_root_depth(es, *, index, root, depth, size=10)`
Get entries by depth of root taxon.

`genomehubs.lib.fill.summarise_attribute_values(attribute, meta, *, values=None, max_value=None, min_value=None)`
Calculate a single summary value for an attribute.

`genomehubs.lib.fill.summarise_attributes(*, attributes, attrs, meta, parent, parents)`
Set attribute summary values.

`genomehubs.lib.fill.traverse_from_root(es, opts, *, template, root=None, max_depth=None, log=True)`
Traverse a tree, filling in values.

`genomehubs.lib.fill.traverse_from_tips(es, opts, *, template, root=None, max_depth=None)`
Traverse a tree, filling in values.

`genomehubs.lib.fill.traverse_handler(es, opts, template)`
Handle single or multi-threaded tree traversal.

`genomehubs.lib.fill.traverse_helper(params)`
Wrap `traverse_tree` for multithreaded traversal.

`genomehubs.lib.fill.traverse_tree(es, opts, template, root, max_depth)`
Propagate values by tree traversal.

CONTRIBUTING

5.1 Bug reports

When [reporting a bug](#) please include:

- Your operating system name and version.
- Any details about your local setup that might be helpful in troubleshooting.
- Detailed steps to reproduce the bug.

5.2 Documentation improvements

Contributions to the official `genomehubs` docs and internal docstrings are always welcome.

5.3 Feature requests and feedback

The best way to send feedback is to file an issue at <https://github.com/genomehubs/genomehubs/issues>.

If you are proposing a feature:

- Explain in detail how it would work.
- Keep the scope as narrow as possible, to make it easier to implement.
- Remember that code contributions are welcome

5.4 Development

To install the development version of *genomehubs*:

1. Clone the *genomehubs* repository:

```
git clone https://github.com/genomehubs/genomehubs
```

2. Install the dependencies using pip:

```
cd genomehubs
pip install -r requirements.txt
```

3. Build and install the *genomehubs* package:

```
python3 setup.py sdist bdist_wheel \  
&& echo y | pip uninstall genomehubs \  
&& pip install dist/genomehubs-2.0.0-py3-none-any.whl
```

To set up *genomehubs* for local development:

1. Fork *genomehubs* <<https://github.com/genomehubs/genomehubs>> - (look for the “Fork” button).
2. Clone your fork locally:

```
git clone git@github.com:USERNAME/genomehubs.git
```

3. Create a branch for local development:

```
git checkout -b name-of-your-bugfix-or-feature
```

Now you can make your changes locally.

4. When you’re done making changes run all the checks and docs builder with `tox` one command:

```
tox
```

5. Commit your changes and push your branch to GitHub:

```
git add .  
git commit -m "Your detailed description of your changes."  
git push origin name-of-your-bugfix-or-feature
```

6. Submit a pull request through the GitHub website.

5.4.1 Pull Request Guidelines

If you need some code review or feedback while you’re developing the code just make the pull request.

For merging, you should:

1. Include passing tests (run `tox`)¹.
2. Update documentation when there’s new API, functionality etc.
3. Add a note to `CHANGELOG.rst` about the changes.
4. Add yourself to `AUTHORS.rst`.

5.4.2 Tips

To run a subset of tests:

```
tox -e envname -- pytest -k test_myfeature
```

To run all the test environments in *parallel*:

```
tox -p
```

¹ If you don’t have all the necessary python versions available locally you can rely on Travis - it will run the tests for each change you add in the pull request.
It will be slower though ...

AUTHORS

- Richard Challis - <https://twitter.com/rjchallis>
- Sujai Kumar - <https://twitter.com/sujaik>

CHANGELOG

7.1 2.0.0 (2020-07-02)

- First release on PyPI.

INDICES AND TABLES

- `genindex`
- `modindex`
- `search`

PYTHON MODULE INDEX

g

`genomehubs.lib.fill`, [10](#)
`genomehubs.lib.index`, [9](#)
`genomehubs.lib.init`, [7](#)
`genomehubs.lib.parse`, [8](#)

INDEX

A

`apply_summary()` (in module *genomehubs.lib.fill*), 11

C

`cli()` (in module *genomehubs.lib.fill*), 11

`cli()` (in module *genomehubs.lib.index*), 10

`cli()` (in module *genomehubs.lib.init*), 8

`cli()` (in module *genomehubs.lib.parse*), 9

`copy_attribute_summary()` (in module *genomehubs.lib.fill*), 11

G

`genomehubs.lib.fill`
module, 10

`genomehubs.lib.index`
module, 9

`genomehubs.lib.init`
module, 7

`genomehubs.lib.parse`
module, 8

`get_max_depth()` (in module *genomehubs.lib.fill*), 11

`get_max_depth_by_lineage()` (in module *genomehubs.lib.fill*), 11

I

`index_file()` (in module *genomehubs.lib.index*), 10

M

`main()` (in module *genomehubs.lib.fill*), 11

`main()` (in module *genomehubs.lib.index*), 10

`main()` (in module *genomehubs.lib.init*), 8

`main()` (in module *genomehubs.lib.parse*), 9

module

`genomehubs.lib.fill`, 10

`genomehubs.lib.index`, 9

`genomehubs.lib.init`, 7

`genomehubs.lib.parse`, 8

S

`set_values_from_descendants()` (in module *genomehubs.lib.fill*), 11

`stream_descendant_nodes_missing_attributes()`
(in module *genomehubs.lib.fill*), 11

`stream_missing_attributes_at_level()` (in module *genomehubs.lib.fill*), 11

`stream_nodes_by_root_depth()` (in module *genomehubs.lib.fill*), 11

`summarise_attribute_values()` (in module *genomehubs.lib.fill*), 11

`summarise_attributes()` (in module *genomehubs.lib.fill*), 11

T

`traverse_from_root()` (in module *genomehubs.lib.fill*), 11

`traverse_from_tips()` (in module *genomehubs.lib.fill*), 11

`traverse_handler()` (in module *genomehubs.lib.fill*), 11

`traverse_helper()` (in module *genomehubs.lib.fill*), 11

`traverse_tree()` (in module *genomehubs.lib.fill*), 11