
genomehubs

Release 2.5.18

genomehubs

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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-source STRING] [--taxonomy-ncbi-root INT] [--taxonomy-ncbi-url URL]
  [--taxonomy-ott-root INT] [--taxonomy-ott-url URL] [--taxonomy-jsonl PATH] [--taxonomy-format STRING] [--taxonomy-root STRING]
  [--taxonomy-url URL] [--taxonomy-file PATH...] [--taxon-preload] [--docker-contain STRING...] [--docker-network STRING]
  [--docker-timeout INT] [--docker-es-container STRING] [--docker-es-image URL] [--reset] [--force-reset] [-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.

--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-source STRING Name of taxonomy to use (ncbi or ott).

--taxonomy-ncbi-root INT Root taxid for NCBI taxonomy index.

--taxonomy-ncbi-url URL Remote URL to fetch NCBI taxonomy.

--taxonomy-ott-root INT Root taxid for Open Tree of Life taxonomy index.

--taxonomy-ott-url URL Remote URL to fetch Open Tree of Life taxonomy.

--taxonomy-format STRING Format of taxonomy (ncbi, ott). Newick support is planned.

--taxonomy-root STRING Root taxid.

--taxonomy-file PATH Taxonomy file names.

--taxonomy-url URL Remote URL to fetch taxonomy.

--taxonomy-jsonl PATH Path to JSON Lines format taxonomy file of additional taxa.

--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.add_jsonl_to_taxonomy(stream, jsonl)`

Add entries from JSON Lines format file to taxonomy stream.

`genomehubs.lib.init.cli()`

Entry point.

`genomehubs.lib.init.extend_lineage(entry)`

Add current taxon to beginning of lineage.

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

Initialise genomehubs.

`genomehubs.lib.init.process_subspecies(data)`

Find species name from subspecies and add to lineage.

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] [-ncbi-datasets-sample PATH]
                 [-refseq-mitochondria] [-refseq-organelles] [-refseq-plastids] [-refseq-root NAME] [-outfile PATH] [-
                 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)
--meta PATH	YAML format file of analysis metadata
--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
--ncbi-datasets-sample PATH	Parse sample data from 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.

`genomehubs.lib.parse.remove_temporary_types(types)`

Remove any keys labelled temporary from a types file.

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] [--feature-dir
  PATH] [--sample-dir PATH] [--taxon-dir PATH] [--taxon-repo URL] [--taxon-exception PATH] [--taxon-
  lookup STRING] [--taxon-lookup-root STRING] [--taxon-lookup-in-memory] [--taxon-id-as-xref STRING]
  [--taxon-matching-ranks INT] [--taxon-spellcheck] [--taxonomy-source STRING] [--file PATH...] [file-dir
  PATH...] [--remote-file URL...] [--remote-file-dir URL...] [--taxon-id STRING] [--assembly-id STRING]
  [--sample-id STRING] [--analysis-id STRING] [--file-title STRING] [--file-description STRING] [--file-
  metadata PATH] [--dry-run] [-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.
--assembly-dir PATH Path to directory containing assembly-level data.
--sample-dir PATH  Path to directory containing sample-level data.
--feature-dir PATH Path to directory containing feature-level data.

--taxon-lookup-root STRING Root taxon Id for in-memory lookup. --taxon-lookup STRING Taxon name class
to lookup (scientific|any). [Default: scientific] --taxon-lookup-in-memory Flag to use in-memory taxon name
lookup. --taxon-id-as-xref STRING Set source DB name to treat taxon_id in file as xref. --taxon-matching-ranks
INT Number of ancestral ranks that must match to import a taxon based on
name match. [Default: 2]
--taxon-spellcheck  Flag to use fuzzy matching to match taxon names.
--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.
--taxonomy-source STRING Name of taxonomy to use (ncbi or ott).
--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.
--sample-id STRING  Sample 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.
--dry-run Flag to run without loading data into the elasticsearch index.
-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.convert_features_to_docs(with_ids)`

Convert features to docs.

`genomehubs.lib.index.group_rows(taxon_id, rows, with_ids, without_ids, taxon_asm_data, imported_rows, types, failed_rows, blanks)`

Group processed rows by available taxon info for import.

`genomehubs.lib.index.index_feature_records(es, opts, taxonomy_name, with_ids, blanks)`

Index a feature records.

`genomehubs.lib.index.index_features(es, opts, *, dry_run=False)`

Index assembly features.

`genomehubs.lib.index.index_file(es, types, names, data, opts, *, taxon_table=None, shared_values=None, exclusions=None)`

Index a file.

`genomehubs.lib.index.index_sample_records(es, taxonomy_name, opts, with_ids, blanks, taxon_types, taxon_asm_data, index_type='sample')`

Index sample records.

`genomehubs.lib.index.index_taxon_records(es, taxonomy_name, opts, with_ids, blanks, types)`

Index a taxon records.

`genomehubs.lib.index.index_taxon_sample(es, opts, index='taxon', *, dry_run=False, taxonomy_name)`

Call taxon- or sample-specific indexing functions.

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

Index files.

`genomehubs.lib.index.not_blank(key, obj, blanks)`

Test value is not blank.

```
genomehubs.lib.index.process_taxon_sample_records(es, taxonomy_name, opts, processed_rows,  
                                                    with_ids, blanks, taxon_asm_data, imported_rows,  
                                                    types, failed_rows, header, taxon_table,  
                                                    taxon_types)
```

Process taxon and sample records.

```
genomehubs.lib.index.set_feature_types(types)
```

Set types for feature properties.

```
genomehubs.lib.index.summarise_imported_taxa(docs, imported_taxa)
```

Summarise taxon information from a stram of taxon docs.

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...] [-taxonomy-source STRING] [-traverse-  
                limit STRING] [-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.  
--taxonomy-source STRING  Name of taxonomy to use (ncbi or ott).  
--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-limit STRING  Maximum rank to ascend to during traversal. [Default: null]  
--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, *, primary_values=None, summary_types=None,
                                   max_value=None, min_value=None, order=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.deduped_list(arr)
```

Remove duplicate values from a list.

```
genomehubs.lib.fill.deduped_list_length(arr)
```

Find number of unique values in a list.

```
genomehubs.lib.fill.earliest(arr, *args)
```

Select earliest date from a list.

```
genomehubs.lib.fill.enum(tup)
```

Use list index to prioritise values.

```
genomehubs.lib.fill.flatten_list(arr)
```

Flatten a list by expanding any nested lists.

```
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.latest(arr, *args)
```

Select earliest date from a list.

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

Initialise genomehubs.

```
genomehubs.lib.fill.range(arr)
```

Calculate difference between max and min values.

```
genomehubs.lib.fill.set_aggregation_source(attribute, source=None)
```

Set attribute aggregation source.

```
genomehubs.lib.fill.set_attributes_to_descend(meta, traverse_limit)
```

Set which attributes should have values inferred from ancestral taxa.

```
genomehubs.lib.fill.set_traverse_values(summaries, values, primary_values, count, max_value,
                                         min_value, meta, attribute, value_type, traverse, source)
```

Set values use for tree traversal.

```
genomehubs.lib.fill.set_values_from_descendants(*, attributes, descendant_values, meta, taxon_id,
                                              parent, taxon_rank, traverse_limit, parents,
                                              descendant_ranks=None, attr_dict=None,
                                              limits=None)
```

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, count=0,
                                                max_value=None, min_value=None, source='direct')
```

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.track_descendant_ranks(node, descendant_ranks)
```

Keep track of descendant ranks.

```
genomehubs.lib.fill.track_missing_attribute_values(node, missing_attributes, attr_dict, desc_attrs,
                                                    desc_attr_limits)
```

Keep track of missing attribute values for in memory traversal.

```
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*.

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 ...

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
```


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.

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