
Python-chado

May 10, 2022

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Contents:

CHAPTER 1

Chado Library

Test Documentation

A Python library for interacting with a Chado database.

1.1 Installation

```
$ pip install chado

# On first use you'll need to create a config file to connect to the database, just
→run:

$ chakin init
Welcome to Chado's Chakin! ()
PGHOST: xxxx
PGDATABASE: xxxx
PGUSER: xxxx
PGPASS:
PGPORT: 5432
PGSCHEMA: public
```

This will create a chakin config file in ~/.chakin.yml

1.2 Examples

```
from chado import ChadoInstance
ci = ChadoInstance(dbhost="localhost", dbname="chado", dbuser="chado", dbpass="chado",
→ dbschema="public", dbport=5432)

# Create human species
org = ci.organism.add_organism(genus="Homo", species="sapiens", common="Human", abbr=
→ "H.sapiens")
```

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```

# Then display the list of organisms
orgs = ci.organism.get_organisms()

for org in orgs:
    print('{} {}'.format(org.genus, org.species))

# Create an analysis
an = ci.analysis.add_analysis(name="My cool analysis",
                             program="Something",
                             programversion="1.0",
                             algorithm="Google",
                             sourcename="src",
                             sourceversion="2.1beta",
                             sourceuri="http://example.org/",
                             date_executed="2018-02-03")

# And load some data
ci.feature.load_fasta(fasta="./test-data/genome.fa", analysis_id=an['analysis_id'],
    ↳organism_id=orgs[0]['organism_id'])
ci.feature.load_gff(gff="./test-data/annot.gff", analysis_id=an['analysis_id'],
    ↳organism_id=orgs[0]['organism_id'])

```

Or with the Chakin client:

```

$ my_org=`chakin organism add_organism --species sapiens Homo Human H.sapiens | jq -r
    ↳'.organism_id'`

$ chakin organism get_organisms
[
  {
    "organism_id": 1133,
    "genus": "Homo",
    "species": "sapiens",
    "abbreviation": "H.sapiens",
    "common_name": "Human",
    "comment": null
  }
]

# Then load some data
$ my_analysis=`chakin analysis add_analysis \
    "My cool analysis" \
    "Something" \
    "v1.0" \
    "src" | jq -r '.analysis_id'`

$ chakin feature load_fasta \
    --analysis_id $my_analysis \
    --sequence_type contig \
    ./test-data/genome.fa $my_org

```


1.3 History

- 2.3.9
 - URL decode GFF ids when loading blast/interpro/others
- 2.3.8
 - Fix connection closed error when loading big interproscan files
- 2.3.7
 - Fix loading of expression data when first column header is not empty
- 2.3.6
 - Fix loading of GO terms from GFF
- 2.3.5
 - Fix has_table() calls with recent sqlalchemy versions
- 2.3.4
 - Now requires biopython >=1.78
 - Fixes biopython sequence usage in recent biopython
- 2.3.3
 - Now requires python >= 3.6
 - Better error reporting for blast loader
- 2.3.2
 - Fix interproscan loader only loading the first result of XML v5
 - Fix interproscan loader failing to load IPR by name
- 2.3.1
 - Fix data loading in Tripal database
- 2.3.0
 - Fix non working `-re_parent` option in fasta loader
 - allow connection using a preformatted url (needed by galaxy tools using pgutil)
 - added loading of Blast and InterProScan data
 - moved `chakin feature load_go` to `chakin load go`
 - fix sequence computing when landmark sequence is available in the db
 - add more options to match features in expression matrix loader (`query_type`, `match_on_name`, `re_name`, `skip_missing`)
- 2.2.6
 - fix requirement name for psycopg2 (name change for version >=2.8)
- 2.2.5
 - Added support for units in expression loaders
 - Fix error in `load_gff` when no source is specified
- 2.2.4

- Fix broken `–skip_missing` option for `load_go`
- 2.2.3
 - Throw a warning instead of an exception when a GFF target feature does not exist
- 2.2.2
 - Bug fixes and improvements to the expression module
- 2.2.1
 - Minor release to fix broken package at pypi, no code change
- 2.2.0
 - Added `feature.load_go()` to load GO annotation (blast2go results)
 - Added `feature.get_feature_analyses()` to fetch the analyses associated with a feature
 - Added `feature.get_feature_cvterms()` to fetch the cvterms associated with a feature
 - Added support for biomaterial/expression data (as used by `tripal_analysis_expression`)
 - New `–protein_id_attr` option for `feature.load_gff()`
- 2.1.5
 - bugfix: fix features deletion when deleting an analysis
- 2.1.4
 - bugfix: fix sporadic errors with `AnalysisFeature` class declaration
- 2.1.3
 - bugfix: make `–species` a mandatory arg for organism creation
 - bugfix: fix features deletion when deleting an analysis or an organism
 - update chado docker image
- 2.1.2
 - skip whole database schema reflection for simple tasks (analysis and organism management)
 - fix polypeptide creation for genes beginning at position 0
 - fix various small bugs in phylogeny and featureprop loading
 - fix bug in cvterm creation
 - fix crashes in gbk/gff exporters
- 2.1.1
 - newick: remove prefix from node labels too
 - newick: fix errors with named internal nodes
- 2.1
 - auto reflect db schema
 - add phylogeny module
 - load features from fasta
 - load features from gff3
 - load featureprops from tabular file

- make chakin util commands work when db is offline
 - add unit tests
- 2.0
 - “Chakin” CLI utility
 - Complete package restructure
 - Nearly all functions renamed

1.4 License

Available under the MIT License

CHAPTER 2

Commands

Chakin is a set of wrappers for accessing Chado. Each utility is implemented as a subcommand of `chakin`. This section of the documentation describes these commands.

2.1 analysis

This section is auto-generated from the help text for the `chakin` command `analysis`.

2.1.1 add_analysis command

Usage:

```
chakin analysis add_analysis [OPTIONS] NAME PROGRAM PROGRAMVERSION
```

Help

Create an analysis

Output

Analysis information

Options:

```
--algorithm TEXT      analysis algorithm
--sourceversion TEXT  analysis sourceversion
--sourceuri TEXT      analysis sourceuri
--description TEXT     analysis description
--date_executed TEXT  analysis date_executed (yyyy-mm-dd)
-h, --help            Show this message and exit.
```

2.1.2 delete_analyses command

Usage:

```
chakin analysis delete_analyses [OPTIONS]
```

Help

Delete analysis

Output

None

Options:

```
--analysis_id INTEGER  analysis_id filter
--name TEXT            analysis name filter
--program TEXT         analysis program filter
--programversion TEXT  analysis programversion filter
--algorithm TEXT       analysis algorithm filter
--sourcename TEXT      analysis sourcename filter
--sourceversion TEXT   analysis sourceversion filter
--sourceuri TEXT       analysis sourceuri filter
--description TEXT     analysis description
-h, --help            Show this message and exit.
```

2.1.3 get_analyses command

Usage:

```
chakin analysis get_analyses [OPTIONS]
```

Help

Get all or some analyses

Output

Analysis information

Options:

```
--analysis_id INTEGER  analysis_id filter
--name TEXT            analysis name filter
--program TEXT         analysis program filter
--programversion TEXT  analysis programversion filter
--algorithm TEXT       analysis algorithm filter
--sourcename TEXT      analysis sourcename filter
--sourceversion TEXT   analysis sourceversion filter
--sourceuri TEXT       analysis sourceuri filter
--description TEXT     analysis description
-h, --help            Show this message and exit.
```

2.2 export

This section is auto-generated from the help text for the chakin command export.

2.2.1 export_fasta command

Usage:

```
chakin export export_fasta [OPTIONS] ORGANISM_ID
```

Help

Export reference sequences as fasta.

Output

None

Options:

```
--file      If true, write to files in CWD  
-h, --help  Show this message and exit.
```

2.2.2 export_gbk command

Usage:

```
chakin export export_gbk [OPTIONS] ORGANISM_ID
```

Help

Export organism features as genbank

Output

None

Options:

```
-h, --help  Show this message and exit.
```

2.2.3 export_gff3 command

Usage:

```
chakin export export_gff3 [OPTIONS] ORGANISM_ID
```

Help

Export organism features as GFF3

Output

None

Options:

```
-h, --help  Show this message and exit.
```

2.3 expression

This section is auto-generated from the help text for the chakin command `expression`.

2.3.1 add_biomaterial command

Usage:

```
chakin expression add_biomaterial [OPTIONS] BIOMATERIAL_NAME ORGANISM_ID
```

Help

Add a new biomaterial to the database

Output

Biomaterial details

Options:

```
--description TEXT      Description of the biomaterial
--biomaterial_provider TEXT  Biomaterial provider name
--biosample_accession TEXT  Biosample accession number
--sra_accession TEXT       SRA accession number
--bioproject_accession TEXT Bioproject accession number
--attributes TEXT         Custom attributes (In JSON dict form)
-h, --help                Show this message and exit.
```

2.3.2 add_expression command

Usage:

```
chakin expression add_expression [OPTIONS] ORGANISM_ID ANALYSIS_ID
```

Help

Add an expression matrix file to the database

Output

Number of expression data loaded

Options:

```
--separator TEXT  Separating character in the matrix file (ex : ','). Default
                  character is tab. [default:      ]
--unit TEXT       The units associated with the loaded values (ie, FPKM,
                  RPKM, raw counts)
--query_type TEXT The feature type (e.g. 'gene', 'mRNA', 'polypeptide',
                  'contig') of the query. It must be a valid Sequence
                  Ontology term. [default: mRNA]
--match_on_name   Match features using their name instead of their uniquename
--re_name TEXT    Regular expression to extract the feature name from the
                  input file (first capturing group will be used).
--skip_missing    Skip lines with unknown features or GO id instead of
                  aborting everything.
-h, --help        Show this message and exit.
```


2.3.3 delete_all_biomaterials command

Usage:

```
chakin expression delete_all_biomaterials [OPTIONS]
```

Help

Delete all biomaterials

Output

None

Options:

```
--confirm    Confirm that you really do want to delete ALL of the biomaterials.
-h, --help   Show this message and exit.
```

2.3.4 delete_biomaterial command

Usage:

```
chakin expression delete_biomaterial [OPTIONS]
```

Help

Output

I have no idea

Options:

```
--names TEXT      JSON list of biomaterial names to delete. [default: []]
--ids TEXT         JSON list of biomaterial ids to delete. [default: []]
--organism_id TEXT Delete all biomaterial associated with this organism id.
--analysis_id TEXT Delete all biomaterial associated with this analysis id.
-h, --help         Show this message and exit.
```

2.3.5 delete_biomaterials command

Usage:

```
chakin expression delete_biomaterials [OPTIONS]
```

Help

Will delete biomaterials based on selector. Only one selector will be used.

Output

Number of deleted biomaterials

Options:

```
--names TEXT          JSON list of biomaterial names to delete.
--ids TEXT            JSON list of biomaterial ids to delete.
--organism_id INTEGER Delete all biomaterial associated with this organism
                      id.
--analysis_id INTEGER Delete all biomaterial associated with this analysis
                      id.
-h, --help           Show this message and exit.
```

2.3.6 get_biomaterials command

Usage:

```
chakin expression get_biomaterials [OPTIONS]
```

Help

List biomaterials in the database

Output

List of biomaterials

Options:

```
--provider_id INTEGER Limit query to the selected provider
--biomaterial_id INTEGER Limit query to the selected biomaterial id
--organism_id INTEGER Limit query to the selected organism
--biomaterial_name TEXT Limit query to the selected biomaterial name
--analysis_id INTEGER Limit query to the selected analysis_id
-h, --help           Show this message and exit.
```

2.4 feature

This section is auto-generated from the help text for the chakin command feature.

2.4.1 delete_features command

Usage:

```
chakin feature delete_features [OPTIONS]
```

Help

Get all or some features

Output

Features information

Options:

```
--organism_id INTEGER organism_id filter
--analysis_id INTEGER analysis_id filter
--name TEXT          name filter
```

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```
--uniquename TEXT      uniquename filter  
-h, --help             Show this message and exit.
```

2.4.2 get_feature_analyses command

Usage:

```
chakin feature get_feature_analyses [OPTIONS] FEATURE_ID
```

Help

Get analyses associated with a feature

Output

Feature analyses

Options:

```
-h, --help  Show this message and exit.
```

2.4.3 get_feature_cvterms command

Usage:

```
chakin feature get_feature_cvterms [OPTIONS] FEATURE_ID
```

Help

Get cvterms associated with a feature

Output

Feature cvterms

Options:

```
-h, --help  Show this message and exit.
```

2.4.4 get_features command

Usage:

```
chakin feature get_features [OPTIONS]
```

Help

Get all or some features

Output

Features information

Options:

```
--organism_id INTEGER  organism_id filter
--analysis_id INTEGER  analysis_id filter
--name TEXT            name filter
--uniquename TEXT      uniquename filter
-h, --help             Show this message and exit.
```

2.4.5 load_fasta command

Usage:

```
chakin feature load_fasta [OPTIONS] FASTA ORGANISM_ID
```

Help

Load features from a fasta file

Output

Number of inserted sequences

Options:

```
--sequence_type TEXT    Sequence type [default: contig]
--analysis_id INTEGER    Analysis ID
--re_name TEXT           Regular expression to extract the feature name from
                        the fasta sequence id (first capturing group will be
                        used).
--re_uniquename TEXT     Regular expression to extract the feature name from
                        the fasta sequence id (first capturing group will be
                        used).
--match_on_name          Match existing features using their name instead of
                        their uniquename
--update                 Update existing feature with new sequence instead of
                        throwing an error
--db INTEGER             External database to cross reference to.
--re_db_accession TEXT    Regular expression to extract an external database
                        accession from the fasta sequence id (first capturing
                        group will be used).
--rel_type TEXT          Relation type to parent feature ('part_of' or
                        'derives_from').
--re_parent TEXT         Regular expression to extract parent uniquename from
                        the fasta sequence id (first capturing group will be
                        used).
--parent_type TEXT       Sequence type of the parent feature
-h, --help               Show this message and exit.
```

2.4.6 load_featureprops command

Usage:

```
chakin feature load_featureprops [OPTIONS] TAB_FILE ANALYSIS_ID
```

Help

Load feature properties from a tabular file (Column1: feature name or uniquename, Column2: property value)

Output

Number of inserted featureprop

Options:

```
--feature_type TEXT  Type of the target features in sequence ontology (will
                      speed up loading if specified)
--match_on_name      Match features using their name instead of their
                      uniqueness
-h, --help           Show this message and exit.
```

2.4.7 load_gff command

Usage:

```
chakin feature load_gff [OPTIONS] GFF ANALYSIS_ID ORGANISM_ID
```

Help

Load features from a gff file

Output

None

Options:

```
--landmark_type TEXT  Type of the landmarks (will speed up loading if
                      provided, e.g. contig, should be a term of the
                      Sequence ontology)
--re_protein TEXT      Replacement string for the protein name using
                      capturing groups defined by --re_protein_capture
--re_protein_capture TEXT Regular expression to capture groups in mRNA name
                      to use in --re_protein (e.g. "^(*?)R([A-Z]+)$",
                      default="^(*?)$") [default: ^(*?)$]
--fasta TEXT           Path to a Fasta containing sequences for some
                      features. When creating a feature, if its sequence
                      is in this fasta file it will be loaded. Otherwise
                      for mRNA and polypeptides it will be computed from
                      the genome sequence (if available), otherwise it
                      will be left empty.
--no_seq_compute       Disable the computation of mRNA and polypeptides
                      sequences based on genome sequence and positions.
--quiet               Hide progress information
--add_only            Use this flag if you're not updating existing
                      features, but just adding new features to the
                      selected analysis and organism. It will speedup
                      loading, and reduce memory usage, but might produce
                      errors in case of already existing feature.
--protein_id_attr TEXT Attribute containing the protein uniqueness. It is
                      searched at the mRNA level, and if not found at CDS
                      level.
-h, --help           Show this message and exit.
```

2.4.8 load_go command

Usage:

```
chakin feature load_go [OPTIONS] INPUT ORGANISM_ID ANALYSIS_ID
```

Help

Load GO annotation from a tabular file

Output

Number of inserted GO terms

Options:

<code>--query_type TEXT</code>	The feature <code>type</code> (e.g. <code>'gene'</code> , <code>'mRNA'</code> , <code>'polypeptide'</code> , <code>'contig'</code>) of the query. It must be a valid Sequence Ontology term. [default: polypeptide]
<code>--match_on_name</code>	Match features using their name instead of their uniquename
<code>--name_column INTEGER</code>	Column containing the feature identifiers (2, 3, 10 or 11; default=2). [default: 2]
<code>--go_column INTEGER</code>	Column containing the GO <code>id</code> (default=5). [default: 5]
<code>--re_name TEXT</code>	Regular expression to extract the feature name <code>from the input</code> file (first capturing group will be used).
<code>--skip_missing</code>	Skip lines <code>with</code> unknown features <code>or</code> GO <code>id</code> instead of aborting everything.
<code>-h, --help</code>	Show this message <code>and</code> exit.

2.5 load

This section is auto-generated from the help text for the chakin command load.

2.5.1 blast command

Usage:

```
chakin load blast [OPTIONS] ANALYSIS_ID ORGANISM_ID INPUT
```

Help

Load a blast analysis, in the same way as does the tripal_analysis_blast module

Output

Number of processed hits

Options:

<code>--blastdb TEXT</code>	Name of the database blasted against (must be <code>in</code> the Chado db table)
<code>--blastdb_id INTEGER</code>	ID of the database blasted against (must be <code>in</code> the Chado db table)
<code>--re_name TEXT</code>	Regular expression to extract the feature name <code>from the input</code> file (first capturing group will be used).
<code>--query_type TEXT</code>	The feature <code>type</code> (e.g. <code>'gene'</code> , <code>'mRNA'</code> , <code>'polypeptide'</code> , <code>'contig'</code>) of the query. It must be a valid Sequence Ontology term. [default: polypeptide]
<code>--match_on_name</code>	Match features using their name instead of their

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	uniquename
--skip_missing	Skip lines with unknown features or GO id instead of aborting everything.
-h, --help	Show this message and exit.

2.5.2 go command

Usage:

```
chakin load go [OPTIONS] INPUT ORGANISM_ID ANALYSIS_ID
```

Help

Load GO annotation from a tabular file, in the same way as does the tripal_analysis_go module

Output

Number of inserted GO terms

Options:

--query_type TEXT	The feature type (e.g. ' gene ', ' mRNA ', ' polypeptide ', ' contig ') of the query. It must be a valid Sequence Ontology term. [default: polypeptide]
--match_on_name	Match features using their name instead of their uniquename
--name_column INTEGER	Column containing the feature identifiers (2, 3, 10 or 11; default=2). [default: 2]
--go_column INTEGER	Column containing the GO id (default=5). [default: 5]
--re_name TEXT	Regular expression to extract the feature name from the input file (first capturing group will be used).
--skip_missing	Skip lines with unknown features or GO id instead of aborting everything.
-h, --help	Show this message and exit.

2.5.3 interpro command

Usage:

```
chakin load interpro [OPTIONS] ANALYSIS_ID ORGANISM_ID INPUT
```

Help

Load an InterProScan analysis, in the same way as does the tripal_analysis_interpro module

Output

Number of processed hits

Options:

--parse_go	Load GO annotation to the database
--re_name TEXT	Regular expression to extract the feature name from the input file (first capturing group will be used).
--query_type TEXT	The feature type (e.g. ' gene ', ' mRNA ', ' polypeptide ', ' contig ') of the query. It must be a valid Sequence

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```
Ontology term. [default: polypeptide]
--match_on_name Match features using their name instead of their uniquename
--skip_missing Skip lines with unknown features or GO id instead of
aborting everything.
-h, --help Show this message and exit.
```

2.6 organism

This section is auto-generated from the help text for the chakin command organism.

2.6.1 add_organism command

Usage:

```
chakin organism add_organism [OPTIONS] GENUS SPECIES COMMON ABBR
```

Help

Add a new organism to the Chado database

Output

Organism information

Options:

```
--comment TEXT A comment / description
-h, --help Show this message and exit.
```

2.6.2 delete_all_organisms command

Usage:

```
chakin organism delete_all_organisms [OPTIONS]
```

Help

Delete all organisms

Output

None

Options:

```
--confirm Confirm that you really do want to delete ALL of the organisms.
-h, --help Show this message and exit.
```

2.6.3 delete_organisms command

Usage:


```
chakin organism delete_organisms [OPTIONS]
```

Help

Delete all organisms

Output

None

Options:

```
--organism_id INTEGER  organism_id filter
--genus TEXT           genus filter
--species TEXT         species filter
--common TEXT          common filter
--abbr TEXT            abbr filter
--comment TEXT         comment filter
-h, --help             Show this message and exit.
```

2.6.4 get_organisms command

Usage:

```
chakin organism get_organisms [OPTIONS]
```

Help

Get all or some organisms

Output

Organisms information

Options:

```
--organism_id INTEGER  organism_id filter
--genus TEXT           genus filter
--species TEXT         species filter
--common TEXT          common filter
--abbr TEXT            abbr filter
--comment TEXT         comment filter
-h, --help             Show this message and exit.
```

2.7 phylogeny

This section is auto-generated from the help text for the chakin command phylogeny.

2.7.1 add_cvterms command

Usage:

```
chakin phylogeny add_cvterms [OPTIONS]
```

Help

Make sure required cvterms are loaded

Output

created cvterms

Options:

```
-h, --help  Show this message and exit.
```

2.7.2 gene_families command

Usage:

```
chakin phylogeny gene_families [OPTIONS]
```

Help

Adds an entry in the featureprop table in a chado database for each family a gene belongs to (for use in https://github.com/legumeinfo/lis_context_viewer/).

Output

None

Options:

```
--family_name TEXT  Restrict to families beginning with given prefix
--nuke              Removes all previous gene families data
-h, --help          Show this message and exit.
```

2.7.3 gene_order command

Usage:

```
chakin phylogeny gene_order [OPTIONS]
```

Help

Orders all the genes in the database by their order on their respective chromosomes in the gene_order table (for use in https://github.com/legumeinfo/lis_context_viewer/).

Output

None

Options:

```
--nuke      Removes all previous gene ordering data
-h, --help  Show this message and exit.
```

2.7.4 load_tree command

Usage:

```
chakin phylogeny load_tree [OPTIONS] NEWICK ANALYSIS_ID
```

Help

Load a phylogenetic tree (Newick format) into Chado db

Output

Number of inserted trees

Options:

<code>--name TEXT</code>	The name given to the phylotree entry in the database (default=<filename>)
<code>--xref_db TEXT</code>	The name of the db to link dbxrefs for the trees (default: "null") [default: null]
<code>--xref_accession TEXT</code>	The accession to use for dbxrefs for the trees (assumed same as name unless otherwise specified)
<code>--match_on_name</code>	Match polypeptide features using their name instead of their uniquename
<code>--prefix TEXT</code>	Comma-separated list of prefix to be removed from identifiers (e.g species prefixes when loading OrthoFinder output)
<code>-h, --help</code>	Show this message and exit.

2.8 util

This section is auto-generated from the help text for the chakin command `util`.

2.8.1 dbshell command

Usage:

```
chakin util dbshell [OPTIONS]
```

Help

Open a psql session to the database

Output

None

Options:

```
-h, --help Show this message and exit.
```

2.8.2 launch_docker_image command

Usage:

```
chakin util launch_docker_image [OPTIONS]
```

Help

Launch a chado docker image.

Output

None

Options:

<code>--background</code>	Launch the image in the background
<code>--no_yeast</code>	Disable loading of example yeast data
<code>-h, --help</code>	Show this message and exit.

3.1 Subpackages

3.1.1 chado.analysis package

Module contents

Contains possible interactions with the Chado Analysis Module

class `chado.analysis.AnalysisClient` (*engine, metadata, session, ci*)

Bases: `chado.client.Client`

Access to the chado analysis table

add_analysis (*name, program, programversion, sourcename, algorithm=None, sourceversion=None, sourceuri=None, description=None, date_executed=None*)

Create an analysis

Parameters

- **name** (*str*) – analysis name
- **program** (*str*) – analysis program
- **programversion** (*str*) – analysis programversion
- **algorithm** (*str*) – analysis algorithm
- **sourcename** (*str*) – analysis sourcename
- **sourceversion** (*str*) – analysis sourceversion
- **sourceuri** (*str*) – analysis sourceuri
- **description** (*str*) – analysis description
- **date_executed** (*str*) – analysis date_executed (yyyy-mm-dd)

Return type dict

Returns Analysis information

delete_analyses (*analysis_id=None, name=None, program=None, programversion=None, algorithm=None, sourcename=None, sourceversion=None, sourceuri=None, description=None*)

Delete analysis

Parameters

- **analysis_id** (*int*) – analysis_id filter
- **name** (*str*) – analysis name filter
- **program** (*str*) – analysis program filter
- **programversion** (*str*) – analysis programversion filter
- **algorithm** (*str*) – analysis algorithm filter
- **sourcename** (*str*) – analysis sourcename filter
- **sourceversion** (*str*) – analysis sourceversion filter
- **sourceuri** (*str*) – analysis sourceuri filter
- **description** (*str*) – analysis description

Return type None

Returns None

get_analyses (*analysis_id=None, name=None, program=None, programversion=None, algorithm=None, sourcename=None, sourceversion=None, sourceuri=None, description=None*)

Get all or some analyses

Parameters

- **analysis_id** (*int*) – analysis_id filter
- **name** (*str*) – analysis name filter
- **program** (*str*) – analysis program filter
- **programversion** (*str*) – analysis programversion filter
- **algorithm** (*str*) – analysis algorithm filter
- **sourcename** (*str*) – analysis sourcename filter
- **sourceversion** (*str*) – analysis sourceversion filter
- **sourceuri** (*str*) – analysis sourceuri filter
- **description** (*str*) – analysis description

Return type list of dict

Returns Analysis information

3.1.2 chado.export package

Module contents

Export data from chado

class chado.export.**ExportClient** (*engine, metadata, session, ci*)

Bases: *chado.client.Client*

Export data from the chado database

export_fasta (*organism_id, file=False*)

Export reference sequences as fasta.

Parameters

- **organism_id** (*int*) – Organism ID
- **file** (*bool*) – If true, write to files in CWD

Return type None

Returns None

export_gbk (*organism_id*)

Export organism features as genbank

Parameters **organism_id** (*int*) – Organism ID

Return type None

Returns None

export_gff3 (*organism_id*)

Export organism features as GFF3

Parameters **organism_id** (*int*) – Organism ID

Return type None

Returns None

3.1.3 chado.expression package

Module contents

Contains possible interactions with the Chado base for expressions and biomaterials

class chado.expression.**ExpressionClient** (*engine, metadata, session, ci*)

Bases: *chado.client.Client*

Interact with expressions

add_biomaterial (*biomaterial_name, organism_id, description="", biomaterial_provider="", biosample_accession="", sra_accession="", bioproject_accession="", attributes={}*)

Add a new biomaterial to the database

Parameters

- **biomaterial_name** (*str*) – Biomaterial name
- **organism_id** (*int*) – The id of the associated organism
- **description** (*str*) – Description of the biomaterial
- **biomaterial_provider** (*str*) – Biomaterial provider name
- **biosample_accession** (*str*) – Biosample accession number
- **sra_accession** (*str*) – SRA accession number

- **bioproject_accession** (*str*) – Bioproject accession number
- **attributes** (*str*) – Custom attributes (In JSON dict form)

Return type dict

Returns Biomaterial details

add_expression (*organism_id*, *analysis_id*, *file_path*, *separator*='\\t', *unit*=None,
 query_type='mRNA', *match_on_name*=False, *re_name*=None,
 skip_missing=False)

Add an expression matrix file to the database

Parameters

- **organism_id** (*int*) – The id of the associated organism
- **analysis_id** (*int*) – The id of the associated analysis
- **file_path** (*str*) – File path
- **separator** (*str*) – Separating character in the matrix file (ex : ';'). Default character is tab.
- **unit** (*str*) – The units associated with the loaded values (ie, FPKM, RPKM, raw counts)
- **query_type** (*str*) – The feature type (e.g. 'gene', 'mRNA', 'polypeptide', 'contig') of the query. It must be a valid Sequence Ontology term.
- **match_on_name** (*bool*) – Match features using their name instead of their uniqueness
- **re_name** (*str*) – Regular expression to extract the feature name from the input file (first capturing group will be used).
- **skip_missing** (*bool*) – Skip lines with unknown features or GO id instead of aborting everything.

Return type str

Returns Number of expression data loaded

delete_all_biomaterials (*confirm*=False)

Delete all biomaterials

Parameters **confirm** (*bool*) – Confirm that you really do want to delete ALL of the biomaterials.

Return type None

Returns None

delete_biomaterials (*names*=None, *ids*=None, *organism_id*="", *analysis_id*="")

Will delete biomaterials based on selector. Only one selector will be used.

Parameters

- **names** (*str*) – JSON list of biomaterial names to delete.
- **ids** (*str*) – JSON list of biomaterial ids to delete.
- **organism_id** (*int*) – Delete all biomaterial associated with this organism id.
- **analysis_id** (*int*) – Delete all biomaterial associated with this analysis id.

Return type str

Returns Number of deleted biomaterials

get_biomaterials (*provider_id*="", *biomaterial_id*="", *organism_id*="", *biomaterial_name*="", *analysis_id*="")

List biomaterials in the database

Parameters

- **organism_id** (*int*) – Limit query to the selected organism
- **biomaterial_id** (*int*) – Limit query to the selected biomaterial id
- **provider_id** (*int*) – Limit query to the selected provider
- **biomaterial_name** (*str*) – Limit query to the selected biomaterial name
- **analysis_id** (*int*) – Limit query to the selected analysis_id

Return type list

Returns List of biomaterials

3.1.4 chado.feature package

Module contents

Contains possible interactions with the Chado Features

class `chado.feature.FeatureClient` (*engine*, *metadata*, *session*, *ci*)

Bases: `chado.client.Client`

Access to the chado features

delete_features (*organism_id*=None, *analysis_id*=None, *name*=None, *uniquename*=None)

Get all or some features

Parameters

- **organism_id** (*int*) – organism_id filter
- **analysis_id** (*int*) – analysis_id filter
- **name** (*str*) – name filter
- **uniquename** (*str*) – uniquename filter

Return type list of dict

Returns Features information

get_feature_analyses (*feature_id*)

Get analyses associated with a feature

Parameters **feature_id** (*int*) – Id of the feature

Return type list

Returns Feature analyses

get_feature_cvterms (*feature_id*)

Get cvterms associated with a feature

Parameters **feature_id** (*int*) – Id of the feature

Return type list

Returns Feature cvterms

get_features (*organism_id=None, analysis_id=None, name=None, uniqueness=None*)

Get all or some features

Parameters

- **organism_id** (*int*) – organism_id filter
- **analysis_id** (*int*) – analysis_id filter
- **name** (*str*) – name filter
- **uniquename** (*str*) – uniqueness filter

Return type list of dict

Returns Features information

load_fasta (*fasta, organism_id, sequence_type='contig', analysis_id=None, re_name=None, re_uniquename=None, match_on_name=False, update=False, db=None, re_db_accession=None, rel_type=None, re_parent=None, parent_type=None*)

Load features from a fasta file

Parameters

- **fasta** (*str*) – Path to the Fasta file to load
- **organism_id** (*int*) – Organism ID
- **sequence_type** (*str*) – Sequence type
- **analysis_id** (*int*) – Analysis ID
- **re_name** (*str*) – Regular expression to extract the feature name from the fasta sequence id (first capturing group will be used).
- **re_uniquename** (*str*) – Regular expression to extract the feature name from the fasta sequence id (first capturing group will be used).
- **match_on_name** (*bool*) – Match existing features using their name instead of their uniqueness
- **update** (*bool*) – Update existing feature with new sequence instead of throwing an error
- **db** (*int*) – External database to cross reference to.
- **re_db_accession** (*str*) – Regular expression to extract an external database accession from the fasta sequence id (first capturing group will be used).
- **rel_type** (*str*) – Relation type to parent feature ('part_of' or 'derives_from').
- **re_parent** (*str*) – Regular expression to extract parent uniqueness from the fasta sequence id (first capturing group will be used).
- **parent_type** (*str*) – Sequence type of the parent feature

Return type dict

Returns Number of inserted sequences

load_featureprops (*tab_file, analysis_id, organism_id, prop_type, feature_type=None, match_on_name=False*)

Load feature properties from a tabular file (Column1: feature name or uniqueness, Column2: property value)

Parameters

- **tab_file** (*str*) – Path to the tabular file to load

- **analysis_id** (*int*) – Analysis ID
- **organism_id** (*int*) – Organism ID
- **prop_type** (*str*) – Type of the feature property (cvterm will be created if it doesn't exist)
- **feature_type** (*str*) – Type of the target features in sequence ontology (will speed up loading if specified)
- **match_on_name** (*bool*) – Match features using their name instead of their uniquename

Return type dict

Returns Number of inserted featureprop

load_gff (*gff*, *analysis_id*, *organism_id*, *landmark_type=None*, *re_protein=None*, *re_protein_capture='^(.*?)\$'*, *fasta=None*, *no_seq_compute=False*, *quiet=False*, *add_only=False*, *protein_id_attr=None*)
Load features from a gff file

Parameters

- **gff** (*str*) – Path to the Fasta file to load
- **analysis_id** (*int*) – Analysis ID
- **organism_id** (*int*) – Organism ID
- **landmark_type** (*str*) – Type of the landmarks (will speed up loading if provided, e.g. contig, should be a term of the Sequence ontology)
- **re_protein** (*str*) – Replacement string for the protein name using capturing groups defined by *re_protein_capture*
- **re_protein_capture** (*str*) – Regular expression to capture groups in mRNA name to use in *re_protein* (e.g. “^(.*?)-R([A-Z]+)\$”, default=“^(.*?)\$”)
- **protein_id_attr** (*str*) – Attribute containing the protein uniquename. It is searched at the mRNA level, and if not found at CDS level.
- **fasta** (*str*) – Path to a Fasta containing sequences for some features. When creating a feature, if its sequence is in this fasta file it will be loaded. Otherwise for mRNA and polypeptides it will be computed from the genome sequence (if available), otherwise it will be left empty.
- **no_seq_compute** (*bool*) – Disable the computation of mRNA and polypeptides sequences based on genome sequence and positions.
- **quiet** (*bool*) – Hide progress information
- **add_only** (*bool*) – Use this flag if you're not updating existing features, but just adding new features to the selected analysis and organism. It will speedup loading, and reduce memory usage, but might produce errors in case of already existing feature.

Return type None

Returns None

load_go (*input*, *organism_id*, *analysis_id*, *query_type='polypeptide'*, *match_on_name=False*, *name_column=2*, *go_column=5*, *re_name=None*, *skip_missing=False*)
Load GO annotation from a tabular file

Parameters

- **input** (*str*) – Path to the input tabular file to load

- **organism_id** (*int*) – Organism ID
- **analysis_id** (*int*) – Analysis ID
- **query_type** (*str*) – The feature type (e.g. ‘gene’, ‘mRNA’, ‘polypeptide’, ‘contig’) of the query. It must be a valid Sequence Ontology term.
- **match_on_name** (*bool*) – Match features using their name instead of their uniquename
- **name_column** (*int*) – Column containing the feature identifiers (2, 3, 10 or 11; default=2).
- **go_column** (*int*) – Column containing the GO id (default=5).
- **re_name** (*str*) – Regular expression to extract the feature name from the input file (first capturing group will be used).
- **skip_missing** (*bool*) – Skip lines with unknown features or GO id instead of aborting everything.

Return type dict

Returns Number of inserted GO terms

3.1.5 chado.load package

Module contents

Contains loader methods

class `chado.load.LoadClient` (*engine, metadata, session, ci*)

Bases: `chado.client.Client`

blast (*analysis_id, organism_id, input, blastdb=None, blastdb_id=None, re_name=None, query_type='polypeptide', match_on_name=False, skip_missing=False*)

Load a blast analysis, in the same way as does the `tripal_analysis_blast` module

Parameters

- **analysis_id** (*int*) – Analysis ID
- **organism_id** (*int*) – Organism ID
- **input** (*str*) – Path to the Blast XML file to load
- **blastdb** (*str*) – Name of the database blasted against (must be in the Chado db table)
- **blastdb_id** (*int*) – ID of the database blasted against (must be in the Chado db table)
- **query_type** (*str*) – The feature type (e.g. ‘gene’, ‘mRNA’, ‘polypeptide’, ‘contig’) of the query. It must be a valid Sequence Ontology term.
- **match_on_name** (*bool*) – Match features using their name instead of their uniquename
- **re_name** (*str*) – Regular expression to extract the feature name from the input file (first capturing group will be used).
- **skip_missing** (*bool*) – Skip lines with unknown features or GO id instead of aborting everything.

Return type dict

Returns Number of processed hits

go (*input*, *organism_id*, *analysis_id*, *query_type*='polypeptide', *match_on_name*=False, *name_column*=2, *go_column*=5, *re_name*=None, *skip_missing*=False)
 Load GO annotation from a tabular file, in the same way as does the tripal_analysis_go module

Parameters

- **input** (*str*) – Path to the input tabular file to load
- **organism_id** (*int*) – Organism ID
- **analysis_id** (*int*) – Analysis ID
- **query_type** (*str*) – The feature type (e.g. 'gene', 'mRNA', 'polypeptide', 'contig') of the query. It must be a valid Sequence Ontology term.
- **match_on_name** (*bool*) – Match features using their name instead of their uniquename
- **name_column** (*int*) – Column containing the feature identifiers (2, 3, 10 or 11; default=2).
- **go_column** (*int*) – Column containing the GO id (default=5).
- **re_name** (*str*) – Regular expression to extract the feature name from the input file (first capturing group will be used).
- **skip_missing** (*bool*) – Skip lines with unknown features or GO id instead of aborting everything.

Return type dict

Returns Number of inserted GO terms

interpro (*analysis_id*, *organism_id*, *input*, *parse_go*=False, *re_name*=None, *query_type*='polypeptide', *match_on_name*=False, *skip_missing*=False)
 Load an InterProScan analysis, in the same way as does the tripal_analysis_intepro module

Parameters

- **analysis_id** (*int*) – Analysis ID
- **organism_id** (*int*) – Organism ID
- **input** (*str*) – Path to the InterProScan file to load
- **parse_go** (*bool*) – Load GO annotation to the database
- **query_type** (*str*) – The feature type (e.g. 'gene', 'mRNA', 'polypeptide', 'contig') of the query. It must be a valid Sequence Ontology term.
- **match_on_name** (*bool*) – Match features using their name instead of their uniquename
- **re_name** (*str*) – Regular expression to extract the feature name from the input file (first capturing group will be used).
- **skip_missing** (*bool*) – Skip lines with unknown features or GO id instead of aborting everything.

Return type dict

Returns Number of processed hits

3.1.6 chado.organism package

Module contents

Contains possible interactions with the Chado Organisms Module

class `chado.organism.OrganismClient` (*engine, metadata, session, ci*)

Bases: `chado.client.Client`

Access to the chado organism table

add_organism (*genus, species, common, abbr, comment=None*)

Add a new organism to the Chado database

Parameters

- **genus** (*str*) – The genus of the organism
- **species** (*str*) – The species of the organism
- **common** (*str*) – The common name of the organism
- **abbr** (*str*) – The abbreviation of the organism
- **comment** (*str*) – A comment / description

Return type dict

Returns Organism information

delete_all_organisms (*confirm=False*)

Delete all organisms

Parameters **confirm** (*bool*) – Confirm that you really do want to delete ALL of the organisms.

Return type None

Returns None

delete_organisms (*organism_id=None, genus=None, species=None, common=None, abbr=None, comment=None*)

Delete all organisms

Parameters

- **organism_id** (*int*) – organism_id filter
- **genus** (*str*) – genus filter
- **species** (*str*) – species filter
- **common** (*str*) – common filter
- **abbr** (*str*) – abbr filter
- **comment** (*str*) – comment filter

Return type None

Returns None

get_organisms (*organism_id=None, genus=None, species=None, common=None, abbr=None, comment=None*)

Get all or some organisms

Parameters

- **organism_id** (*int*) – organism_id filter
- **genus** (*str*) – genus filter

- **species** (*str*) – species filter
- **common** (*str*) – common filter
- **abbr** (*str*) – abbr filter
- **comment** (*str*) – comment filter

Return type list of dict

Returns Organisms information

3.1.7 chado.phylogeny package

Module contents

Contains possible interactions with the Chado Phylogeny Module http://gmod.org/wiki/Chado_Phylogeny_Module
As implemented in https://github.com/legumeinfo/tripal_phylotree and https://github.com/legumeinfo/lis_context_viewer/

class `chado.phylogeny.PhylogenyClient` (*engine, metadata, session, ci*)

Bases: `chado.client.Client`

Access to the chado phylogeny content

add_cvterms ()

Make sure required cvterms are loaded

Return type list of dict

Returns created cvterms

gene_families (*family_name="", nuke=False*)

Adds an entry in the featureprop table in a chado database for each family a gene belongs to (for use in https://github.com/legumeinfo/lis_context_viewer/).

Parameters

- **family_name** (*str*) – Restrict to families beginning with given prefix
- **nuke** (*bool*) – Removes all previous gene families data

Return type None

Returns None

gene_order (*nuke=False*)

Orders all the genes in the database by their order on their respective chromosomes in the gene_order table (for use in https://github.com/legumeinfo/lis_context_viewer/).

Parameters **nuke** (*bool*) – Removes all previous gene ordering data

Return type None

Returns None

load_tree (*newick, analysis_id, name=None, xref_db='null', xref_accession=None, match_on_name=False, prefix=""*)

Load a phylogenetic tree (Newick format) into Chado db

Parameters

- **newick** (*str*) – Newick file to load (or directory containing multiple newick files to load)

- **analysis_id** (*int*) – Analysis ID
- **name** (*str*) – The name given to the phylotree entry in the database (default=<filename>)
- **xref_db** (*str*) – The name of the db to link dbxrefs for the trees (default: “null”)
- **xref_accession** (*str*) – The accession to use for dbxrefs for the trees (assumed same as name unless otherwise specified)
- **match_on_name** (*bool*) – Match polypeptide features using their name instead of their uniquename
- **prefix** (*str*) – Comma-separated list of prefix to be removed from identifiers (e.g species prefixes when loading OrthoFinder output)

Return type dict

Returns Number of inserted trees

3.1.8 chado.util package

Module contents

class `chado.util.UtilClient` (*engine, metadata, session, ci*)

Bases: `chado.client.Client`

Some chado utilities

dbshell ()

Open a psql session to the database

Return type None

Returns None

launch_docker_image (*background=False, no_yeast=False*)

Launch a chado docker image.

Parameters

- **background** (*bool*) – Launch the image in the background
- **no_yeast** (*bool*) – Disable loading of example yeast data

Return type None

Returns None

3.2 Submodules

3.3 chado.client module

Base chado client

class `chado.client.Client` (*engine, metadata, session, ci*)

Bases: object

Base client class implementing methods to make queries to the server

3.4 chado.exceptions module

exception `chado.exceptions.RecordNotFoundError`

Bases: `Exception`

Raised when a db select failed.

3.5 chado.util module

class `chado.util.UtilClient(engine, metadata, session, ci)`

Bases: `chado.client.Client`

Some chado utilities

dbshell ()

Open a psql session to the database

Return type `None`

Returns `None`

launch_docker_image (*background=False, no_yeast=False*)

Launch a chado docker image.

Parameters

- **background** (*bool*) – Launch the image in the background
- **no_yeast** (*bool*) – Disable loading of example yeast data

Return type `None`

Returns `None`

3.6 Module contents

class `chado.ChadoInstance(dbhost='localhost', dbname='chado', dbuser='chado', dbpass='chado', dbschema='public', dbport=5432, dburl=None, offline=False, no_reflect=False, reflect_tripal_tables=False, pool_connections=True, **kwargs)`

Bases: `object`

create_cvterm (*term, cv_name, db_name, term_definition="", cv_definition="", db_definition="", accession=""*)

get_cvterm_id (*name, cv, allow_synonyms=False*)

`get_cvterm_id` allows lookup of CV terms by their name. This method caches the result in order to not hit the DB for every query. Maybe should investigate pre-loading popular terms? (E.g. gene, mRNA, etc)

get_cvterm_name (*cv_id*)

`get_cvterm_name` allows lookup of CV terms by their ID. This method caches the result in order to not hit the DB for every query. Maybe should investigate pre-loading popular terms? (E.g. gene, mRNA, etc)

get_pub_id (*name*)

Allows lookup of publication by their unique name. This method caches the result in order to not hit the DB for every query.

```
class chado.ChadoModel
    Bases: object
```

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