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# **eutils Documentation**

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## 1.1 Introduction

eutils is a Python package to simplify searching, fetching, and parsing records from NCBI using their [E-utilities](#) interface.

### 1.1.1 Features

- simple Pythonic interface for searching and fetching
- automatic query rate throttling per NCBI guidelines
- optional sqlite-based caching of compressed replies
- “façades” that facilitate access to essential attributes in XML replies

### 1.1.2 Important Notes

- **You are encouraged to [browse issues](#).** Please report any issues you find.
- **Use a pip package specification to ensure stay within minor releases for API stability.** For example, `eutils >=0.1,<0.2`.

## 1.2 Using eutils

### 1.2.1 Installation

The easiest way to install the eutils package is to use pre-build Python package from PyPI, like so:

```
$ pip install eutils
```

Consider using [virtualenvwrapper](#) or [pyenv](#) to setup virtual environments before installing utils.

Code that relies on utils should specify a version bracket to ensure that utils receives bug fixes but not updates that might break compatibility. In your package's setup.py:

```
setup(
    ...
    install_requires = [
        'utils>=0.4,<0.3',
    ],
    ...
)
```

Alternatively, you may install from source; please see *Installation for Development* for details.

## 1.2.2 Examples

### Common setup

Instantiating an utils `utils.Client` is this easy:

```
>>> import utils

# Initialize a client. This client handles all caching and query
# throttling
>>> ec = utils.Client()
```

### Fetching gene information

```
# search for tumor necrosis factor genes
# any valid NCBI query may be used
>>> esr = ec.esearch(db='gene',term='tumor necrosis factor')

# fetch one of those (gene id 7157 is human TNF)
>>> egs = ec.efetch(db='gene',id=7157)

# One may fetch multiple genes at a time. These are returned as an
# EntrezgeneSet. We'll grab the first (and only) child, which returns
# an instance of the Entrezgene class.
>>> eg = egs.entrezgenes[0]

# Easily access some basic information about the gene
>>> eg.hgnc, eg.maploc, eg.description, eg.type, eg.genus_species
('TP53', '17p13.1', 'tumor protein p53', 'protein-coding', 'Homo sapiens')

# get a list of genomic references
>>> [str(r) for r in eg.references]
['GeneCommentary(acv=NC_000017.11,type=genomic,heading=Reference GRCh38.p2 Primary_
↳Assembly,label=Chromosome 17 Reference GRCh38.p2 Primary Assembly)',
 'GeneCommentary(acv=NG_017013.2,type=genomic,heading=None,label=RefSeqGene)',
 'GeneCommentary(acv=NC_018928.2,type=genomic,heading=Alternate CHM1_1.1,
↳label=Chromosome 17 Alternate CHM1_1.1)']

# Get all products defined on GRCh38
>>> [p.acv for p in eg.references[0].products]
```

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```
[u'NM_001126112.2', u'NM_001276761.1', u'NM_000546.5',
u'NM_001276760.1', u'NM_001126113.2', u'NM_001276695.1',
u'NM_001126114.2', u'NM_001276696.1', u'NM_001126118.1',
u'NM_001126115.1', u'NM_001276697.1', u'NM_001126117.1',
u'NM_001276699.1', u'NM_001126116.1', u'NM_001276698.1']

# As a sample, grab the first product defined on this reference (order is arbitrary)
>>> mrna = eg.references[0].products[0]
>>> str(mrna)
'GeneCommentary(acv=NM_001126112.2,type=mRNA,heading=Reference,label=transcript_
↳variant 2) '

# mrna.genomic_coords provides access to the exon definitions on this
reference

>>> mrna.genomic_coords.gi, mrna.genomic_coords.strand
('568815581', -1)

>>> mrna.genomic_coords.intervals
[(7687376, 7687549), (7676520, 7676618), (7676381, 7676402),
(7675993, 7676271), (7675052, 7675235), (7674858, 7674970),
(7674180, 7674289), (7673700, 7673836), (7673534, 7673607),
(7670608, 7670714), (7668401, 7669689)]

# and the mrna has a product, the resulting protein:
>>> str(mrna.products[0])
'GeneCommentary(acv=NP_001119584.1,type=peptide,heading=Reference,label=isoform a) '
```

## Fetch PubMed information

```
# search pubmed by author
>>> esr = c.esearch(db='pubmed', term='Nussbaum RL')

# fetch all of them
>>> paset = c.efetch(db='pubmed', id=esr.ids)

# paset represents PubmedArticleSet, a collection of
PubmedArticles. The major interface component is to iterate over
PubmedArticles with constructs like `for pa in paset: ...`. We
fetch the first PubmedArticle like this:
>>> pa = iter(paset).next()

PubmedArticle provides accessors to essential data:
>>> pa.title
'High incidence of functional ion-channel abnormalities in a
consecutive Long QT cohort with novel missense genetic variants of
unknown significance.'

>>> pa.authors
[u'Steffensen AB', u'Refaat MM', u'David JP', u'Mujezinovic A',
u'Calloe K', u'Wojciak J', u'Nussbaum RL', u'Scheinman MM',
u'Schmitt N']

>>> pa.jrnl, pa.volume, pa.issue, pa.year
('Sci Rep', '5', None, '2015')
```

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```
>>> pa.jrnl, pa.volume, pa.issue, pa.year, pa.pages
('Sci Rep', '5', None, '2015', '10009')

>>> pa.pmid, pa.doi, pa.pmc
('26066609', '10.1038/srep10009', '4464365')
```

## 1.3 Modules

### 1.3.1 Main Classes

**class** `eutils.Client` (*cache=False, api\_key=None*)

Bases: `object`

class-based access to NCBI E-Utilities, returning Python classes with rich data accessors

#### Parameters

- **cache** (*str*) – passed to QueryService, which see for explanation
- **api\_key** (*str*) – API key from NCBI

**Raises** `EutilsError` – if cache file couldn't be created

#### databases

list of databases available from eutils (per einfo query)

#### efetch (*db, id*)

query the efetch endpoint

#### einfo (*db=None*)

query the einfo endpoint

**Parameters** *db* – string (optional)

**Return type** EInfo or EInfoDB object

If *db* is None, the reply is a list of databases, which is returned in an EInfo object (which has a `databases()` method).

If *db* is not None, the reply is information about the specified database, which is returned in an EInfoDB object. (Version 2.0 data is automatically requested.)

#### esearch (*db, term*)

query the esearch endpoint

**class** `eutils.QueryService` (*email='biocommons-dev@googlegroups.com', cache=False, default\_args={'retmax': 250, 'retmode': 'xml', 'usehistory': 'y'}, request\_interval=None, tool=None, api\_key=None*)

Bases: `object`

*provides throttled and cached querying of NCBI E-utilities services*

QueryService has three functions:

- construct URLs appropriate for eutils endpoints
- throttle queries per NCBI guidelines
- cache results in persistent cache (sqlite)



QueryService works with any valid query arguments, passed as dictionaries.

Implemented interfaces:

- `esearch`
- `efetch`
- `elink`
- `einfo`
- `esummary`

Implementing other query modes should be straightforward.

See also

- <http://www.ncbi.nlm.nih.gov/books/NBK25500/> :the NCBI's Entrez Programming Utilities Help
- <http://www.ncbi.nlm.nih.gov/books/NBK25499/> :NCBI E-utilities

#### Parameters

- **email** (*str*) – email of user (for abuse reports)
- **cache** (*str*) – if True, cache at `~/.cache/eutils-db.sqlite`; if string, cache there; if False, don't cache
- **default\_args** (*dict*) – dictionary of query args that should accompany all requests
- **request\_interval** (*int* or a callable returning an *int*) – seconds between requests; default: auto-select based on API key
- **api\_key** (*str*) – api key assigned by NCBI
- **tool** (*str*) – name of client

**Return type** `None`

**Raises** `OSError` – if sqlite file can't be opened

**efetch** (*args*)

execute a cached, throttled efetch query

**Parameters** **args** (*dict*) – dict of query items

**Returns** content of reply

**Return type** `str`

**Raises** `EutilsRequestError` – when NCBI replies, but the request failed (e.g., bogus database name)

**einfo** (*args=None*)

execute a NON-cached, throttled einfo query

`einfo.fcgi?db=<database>`

Input: Entrez database (&db) or None (returns info on all Entrez databases)

Output: XML containing database statistics

Example: Find database statistics for Entrez Protein.

`QueryService.einfo({"db": "protein"})`

Equivalent HTTP request:

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/einfo.fcgi?db=protein>

**Parameters** *args* (*dict*) – dict of query items (optional)

**Returns** content of reply

**Return type** *str*

**Raises** *EutilsRequestError* – when NCBI replies, but the request failed (e.g., bogus database name)

**elink** (*args*)

execute a cached, throttled elink query

Input: List of UIDs (&id); Source Entrez database (&dbfrom); Destination Entrez database (&db)

Output: XML containing linked UIDs from source and destination databases

Example: Find one set of Gene IDs linked to nuccore GIs 34577062 and 24475906

QueryService.elink({"dbfrom": "nuccore", "db": "gene", "id": "34577062,24475906"})

Equivalent HTTP request:

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=nuccore&db=gene&id=34577062,24475906>

**Parameters** *args* (*dict*) – dict of query items containing at least the “db”, “dbfrom”, and “id” keys.

**Returns** content of reply

**Return type** *str*

**Raises** *EutilsRequestError* – when NCBI replies, but the request failed (e.g., bogus database name)

**esearch** (*args*)

execute a cached, throttled esearch query

**Parameters** *args* (*dict*) – dict of query items, containing at least “db” and “term” keys

**Returns** content of reply

**Return type** *str*

**Raises** *EutilsRequestError* – when NCBI replies, but the request failed (e.g., bogus database name)

**esummary** (*args*)

execute a cached, throttled esummary query

Input: List of UIDs (&id); Entrez database (&db)

Output: XML document summary for requested ID(s) [comma-separated]

Example:

QueryService.esummary({"db": "medgen", "id": 134 })

Equivalent HTTP request:

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/esummary.fcgi?db=medgen&id=134>

**Parameters** *args* (*dict*) – dict of query items containing at least “db” and “id” keys.

**Returns** content of reply

**Return type** `str`

**Raises** `EutilsRequestError` – when NCBI replies, but the request failed (e.g., bogus database name)

## 1.3.2 Exceptions

**class** `eutils.EutilsError`

Bases: `Exception`

Base class for all Eutils exceptions, and also used to raise general exception.

**class** `eutils.EutilsNCBIError`

Bases: `eutils._internal.exceptions.EutilsError`

Raised when NCBI returns data that appears to be incorrect or invalid.

**class** `eutils.EutilsNotFoundError`

Bases: `eutils._internal.exceptions.EutilsError`

Raised when the requested data is not available. (Used only by the `eutils.sketchy.clientx` interface currently.)

**class** `eutils.EutilsRequestError`

Bases: `eutils._internal.exceptions.EutilsError`

Raised when NCBI responds with an error, such as when a non-existent database is specified.

## 1.3.3 Experimental

**class** `eutils.sketchy.clientx.ClientX(cache=False, api_key=None)`

Bases: `eutils._internal.client.Client`

*warning* This class is subject to rapid development and api changes.

A subclass of `eutils.client.Client` that provides specific lookup functions.

This functionality is in a separate class because the API is experimental.

### Parameters

- **cache** (`str`) – passed to QueryService, which see for explanation
- **api\_key** (`str`) – API key from NCBI

**Raises** `EutilsError` – if cache file couldn't be created

**fetch\_gbseq\_by\_ac** (`acv`)

**fetch\_gene\_by\_hgnc** (`hgnc`)

**fetch\_nuccore\_by\_ac** (`acv`)

**fetch\_snps\_for\_gene** (`hgnc, organism='human'`)

## 1.4 Contributing

Development occurs in the default branch. Please work in feature branches or bookmarks from the default branch. Feature branches should be named for the eutils issue they fix, as in *121-update-xml-facades*. When merging, use a commit message like “closes #121: update xml facades to new-style interface”. (“closes #n” is recognized automatically and closes the ticket upon pushing.)

The included Makefile automates many tasks. In particular, *make develop* prepares a development environment and *make test* runs unittests. (Please run tests before committing!)

Again, thanks for your contributions.

### 1.4.1 Development

This section is intended for developers seeking to extend the eutils package. You should be familiar with the architecture, conventions, and basic functionality elsewhere in this documentation.

#### Get Cozy with make

The eutils package includes a GNU Makefile that aids nearly all developer tasks. It subsumes much of the functionality in setup.py. While using the Makefile isn’t required to develop, it is the official way to invoke tools, tests, and other development features. Type *make* for eutils-specific help.

Some of the key targets are:

**develop** Prepare the directory for local development.

**install** Install eutils (as with python setup.py install).

**test** Run the default test suite

**clean, cleaner, cleanest** Remove extraneous files, leaving a directory in various states of tidiness.

**docs** Make the sphinx docs in doc/build/html/.

**upload, upload\_docs** Upload package to PyPI or docs to pythonhosted.org.

#### Installation for Development

You will need [Mercurial](#) to clone the eutils repository.

```
$ hg clone ssh://hg@bitbucket.org/biocommons/eutils
$ cd eutils
$ make develop
```

#### Submitting Patches

Yes! We’ll be thrilled to have your contributions!

The preferred way to submit a patch is by forking the project on BitBucket, committing your changes there, then sending a pull request.

If you have a really worthwhile patch, we’ll probably accept a diff-formatted patch, but that’ll make it harder for us and impossible for you to get credit.

## Developing and Contributing to eutils

- Fork the project at <https://bitbucket.org/biocommons/eutils/>
- Clone the project locally with:

```
$ hg clone https://bitbucket.org/<your_username>/eutils
```

- Create a virtualenv:

```
$ mkvirtualenv eutils
```

mkvirtualenv is part of the virtualenvwrapper package. Python3 users should prefer pyenv.

- Prepare your environment:

```
$ make develop
```

(The Makefile in eutils wraps functionality in setup.py, and also provides many useful utilitarian rules. Type `make` to see a list of targets.)

- Create an issue at <https://github.com/biocommons/eutils/issues/> for the feature you want to work on. This helps tracking for changelogs.
- Create a mercurial bookmark for your feature. Please name the bookmark like 141-implement-caching (where 141 is the issue number).
- Code away, then commit and push:

```
$ hg commit -m 'fixes #141: implemented caching'
$ hg push
```

- If you'd like to contribute back, create a pull request.

## 1.5 ChangeLog

### 1.5.1 0.6 Series

#### 0.6.0 (2019-12-17)

Changes since 0.5.2 (2019-05-15).

#### Special Attention

Support for Python 2.7 has been dropped.

#### Deprecations

#### Bug Fixes

- Closes [#164](#): Handle cases of NCBI error response without ERROR message [[2e55029](#)] (Reece Hart)

## New Features

## Other Changes

- Replace deprecated time.clock function (#165) [caeff2b] (Jeff van Santen)
- Replaced process\_time() with monotonic(), which measures elapsed time [d4508f8] (Reece Hart)

## Internal and Developer Changes

- Add .deepsources.toml, Fix issues raised by DeepSource (#163) [db41c8b] (Mohit Solanki)
- Dropped python 2.7 support [3e53fa2] (Reece Hart)
- Closes #166: Remove six and \_internal/compat.py [b5d4e84] (Reece Hart)
- Sync with current biocommons conventions: use setup.cfg, use src/, Makefile updates, drop req files [a232d9b] (Reece Hart)
- Add support for testing on Python 3.8 on travis and tox [0e6e2f0] (Reece Hart)

## 1.5.2 0.5 Series

### 0.5.0 (2018-11-19)

Changes since 0.4.1 (2018-10-10).

## Special Attention

Support for Python < 3.6 will be dropped on 2019-03-31. This release will issue warnings when imported by a python version < 3.6. See <https://github.com/biocommons/org/wiki/Migrating-to-Python-3.6>

## New Features

- #159: Adding publication types, mesh qualifiers and chemicals properties for medline citations [d28dbd0]. Thanks to @VincentMatthys for this contribution!

## Internal and Developer Changes

- removed py 3.5 from travis config; updated badges in README [5ab476c]
- sync project files with bioutils; use travis stages for test+deploy [2a2222e]
- deprecate python < 3.6; see <https://github.com/biocommons/org/wiki/Migrating-to-Python-3.6> [57c41cc]

## 1.5.3 0.4 Series

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**Important:** Clients should import only from eutils (e.g., `import eutils`). Importing from submodules (e.g., `import eutils.client`) will fail in the 0.5 release.

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### 0.4.1 (2018-10-11)

Changes since 0.4.0 (2018-05-28).

#### Bug Fixes

- closes #157: edge case results in error being thrown when extracting abstract text (#158) [@pmartin23]

### 0.4.0 (2018-05-28)

Changes since 0.3.2 (2017-11-02).

#### Special Attention

- fixes #152: support NCBI API keys [1175630]

Removed time-based throttling and added support for NCBI API keys. Without an API key, NCBI returns an error if clients make more than 3 requests/second. With an API, clients may make 10 requests/second. See <https://www.ncbi.nlm.nih.gov/books/NBK25497/>. The API key may be passed as argument to Client and QueryService.

#### New Features

- #153: efetch for protein db

#### Internal and Developer Changes

- closes #132: Fix functions default argument (#156)

## 1.5.4 0.3 Series

### 0.3.2 (2017-11-02)

Changes since 0.3.1 (2017-08-22).

#### Internal and Developer Changes

- Fix for #150 drop gi assertion in tests [e857856]

### 0.3.1 (2017-08-22)

Changes since 0.3.0.post0 (2017-03-01).

#### Bug Fixes

- closes #149: fix bug in which multi-line abstracts were truncated [df491f8]

### 0.3.0 (2017-02-28)

Changes since 0.2.4 (2017-02-21).

#### Special Attention

- closes #147: Do not use cache by default (use *cache=True* for current behavior) [abfa129]

#### Internal and Developer Changes

- closes #140: migrate tests to vcrpy (and delete test data) [7862548]

## 1.5.5 0.2 Series

### 0.2.4 (2017-02-21)

Changes since 0.2.3 (2017-02-03).

#### Special Attention

#### Deprecations

#### Bug Fixes

#### New Features

#### Other Changes

#### Internal and Developer Changes

- Implemented wheel support

### 0.2.3 (2017-02-03)

Changes since 0.2.2 (2016-12-10).

#### New Features

- Merge pull request #143 from diekhans/betterResponseParseErrors
- Merge pull request #144 from diekhans/nucestSupport [f26636c]

#### Other Changes

- include error message from XML parser when can't parse NCBI response [47d0673]



## Internal and Developer Changes

- use exception syntax compatible with py 3 [858cbdc]

### 0.2.2 (2016-12-10)

Changes since 0.2.1 (2016-10-19).

## Internal and Developer Changes

- closes #141: updates issue links from bitbucket to github [c41c501]

### 0.2.1 (2016-10-19)

Changes since 0.2.0 (2016-09-15).

## Bug Fixes

- Merge pull request #139 from timothyjlaurent/138-catch-malformed-xml-on-error

### 0.2.0 (2016-09-15)

Changes since 0.1.1 (2016-07-22).

## New Features

- fixes #8: use https for eutilities (required by 2016-09-30) [0ce382f]
- Update ExchangeSet handling for switch to https [399b330]
- basic support for pubmedcentral [18b3a63]

## 1.6 License

eutils is released under the [Apache License 2.0](#), the text of which appears below:

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