
Bio2BEL CTD Documentation

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CHAPTER 1

Enrichment

`bio2bel_ctd.enrich.enrich_chemicals(graph, connection=None)`
Enriches chemicals in the graph

Parameters `graph` (`pybel.BELGraph`) – A BEL graph

CHAPTER 2

Manager

Bio2BEL CTD Manager.

```
class bio2bel_ctd.manager.Manager(*args, **kwargs)
    Bio2BEL manager for the CTD.

    is_populated() → bool
        Check if the database is already populated.

    populate(urls=None, force_download=False, only_tables=None, exclude_tables=None) → None
        Updates the CTD database
        1. downloads all files from CTD
        2. drops all tables in database
        3. creates all tables in database
        4. import all data from CTD files
```

Parameters

- **urls** (*iter[str]*) – An iterable of URL strings
- **force_download** (*bool*) – force method to download

```
count_genes() → int
    Count the genes in the database.
```

```
list_chemicals() → List[pyctd.manager.models.Chemical]
    List all chemicals.
```

```
count_chemicals() → int
    Count the chemicals in the database.
```

```
list_chemical_gene_interactions() → List[pyctd.manager.models.ChemGeneIx]
    List all chemical-gene interactions.
```

```
count_chemical_gene_interactions() → int
    Count the chemical-gene interactions in the database.
```

count_pathways() → int

Count the pathways in the database.

count_diseases() → int

Count the diseases in the database.

summarize() → Mapping[str, int]

Return a summary dictionary of the database.

get_chemical_by_mesh(mesh_id: str) → Optional[pyctd.manager.models.Chemical]

Get a chemical by its MeSH identifier, if it exists.

Parameters **mesh_id** – A MeSH identifier of a chemical

get_chemical_by_cas(cas_rn: str) → Optional[pyctd.manager.models.Chemical]

Get a chemical by its CAS Registry Number, if it exists.

Parameters **cas_rn** (*str*) – A CAS Registry Number

Return type Optional[Chemical]

get_gene_by_entrez_id(entrez_id: str) → Optional[pyctd.manager.models.Gene]

Get a gene by its Entrez Gene identifier, if it exists.

Parameters **entrez_id** – An Entrez Gene identifier of a gene

Return type Optional[Gene]

get_interaction_by_id(ixn_id: int) → Optional[pyctd.manager.models.ChemGeneIxN]

Get an interaction by its database identifier

Parameters **ixn_id** – An interaction database identifier

enrich_graph_chemical(graph: pybel.struct.graph.BELGraph, mesh_id: str) → None

Enrich the BEL graph with chemical-gene interactions for the given chemical.

Parameters

- **graph** – A BEL graph
- **mesh_id** – A MeSH identifier of a chemical

enrich_graph_gene(graph: pybel.struct.graph.BELGraph, entrez_id: str) → None

Enrich the BEL graph with chemical-gene interactions for the given gene.

Parameters

- **graph** – A BEL graph
- **entrez_id** – An Entrez Gene identifier of a gene

enrich_graph_genes(graph: pybel.struct.graph.BELGraph) → None

Enrich the BEL graph with chemical-gene interactions for all Entrez genes.

Parameters **graph** – A BEL graph

enrich_chemicals(graph: pybel.struct.graph.BELGraph) → None

Find chemicals that can be mapped and enriched with the CTD.

Parameters **graph** (*pybel.BELGraph*) – A BEL graph

to_bel() → pybel.struct.graph.BELGraph

Convert all possible aspects of the database to BEL.

Warning: Not complete!

To do:

- add namespaces
- use cursors
- multiprocessing

CHAPTER 3

Indices and tables

- genindex
- modindex
- search

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