Bio2BEL CTD Documentation

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Contents:

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.ChemGeneIxn]

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

Python Module Index

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