Bio2BEL GO Documentation

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Contents:

Bio2BEL GO.

Contents:

Enrichment

Manager for Bio2BEL GO.

bio2bel_go.manager.**add_parents**(*go*, *identifier: str*, *graph: pybel.struct.graph.BELGraph*, *child: pybel.dsl.node_classes.BaseEntity*)

>   Add parents to the network.
>
>   **Parameters**
>
>   - **go** – GO Network
>
>   - **identifier** – GO Identifier of the child
>
>   - **graph** – A BEL graph
>
>   - **child** – A BEL node

bio2bel_go.manager.**normalize_go_id**(*identifier: str*) → str

>   If a GO term does not start with the GO: prefix, add it.

class bio2bel_go.manager.**Manager**(**args*, ***kwargs*)

>   Biological process multi-hierarchy.
>
>   **namespace_model**
>   >   alias of bio2bel_go.models.Term
>
>   **is_populated**() → bool
>   >   Check if the database is already populated.
>
>   **get_term_by_id**(*go_id: str*) → Optional[bio2bel_go.models.Term]
>   >   Get a GO entry by its identifier.
>
>   **get_term_by_name**(*name: str*) → Optional[bio2bel_go.models.Term]
>   >   Get a GO entry by name.
>
>   **populate**(*path=None*, *force_download=False*) → None
>   >   Populate the database.
>   >
>   >   **Parameters**
>   >
>   >   - **path** – Path to the GO OBO file

- **force_download** –

count_terms() → int
    Count the number of entries in GO.

count_synonyms() → int
    Count the number of synonyms in GO.

count_hierarchies() → int
    Count the number of synonyms in GO.

list_hierarchies() → List[bio2bel_go.models.Hierarchy]
    List hierarchy entries.

count_annotations() → int
    Count the number of annotations.

list_annotations() → List[bio2bel_go.models.Annotation]
    List annotation entries.

summarize() → Mapping[str, int]
    Return a summary dictionary over the content of the database.

lookup_term(*node: pybel.dsl.node_classes.BaseEntity*) → Optional[bio2bel_go.models.Term]
    Guess the identifier from a PyBEL node data dictionary.

iter_terms(*graph: pybel.struct.graph.BELGraph*, *use_tqdm: bool = False*) → Iterable[Tuple[pybel.dsl.node_classes.BaseEntity, bio2bel_go.models.Term]]
    Iterate over nodes in the graph that can be looked up.

normalize_terms(*graph: pybel.struct.graph.BELGraph*, *use_tqdm: bool = False*) → None
    Add identifiers to all GO terms.

enrich_bioprocesses(*graph: pybel.struct.graph.BELGraph*, *use_tqdm: bool = False*) → None
    Enrich a BEL graph's biological processes.

get_release_date() → str
    Convert the OBO release date to a ISO 8601 version.

    Example: 'releases/2017-03-26'

to_bel() → pybel.struct.graph.BELGraph
    Convert Gene Ontology to BEL, with given strategies.

Constants

Constants for Bio2BEL GO.

bio2bel_go.constants.**GO_OBO_URL = 'http://purl.obolibrary.org/obo/go/go-basic.obo'**
  The web location of the GO OBO file

bio2bel_go.constants.**GO_OBO_PATH = '/home/docs/.bio2bel/go/go-basic.obo'**
  The local cache location where the GO OBO file is stored

bio2bel_go.constants.**GO_OBO_PICKLE_PATH = '/home/docs/.bio2bel/go/go-basic.obo.gpickle'**
  The local cache location where the parsed and pickled GO OBO file is stored

bio2bel_go.constants.**GAF_COLUMNS = ['db', 'db_id', 'db_symbol', 'qualifier', 'go_id', 'prov**
  GAF columns, see: http://geneontology.org/docs/go-annotation-file-gaf-format-2.1/

CHAPTER 3

Indices and tables

- genindex
- modindex
- search

Python Module Index

b

Index

A

add_parents() (*in module bio2bel_go.manager*), 3

B

bio2bel_go (*module*), 1
bio2bel_go.constants (*module*), 5
bio2bel_go.manager (*module*), 3

C

count_annotations()
(*bio2bel_go.manager.Manager method*),
4
count_hierarchies()
(*bio2bel_go.manager.Manager method*),
4
count_synonyms() (*bio2bel_go.manager.Manager method*), 4
count_terms() (*bio2bel_go.manager.Manager method*), 4

E

enrich_bioprocesses()
(*bio2bel_go.manager.Manager method*),
4

G

GAF_COLUMNS (*in module bio2bel_go.constants*), 5
get_release_date()
(*bio2bel_go.manager.Manager method*),
4
get_term_by_id() (*bio2bel_go.manager.Manager method*), 3
get_term_by_name()
(*bio2bel_go.manager.Manager method*),
3
GO_OBO_PATH (*in module bio2bel_go.constants*), 5
GO_OBO_PICKLE_PATH (*in module bio2bel_go.constants*), 5
GO_OBO_URL (*in module bio2bel_go.constants*), 5

I

is_populated() (*bio2bel_go.manager.Manager method*), 3
iter_terms() (*bio2bel_go.manager.Manager method*), 4

L

list_annotations()
(*bio2bel_go.manager.Manager method*),
4
list_hierarchies()
(*bio2bel_go.manager.Manager method*),
4
lookup_term() (*bio2bel_go.manager.Manager method*), 4

M

Manager (*class in bio2bel_go.manager*), 3

N

namespace_model (*bio2bel_go.manager.Manager attribute*), 3
normalize_go_id() (*in module bio2bel_go.manager*), 3
normalize_terms() (*bio2bel_go.manager.Manager method*), 4

P

populate() (*bio2bel_go.manager.Manager method*), 3

S

summarize() (*bio2bel_go.manager.Manager method*), 4

T

to_bel() (*bio2bel_go.manager.Manager method*), 4