Bio2BEL Reactome Documentation

Release 0.2.0

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Contents:

Enrichment

This module contains all enrichment functions that allow to integrate Reactome information in BEL networks.

Manager

Database Manager and query functions

Command Line Interface

The command line interface allows you to communicate with the package and perform basic functions such as:

- Populate the database: `python3 -m bio2bel_reactome populate`. By default this command populates the database only with human information. In order to populate all species pathway information you can add the "–not-only-human" argument. By default the database is reset every time is populated. However, another optional parameter "–reset-db=False", allows you to avoid the reset. More logging can be activated by added "-vv" or "-v" as an argument.

- Drop the database: `python3 -m bio2bel_reactome drop`. More logging can be activated by added "-vv" or "-v" as an argument.

- Export gene sets as an excel file: `python3 -m bio2bel_reactome export`. By default, the excel will contain all pathways from all species. However, you can add the argument "species" and type the name of a particular one to get only those pathways (e.g., "–species='Homo sapiens'""). Since Reactome has a hierarchy pathway structure, you can get only the major pathways with the optional parameter "–top-hierarchy".

Constants

This module contains all the constants used in this package.

Models

Database models.

CHAPTER 6

Web

This module contains the web application to explore the database

Utils

Some various methods used in this package

CHAPTER 8

Indices and tables

- genindex
- modindex
- search