Bio2BEL WikiPathways Documentation

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CHAPTER 1

Manager

Database Manager and useful query methods.

CHAPTER 2

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_wikipathways populate`. 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_wikipathways drop`. More logging can be activated by added "-vv" or "-v" as an argument.
- Export gene sets as an excel file: `python3 -m bio2bel_wikipathways export`.

CHAPTER 3

Models

Database models.

CHAPTER 4

Constants

This module contains all the constants used in this package.

CHAPTER 5

Web

This module contains the web application to explore the database

CHAPTER 6

Indices and tables

- genindex
- modindex
- search