
Bio2BEL WikiPathways Documentation

Release 0.2.4-dev

Daniel Domingo-Fernández and Charles Tapley Hoyt

Nov 20, 2019

Contents:

1	Manager	1
2	Command Line Interface	3
3	Models	5
4	Constants	7
5	Parser	9
6	Web	11
7	Indices and tables	13

CHAPTER 1

Manager

Database Manager and useful query methods.

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

Parser

This module contains all methods that allow to parse the requests to the WikiPathways API

CHAPTER 6

Web

This module contains the web application to explore the database

CHAPTER 7

Indices and tables

- `genindex`
- `modindex`
- `search`