Bio2BEL KEGG Documentation

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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_kegg 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_kegg drop`. More logging can be activated by added "-vv" or "-v" as an rgument.

- Export gene sets as an excel file: `python3 -m bio2bel_kegg export`.

MANAGER

MODELS

FOUR

CONSTANTS

WEB

INDICES AND TABLES

- genindex
- modindex
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