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# **Bio2BEL MSIG Documentation**

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## Command Line Interface

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

- Populate the database: `python3 -m bio2bel_msig 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_msig drop`. More logging can be activated by added “`-vv`” or “`-v`” as an rgument.
- Export gene sets as an excel file: `python3 -m bio2bel_msig export`.



## CHAPTER 2

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Manager

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## CHAPTER 3

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### Models

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## CHAPTER 4

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### Constants

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Constant module. Define here the link of the gene set gmt file to populate the database.



## CHAPTER 5

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Web

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## CHAPTER 6

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### Indices and tables

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