## **Bio2BEL KEGG Documentation**

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**CHAPTER** 

**ONE** 

#### **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.

# CHAPTER TWO

#### **MANAGER**

## CHAPTER THREE

## **MODELS**

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# CHAPTER FOUR

## **CONSTANTS**

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#### CHAPTER

## SIX

## **INDICES AND TABLES**

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