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# **FLUTE**

***Release version 1.0***

**Emilee Holtzapple**

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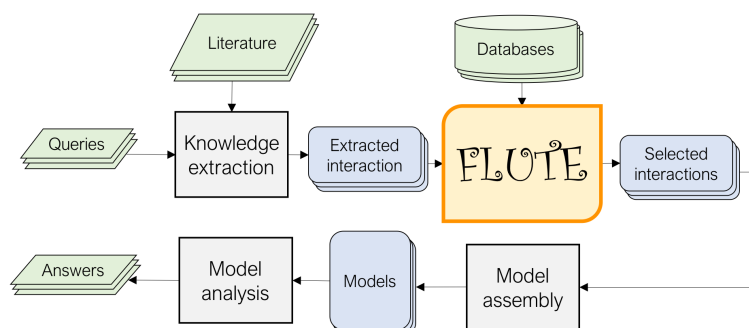
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Understanding disease at the cellular level requires detailed knowledge of signaling networks. To aid in this task, many advances have been made in the field of natural language processing (NLP) to extract signaling events from biomedical literature.

However, even state-of-the-art NLP methods incorrectly interpret some signaling events described in the literature.



The FiLter for Understanding True Events (FLUTE) tool seeks to identify high-confidence signaling events from biomedical NLP output by comparing with existing biological databases. As such, FLUTE can reliably determine the confidence in the biomolecular events extracted by NLP methods and at the same time provide a speedup in event filtering by three orders of magnitude.



## INSTALLATION INSTRUCTIONS

### 1.1 MySQL

1. Download the appropriate distribution of [MySQL](#).
2. Restart your computer and add to path if necessary.
3. From the command line, access the MySQL environment by typing:

```
mysql -u root
```

If the first prompt fails, you may need to enter the password associated with your computer user account:

```
mysql -u root -p
```

3. You may choose to create a local username and password to keep your database private.
4. Install [MySQL Python connector](#).

### 1.2 FLUTE database

1. Un-zip the FLUTE.sql file downloaded from BitBucket.
2. Log in to the MySQL environment using your username and password.
3. From there, create an empty database.
4. Log back out, and again from the command line:

```
mysql -u username -p database_name < FLUTE.sql
```

5. If you created a username and password, this will be your username in the above command, but do not enter your password above! Once you hit enter, it will prompt you for the password.
6. You can now run the “run\_FLUTE.py” script, you will need to enter the database, host, username, etc. as an argument from the command line.





## FLUTE USAGE

1. To filter interactions, run “run\_FLUTE.py”. You must have Python3 installed.

2. **The script takes several parameters:**

- A. MySQL username
- B. MySQL password
- C. Host name - “localhost” for MacOSX, desktop name for Windows
- D. Database name (see step 3 from FLUTE DB installation instructions)
- E. Input filename
- F. Output filename for interactions
- G. Output filename for scores

3. Input files must have the following headers:

Regulated- Name	Regulate- dID	Regulated- Type	Regulator- Name	Regula- torID	Regula- torType	Pa- perID
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4. Output files include list of reading interactions that pass filtration, and the filtration scores for those filtered interactions.



## RUN\_FLUTE

This page describes the script that accesses the FLUTE database. The functions in this module ground element names and check against the FLUTE database.

### 3.1 Functions

**run\_FLUTE.getRelatedPapers**(*db\_user, db\_pass, db\_host, db\_name, prot*)

This function retrieves related papers based on a protein name.

**db\_user: str** Name of the MySQL user where the FLUTE DB is stored.

**db\_pass: str** Password for the MySQL user where the FLUTE DB is stored.

**db\_host: str** Host name for the local machine where the copy of the FLUTE DB is stored.

**db\_name: str** Name of the local copy of the FLUTE DB.

**prot: str** Input protein

Saves a file of related paper IDs

**run\_FLUTE.getRelatedInts**(*db\_user, db\_pass, db\_host, db\_name, f*)

This function retrieves interactions from the same papers as

**db\_user: str** Name of the MySQL user where the FLUTE DB is stored.

**db\_pass: str** Password for the MySQL user where the FLUTE DB is stored.

**db\_host: str** Host name for the local machine where the copy of the FLUTE DB is stored.

**db\_name: str** Name of the local copy of the FLUTE DB.

**f: str** File name of the list of papers

**run\_FLUTE.getRecentPapers**(*f*)

This function should search the OA file and find all interactions occurring in papers less than X years old

**f: str** Input filename that contains list of interactions

None

**run\_FLUTE.getDups**(*f*)

This function calculates the number of occurrences of an interaction in a reading set.

**f: str** Filename of the list of interactions to be counted.

None

**run\_FLUTE.getArgs**()

**run\_FLUTE.convID**(*db\_user, db\_pass, db\_host, db\_name, X*)

This function uses the FLUTE DB to ground interactions

**db\_user: str** Name of the MySQL user where the FLUTE DB is stored.

**db\_pass: str** Password for the MySQL user where the FLUTE DB is stored.

**db\_host: str** Host name for the local machine where the copy of the FLUTE DB is stored.

**db\_name: str** Name of the local copy of the FLUTE DB.

**X: numpy array** Array containing all grounded interactions

**X: numpy array** Grounded interactions

`run_FLUTE.findInts(db_user, db_pass, db_host, db_name, ints, es, ts, ds)`

This function uses the FLUTE DB to filter interactions

**db\_user: str** Name of the MySQL user where the FLUTE DB is stored.

**db\_pass: str** Password for the MySQL user where the FLUTE DB is stored.

**db\_host: str** Host name for the local machine where the copy of the FLUTE DB is stored.

**db\_name: str** Name of the local copy of the FLUTE DB.

**X: numpy array** Array containing all filtered interactions

**X: numpy array** Filtered interactions

`run_FLUTE.uniOnly(allInts)`

This function returns only proteins

**allInts: numpy array** All interactions from the input file

**rel\_ints: numpy array** Protein-protein interactions only

`run_FLUTE.getChem(X)`

This function returns only protein-chemical interactions

**X: numpy array** All interactions from the input file

**X: numpy array** Protein-chemical interactions only

`run_FLUTE.getGo(a)`

This function returns only protein-biological process interactions

**a: numpy array** All interactions from the input file

**a: numpy array** Protein-biological process interactions only

## 3.2 Dependencies

### Python:

[pandas](#) library

[csv](#) module

[numpy](#) library

[MySQL Connector for Python3](#) library

[argparse](#) library [re](#) library

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**CHAPTER  
FOUR**

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**LEGAL**

Add here any information concerning usage, downloads, and repurposing.



## **LICENSING AND FUNDING**

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## INDICES AND TABLES

- `genindex`
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