

# **Mutual Information Analyzer**

## **version 1.0.0**

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### 1. How to install?

There are two ways to install:

- clone the project via github;
- download the project

### 2. How to clone?

Here are the commands to clone MIA project:

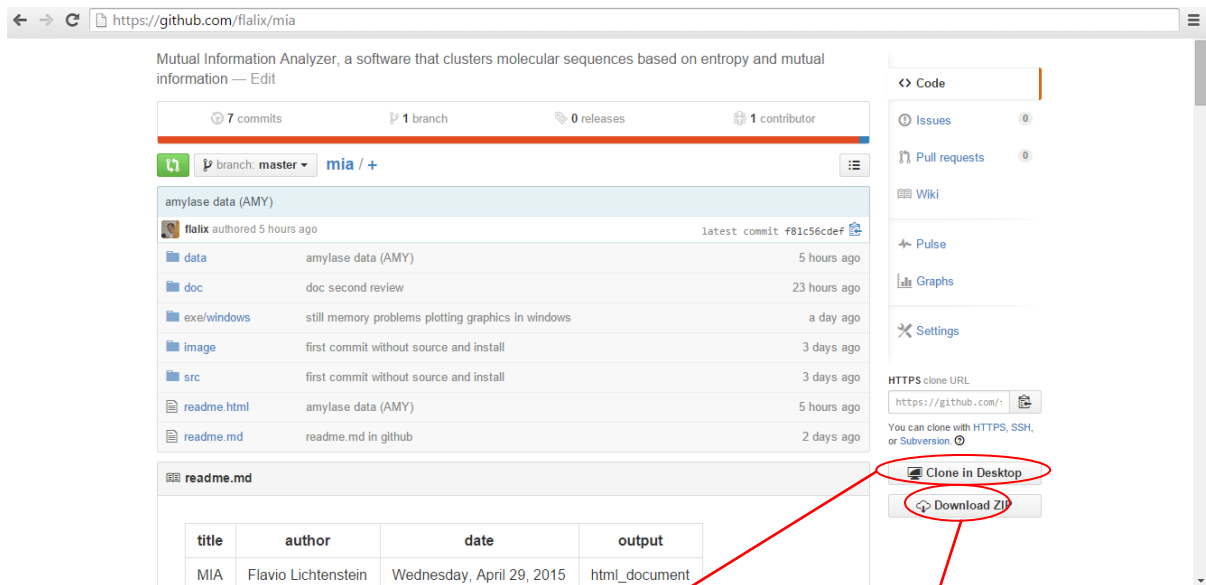
- Install GitHub application
  - for windows: <https://windows.github.com/>
  - for linux give the following command: `sudo apt-get install git`
- Run GitHub and write the following commands:

```
git init
```

```
git clone https://github.com/flalix/mia
```

### 3. How to download?

Go to MIA URL (<https://github.com/flalix/mia>) and click in download



also to clone

to download

- Create a directory:
  - if windows: c:\user\your\_name\mia
  - if linux: ~/mia
- and decompress the zip file here

#### 4. Running MIA

Once cloned or downloaded (and unzipped) MIA archives, you will find the executable file (binary) at:

- if windows: c:\user\your\_name\mia\exe\windows
- if linux: ~/mia/exe/linux

Give a double click in MIA and start it.

## 5. First time at front end and what to do?

If you started MIA correctly this front end will appear:

NCBI Gbk-Fasta Alignment Purging Consensus VMI HMI JSD Cluster Entropy Root

Search Species and Genes in NCBI

Organism: Drosophila - Adh - New Search Delete

Gene list:

Gene: Adh

Species list:

Title:

Database: Nucleotide

Title filters:

|                    |    |     |     |                  |    |     |     |               |    |     |     |
|--------------------|----|-----|-----|------------------|----|-----|-----|---------------|----|-----|-----|
| CDS:               | no | yes | --- | mRNA             | no | yes | --- | Partial CDS:  | no | yes | --- |
| Complete Sequence: | no | yes | --- | Complete Genome: | no | yes | --- | Shotgun:      | no | yes | --- |
| Chromosome:        | no | yes | --- | Contig:          | no | yes | --- | Super-Contig: | no | yes | --- |

Log Gbk Filename: log\_gbk\_Drosophila\_Adh.txt

Output: Drosophila\_Adh.gbk

retmax: 10000

e-mail: xxx@xxx.com

Message:

Could not find C:/Users/Flavio/data/Drosophila/Adh/files/Drosophila\_Adh\_species\_list.txt

Get GBK from NCBI Save Exit Clear

Now you have four alternatives to start your analysis:

1. Click in <Get GBK from NCBI> and you will download all gbk from the organism "Drosophila" and gene "Adh".
2. Change "Adh" to "AMY" and in Gene List write "AMY, AMYREL", and click in <Get GBK from NCBI> and you will analyze a short and interesting sample data.
3. You also may define your own Organism and Gene. If necessary you may define words in Title to find any desired gene-experiment.
4. Another possible way is to see a previous analysis that we did. In mia/data you will find 2 set of samples. One for "Adh" and the other for "AMY".
  - click in "save" and exit the MIA program
  - look for:
    - in windows: c:\user\your\_name\ Drosophila \data
    - in linux: ~/Drosophila/data
  - you will find /data/Adh
  - create also /data/AMY
  - go to your clone/download directory and find data/adh and data/AMY
  - copy each fasta.rar and files.rar to its respective directory
  - decompress and you will find:
    - ../ Drosophila/ data /Adh/fasta
    - ../ Drosophila/ data/Adh/files
    - both directories have files inside
  - in mia/data you will find "default.ini", overwrite it in ../ Drosophila/ data

- find again MIA executable (binary) and restart it
- in the first combo box you will find " Drosophila - Adh" and " Drosophila - AMY".
- choose one of these options
- jump (click) in VMI, or HMI, or JSD or Cluster tab and see the results
- any other information search in the MIA manual, please