Mutual Information Analyzer

How to install?

version 1.0.0

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DIS - Bioinformatics

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Summary

1.   How to install?

There are two ways to install:

- clone the project via github;
- download the project

2.   How to clone?
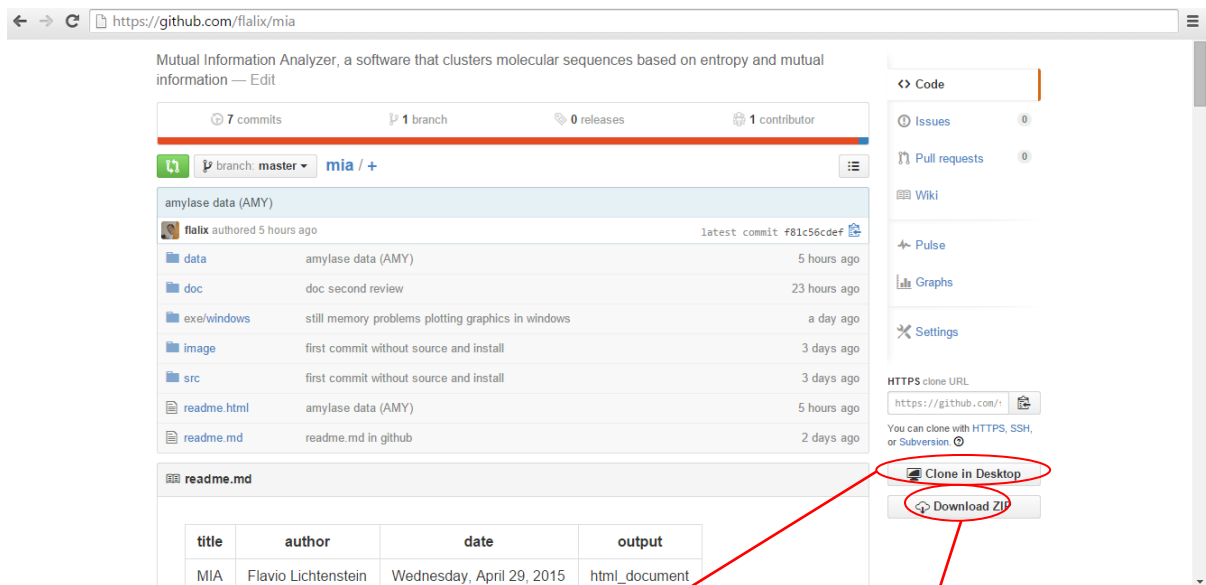
Here are the commands to clone MIA project:

- 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 in Windows:

cd c:\\Users\\your_name

md mia

- and decompress the zip file here

- Create a directory in <u>Linux</u>:

cd ~

mkdir 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:

- in Windows: c:\Users\your_name\mia\exe\windows
- n 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:

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 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 by NCBI titles.
4. Another possible way is to get Adh or AMY gene data already analyzed. 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
   - go to your clone/download directory and find data/Adh and data/AMY:
     - in windows: clone_dir\data\Drosophila
     - in linux: clone_dir /data/Drosophila
   - you will find …/data/Drosophila /Adh
   - and also …/data/Drosophila /AMY

   - copy each fasta.rar and files.rar to to the Adh root (ou AMY) .../data/Drosophyla/Adh:
   - decompress and you will observe data at:
     - .../data/ Drosophila/ data /Adh/fasta
     - …/data / Drosophila/ data/Adh/files

- both directories have ASCII files inside
- in mia/data you will find "default.ini", overwrite it in ../Drosophila/data default.ini form the clone directory (to get access to AMY in MIA).
- find again MIA executable (binary) and restart it
- in the first combo box you will find " Drosophila - Adh" and the second "Drosophila - AMY" if you have copied "default .ini" correctly.
- then choose one of these options:
  - jump (click) in VMI, or HMI, or JSD or Cluster tab and see the results (don't save neither recalculate again, reset the check buttons).
  - any other information access MIA manual, please