

# Manual

## RNAplonc: A tool for identification of plant long non-coding RNAs.

### Pipeline

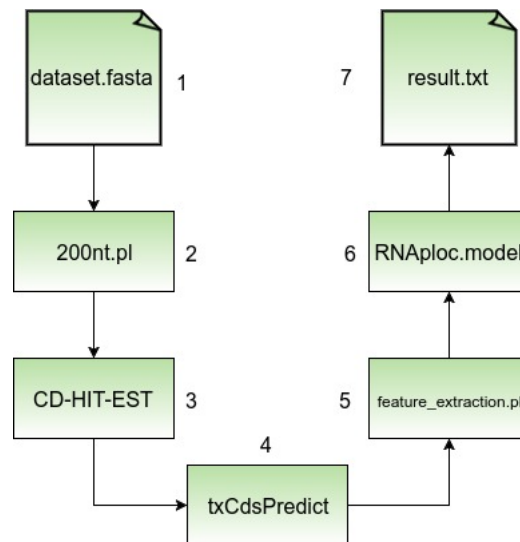


Figura 1:

Before to start, it is necessary to install CD-HIT-EST and txCdsPredict. After, it just unzips the RNAplonc.zip.

**PS:** path is the location of the RNAplonc folder.

## 1 - dataset.fasta

**Input of data:** The input sequences must be in fasta format, according to the model below:

```
>12345xyz this is a nice sequence of the Foo gene
atgcatgataggactatttttttttctactaccatcaccncacttaaagcatgggcggatttacta
>12345xyz this is a nice sequence of the Foo gene
atgcatgataggactatttttttttctactaccatcaccncacttaaagcatgggcggatttacta
```

## 2 - 200nt.pl

The 200nt.pl file, compacted in RNAPlonc.zip in the download section, will be executed to remove sequences smaller than 200 nucleotides.

Open the command terminal (Ctrl + Alt+ t)

**Command to execute:** perl path/200nt.pl path/file.fasta

**OBS: path = Path of the file**

The output file will have the same name as the input file with \_ at the end, eg. dataset\_.fasta

## 3 - CD-HIT-EST

The CD-HIT-EST program is presented in the download section. Your installation is explained in the install section. Its execution is a little slow, due to it removes all sequences with similarity of 80%.

It will run with the file resulting from step 2.

**Command to execute:** cd path

```
./cd-hit-est -i dataset_.fasta -o result.fasta -c 0.8
```

-i = Name of the input file from step 2

-o = Output file name

-c = Percentage cut used of 80% similarity

The output file will have the name you put after the -o

## 4 - txCdsPredict

The txCdsPredict program is presented in the download section. Your installation is explained in the install section.

The file resulting from step 3 (result.fasta) will be entered in the txCdsPredict

**Command to execute:** cd path/kentUtils/src/hg/txCds/txCdsPredict/

./txCdsPredict result.fasta result.cds

result.fasta = Name of the output file from step 3 - CD-HIT-EST

result.cds = Output file name

## 5 - feature\_extraction.pl

The entry in this step 5 will be the resulting files of steps 3 will be the results files of steps 3 - CD-HIT-EST and 4 - txCdsPredict

**Command to execute:** perl feature\_extraction.pl result.fasta result.cds >result.arff

result.fasta = Name of the output file from step 3 - CD-HIT-EST

result.cds = Name of the output file from step 4 - txCdsPredict

The output file will have the extension .arff

## 6 - RNAploc.model

The entry in this step 6 is the resulting file from step 5 - feature\_extraction.pl

**Command to execute:** java -Xmx10G -cp path/weka.jar weka.classifiers.trees.J48 -l path/RNAploc.model -T path/result.arff -p 0 >resultado\_end.txt

The file weka.jar is in the download section in the compressed file RNAploc.zip

## 7 - result

RNAploc.model file results from step 6

>resultado\_end.txt final result

**Any questions please contact us.**