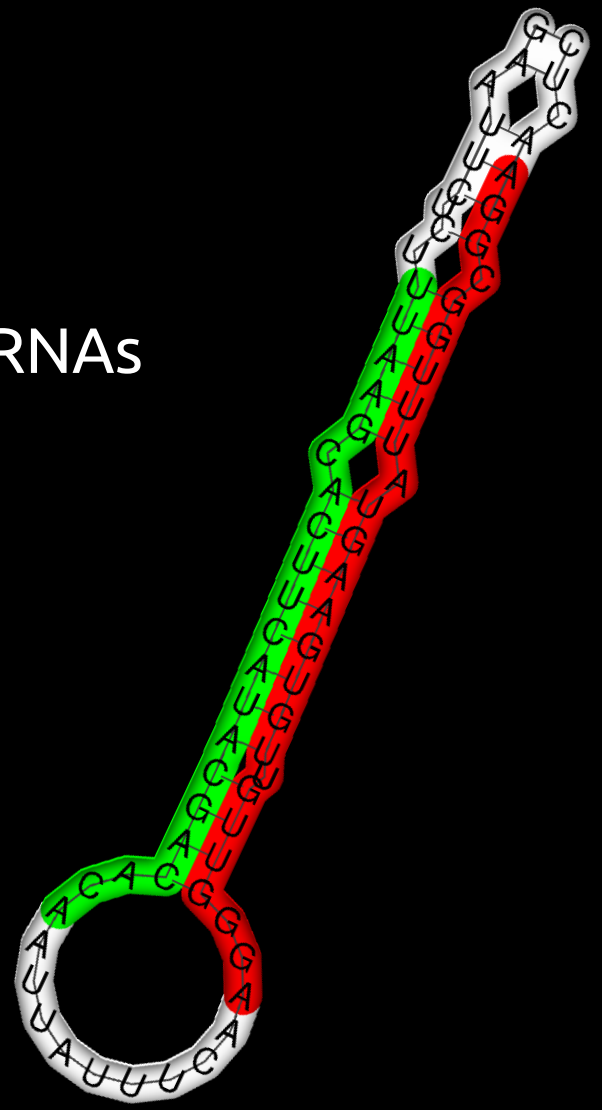
pre-miRNA-plot

quick and easy tool for generating images of pre-miRNAs



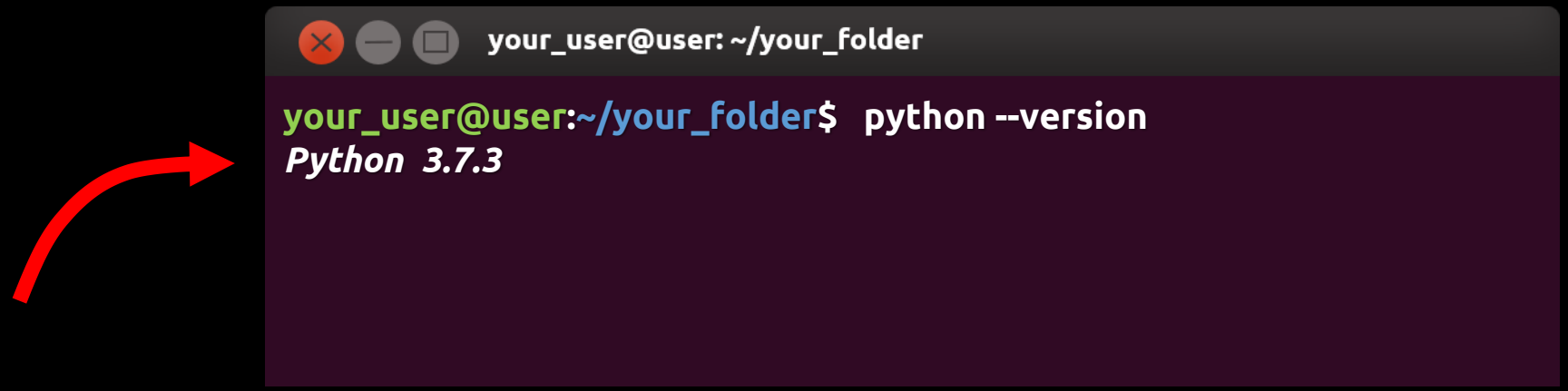
Genomics and Plant Population Laboratory
Federal University of Rio Grande do Sul (UFRGS) - Brazil
Contact: igorpaim8@gmail.com

1. **Configuration**
    1.1 Python
    1.2 Matplotlib
    1.3 Ghostscript
    1.4 Vienna RNA package
2. **Installation**
3. **How to use**
    3.1 Input files
    3.2 Installation
    3.2 Exploring the parameters

1. Configuration

1.1 Python

Pre-miRNA-plot runs in Python3.5+. You can check which version of Python you have installed in your machine with the command bellow; anything 3.5 or higher should work just fine.

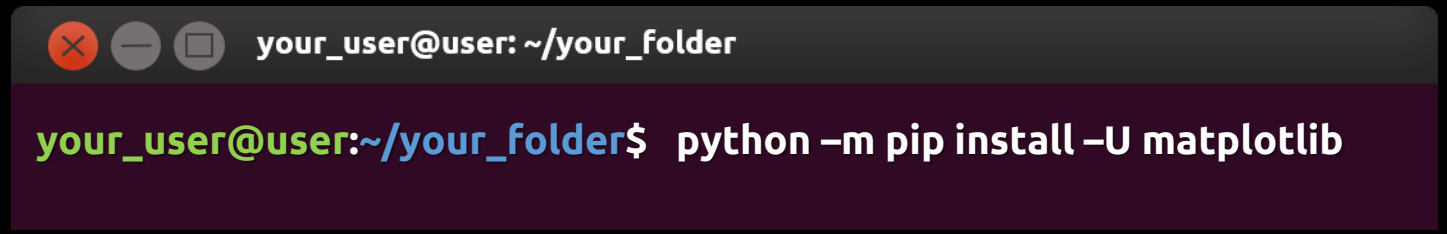


In case you have an older version, you can go to the Python website (https://www.python.org/downloads/) and follow their tutorial to update the platform to a more recent release.

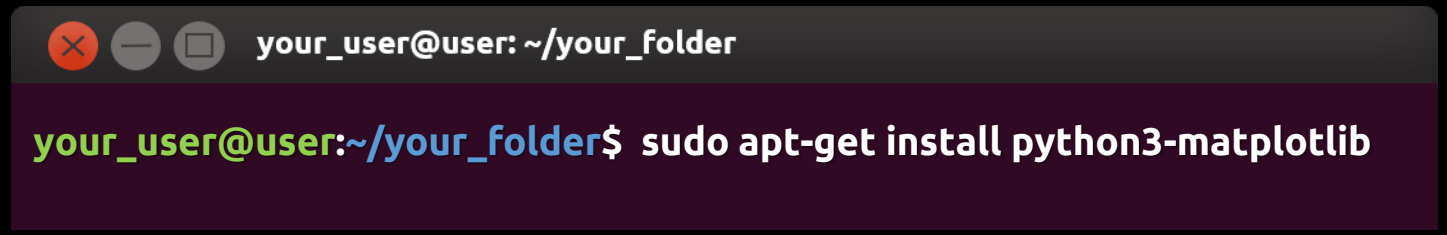
1. Configuration

1.1 Matplotlib

Matplotlib is a graphing package for Python; pre-miRNA-plot uses it to generate diferente plots. You can install it using the pip Python package manager.



If you don't have pip installed, you can use apt instead.



If you are having trouble, please visit https://matplotlib.org/3.1.1/users/installing.html for more details.

1. Configuration

1.2 Ghostscript

Ghostscript is used to convert the Postscript files (.ps) to Portable Network Graphics images (.png). If you do not have it installed, we have to download the tar ball file containing the program, decompress it and then compile it.

```
your_user@user: ~/your_folder
your_user@user:~/your_folder$ wget https://github.com/ArtifexSoftware/ghostpdl-downloads/releases/download/gs927/ghostscript-9.27.tar.gz
<output>
your_user@user:~/your_folder$ tar xvzf ghostscript-9.27.tar.gz
<output>
your_user@user:~/your_folder$ cd ghostscript-9.27/
your_user@user:~/your_folder/ghostscript-9.27$ ./configure
<output>
your_user@user:~/your_folder/ghostscript-9.27$ make
<output>
your_user@user:~/your_folder/ghostscript-9.27$ sudo make install
```

1. Configuration

1.3 Vienna RNA package

Vienna RNA package contains RNAfold and RNAplot, used to predict the secondary structure of the pre-miRNA and to "costumize" it, respectively. You can visit their website to have more details and get to know more about this amazing package.

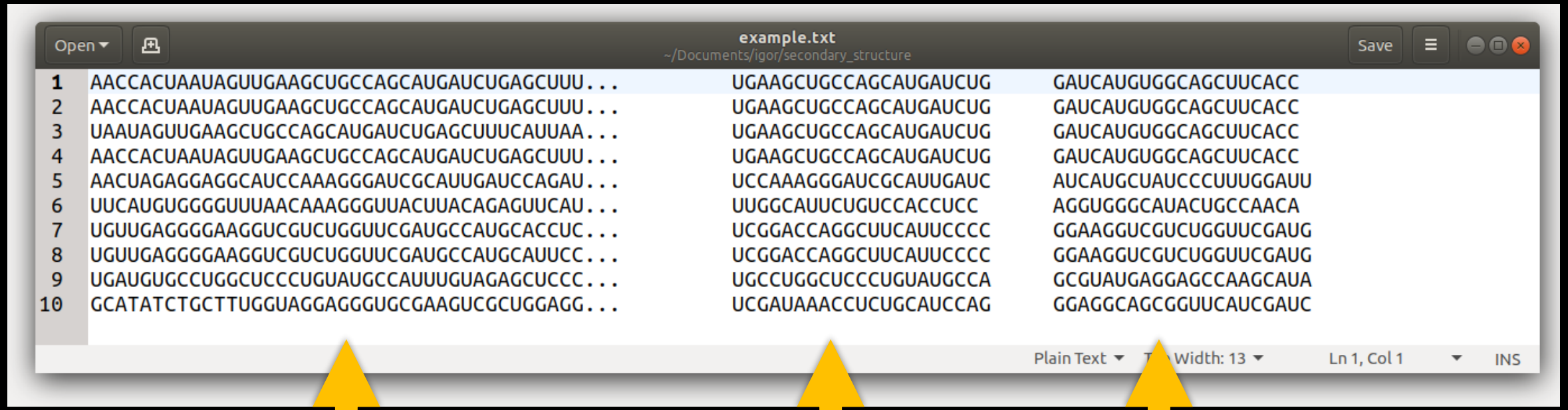
your_user@user: ~/your_folder

```
your_user@user:~/your_folder$ wget https://www.tbi.univie.ac.at/RNA/download/sourcecode/2_4_x/ViennaRNA-2.4.13.tar.gz
<output>
your_user@user:~/your_folder$ tar xvzf ViennaRNA-2.4.13.tar.gz
<output>
your_user@user:~/your_folder$ cd ViennaRNA-2.4.13/
your_user@user:~/your_folder/ViennaRNA-2.4.13$ ./configure
<output>
your_user@user:~/your_folder/ViennaRNA-2.4.13$ make
<output>
your_user@user:~/your_folder/ViennaRNA-2.4.13$ sudo make install
```

2. How to use

2.1 Input files

To use pre-miRNA-plot, your input files should look like this:

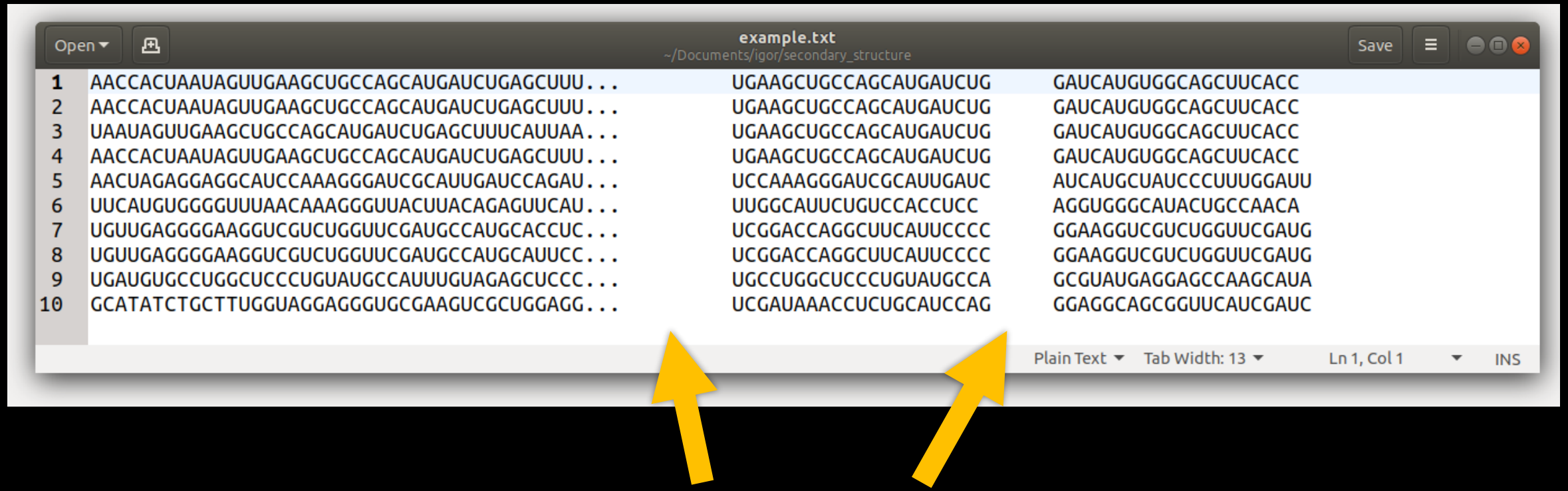


pre-miRNA sequence **miRNA sequence** **another miRNA seq.**

2. How to use

2.1 Input files

To use pre-miRNA-plot, your input files should look like this:



Each data column should be separated by tabs (\t)

2. How to use

2.1 Input files

You can also add some label/annotation to the input file, necessarly on the first column

Open ▾ | example.txt — ~/Documents/igor/secondary_structure | Save

1	pre-mir1	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
2	pre-mir2	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
3	pre-mir3	UAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUUCAUUAA...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
4	pre-mir4	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
5	pre-mir5	AACUAGAGGAGGCAUCCAAAGGGAUCGCAUUGAUCCAGAU...	UCCAAAGGGAUCGCAUUGAUC	AUCAUGCUAUCCCUUUGGAUU
6	pre-mir6	UUCAUGUGGGGUUUAACAAAGGGUUACUUACAGAGUUCAU...	UUGGCAUUCUGUCCACCUCC	AGGUGGGCAUACUGCCAACA
7	pre-miR7	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACCUC...	UCGGACCAGGCUUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG
8	pre-miR8	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCAUUCC...	UCGGACCAGGCUUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG
9	pre-mir9	UGAUGUGCCUGGCUCCCUGUAUGCCAUUUGUAGAGCUCCC...	UGCCUGGCUCCCUGUAUGCCA	GCGUAUGAGGAGCCAAGCAUA
10	pre-mir10	GCATATCTGCTTUGGUAGGAGGGUGCGAAGUCGCUGGAGG...	UCGAUAAACCUCUGCAUCCAG	GGAGGCAGCGGUUCAUCGAUC

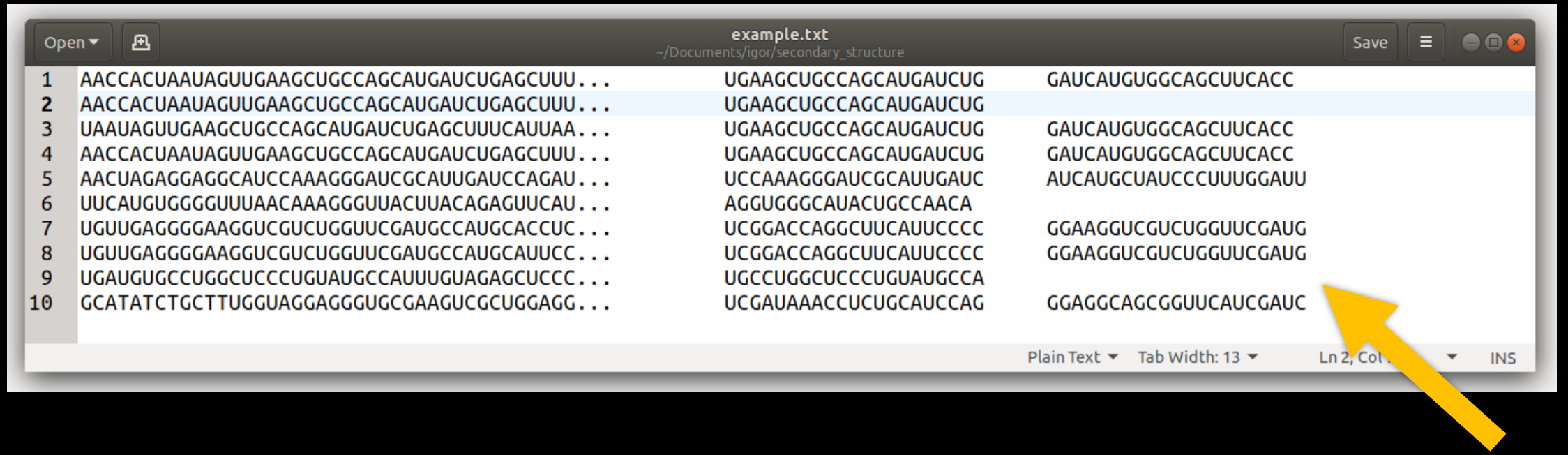
Plain Text ▾ | Tab Width: 13 ▾ | Ln 1, Col 13 ▾ | INS

Label/annotation

2. How to use

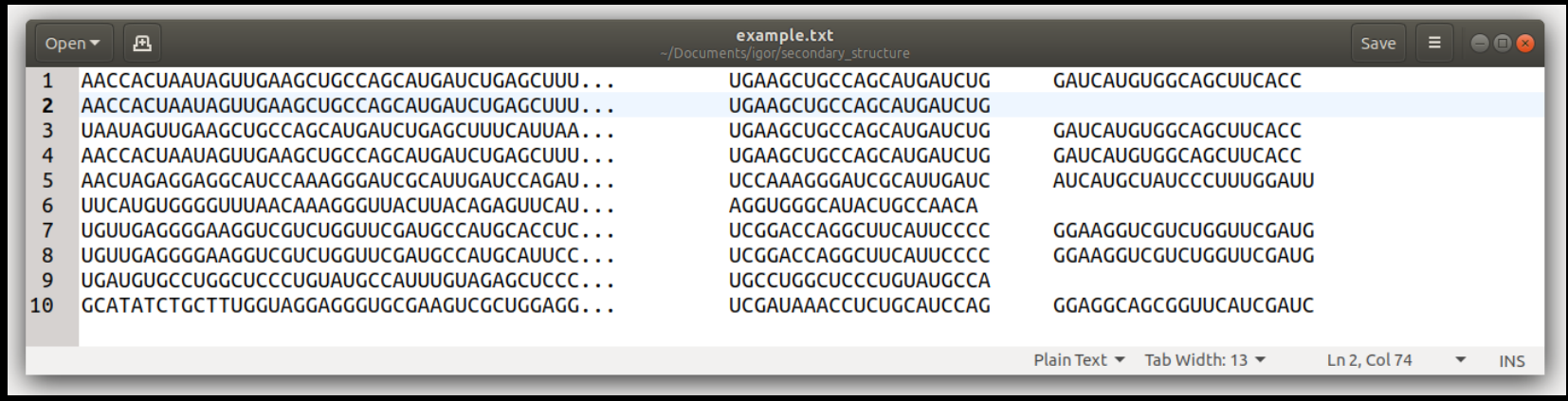
2.1 Input files

Also, you can have data where you have just one of the miRNA sequences:



2. How to use

2.1 Running

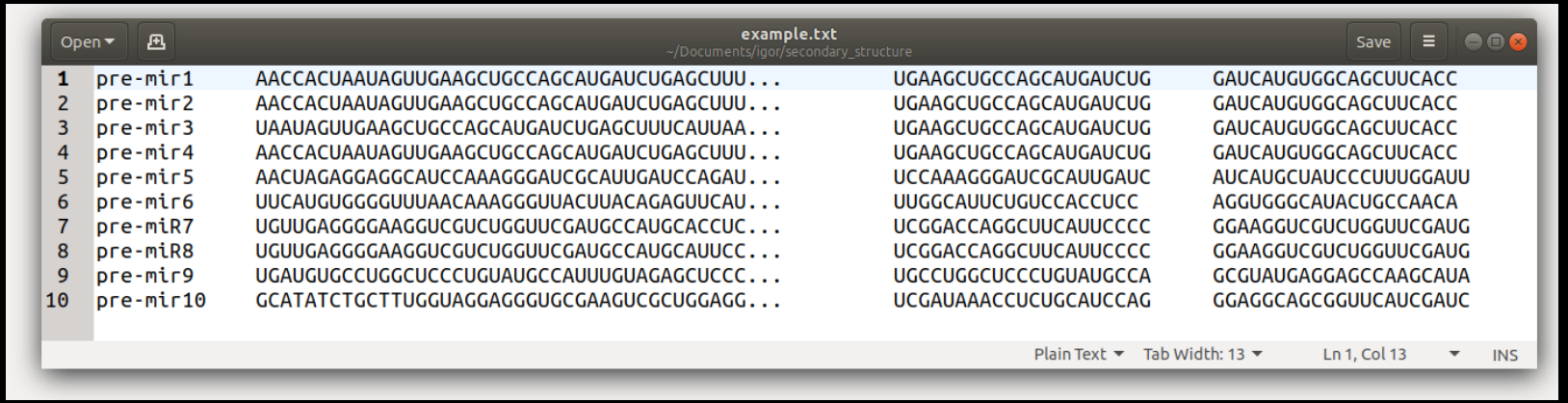


To run pre-miRNA-plot with simple files you can use:

```
python premirnaplot.py file1.txt

python premirnaplot.py file1.txt file2.txt file3.txt ...

python premirnaplot.py -i file1.txt file2.txt

python premirnaplot.py --input file1.txt file2.txt
```

2. How to use

2.1 Running

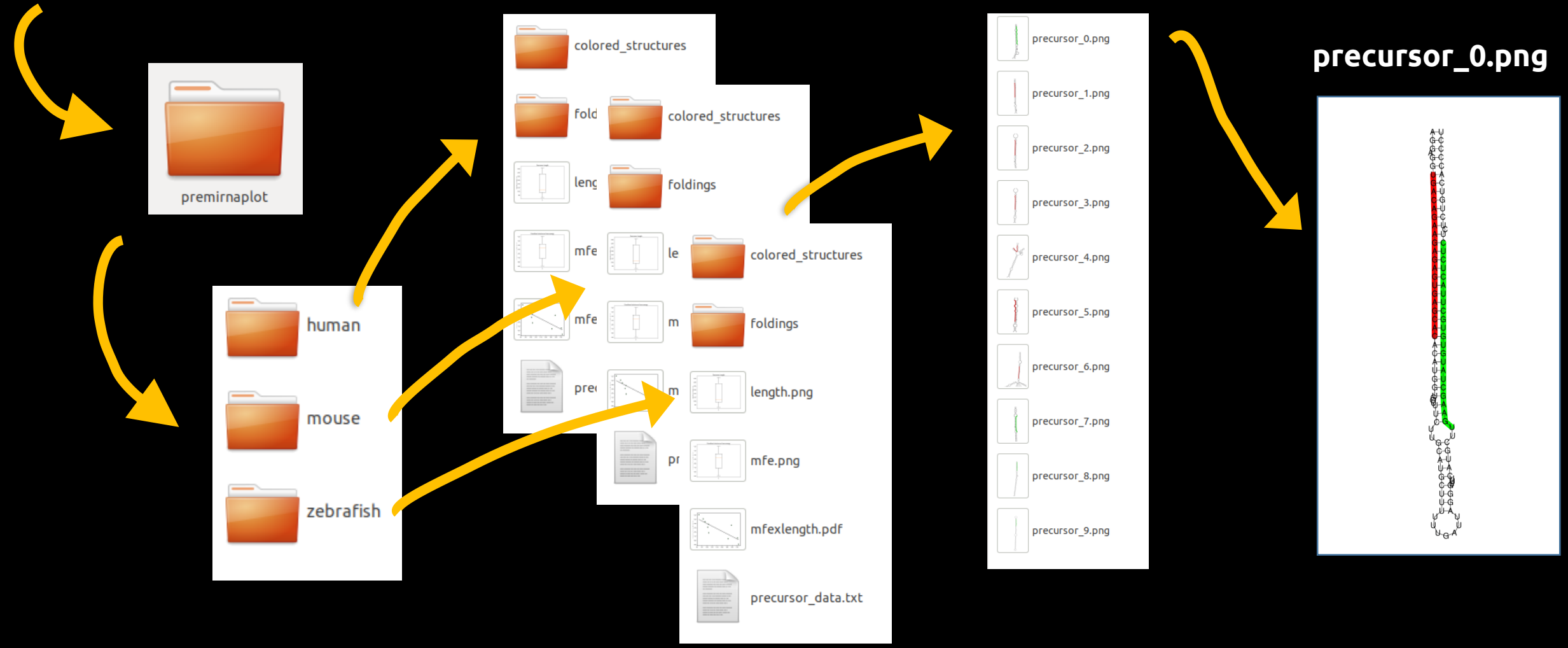


If you have labels in your input, you have to use the parameter “–a” as True:

```
python premirnaplot.py file1.txt –a T

python premirnaplot.py file1.txt file2.txt file3.txt ... –a T

python premirnaplot.py -i file1.txt file2.txt –a T

python premirnaplot.py --input file1.txt file2.txt --annotation T
```

The basic workflow of pre-miRNA-plot:

python premirnaplot.py human.txt mouse.txt zebrafish.txt ...



The basic workflow of pre-miRNA-plot:

python premirnaplot.py human.txt mouse.txt zebrafish.txt ... –a T

2. How to use

2.1 Exploring the parameters

You can choose which colors will be used to highlight the 5p and 3p miRNAs, respectively. You can use predefined colors' names or specify the RGB codes corresponding to the colors. There is no problem if you have just one color. By default, the sequences will be colored red (5p) and green (3p).

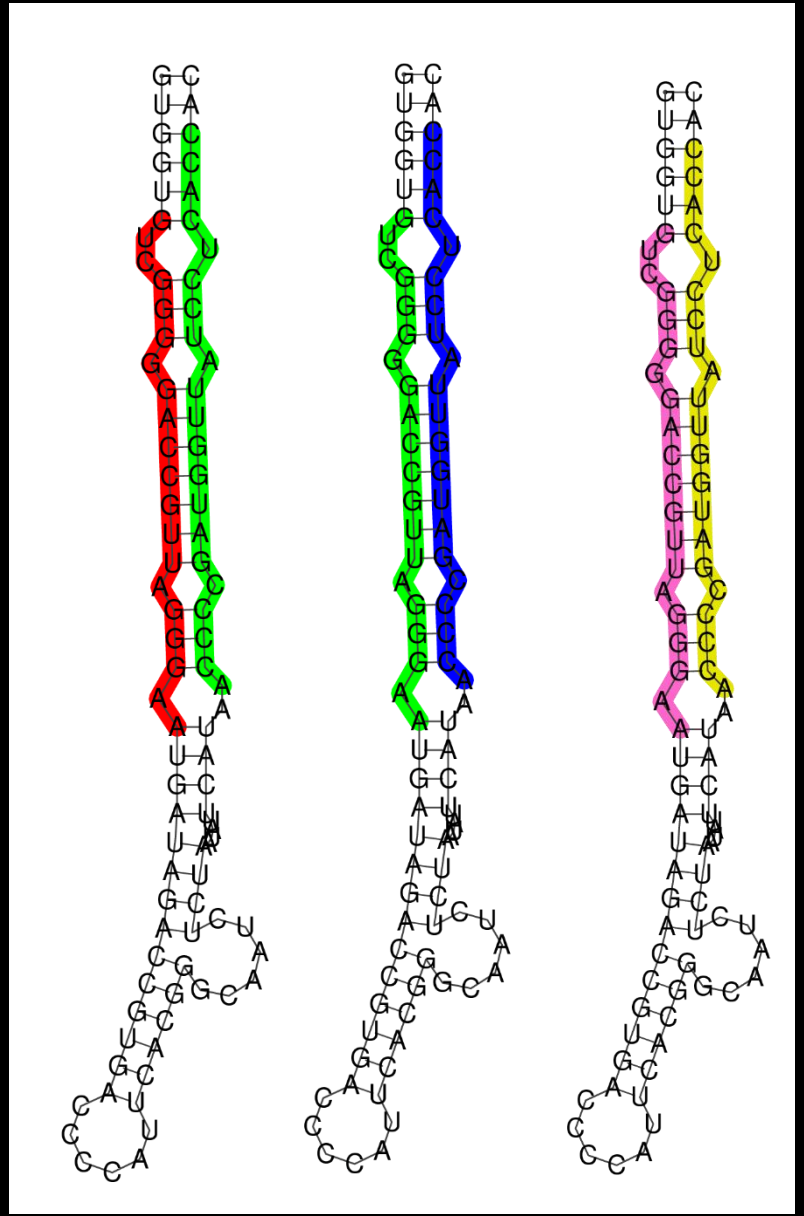
1 python premirnaplot.py file1.txt

2 python premirnaplot.py file1.txt –c green blue

3 python premirnaplot.py file1.txt –c 255 102 204 230 230 0

Default colors are: green, black, red, blue, white

You can choose colors and get their RGB codes in this website



1 2 3

2. How to use

2.1 Exploring the parameters

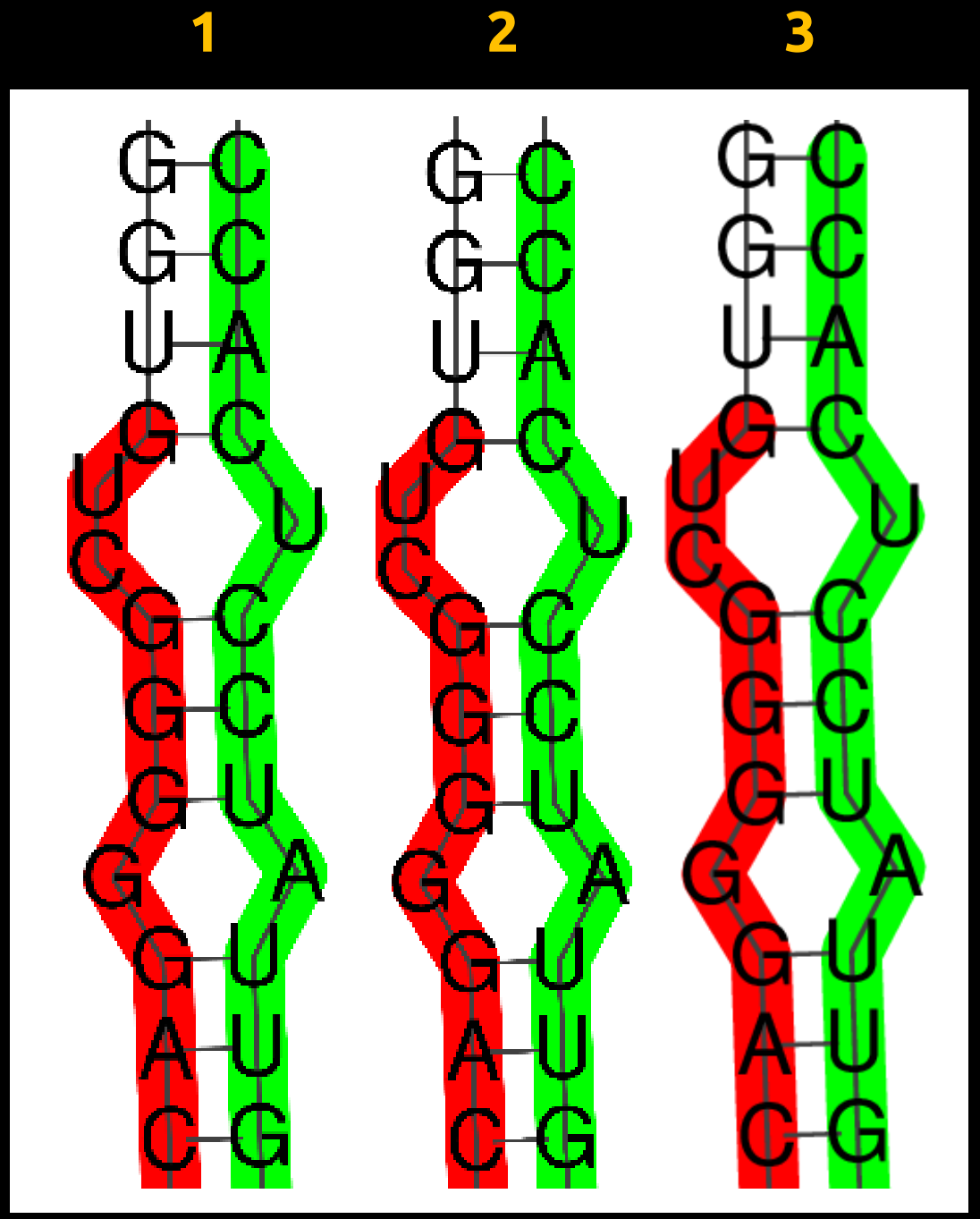
You can also choose the quality of the images, the default is 200 pixels. You can increase this value for better images for publications, for example, but be aware that this increases the program execution time.

1 python premirnaplot.py file1.txt –q 200

2 python premirnaplot.py file1.txt –q 800

3 python premirnaplot.py file1.txt –q 1200

A superzoom in the image can reveal the resolution increase effect.



That’s it! (for now)

Hope you enjoy our program.

Please cite us as: ... (link?)

Any doubts, suggestions or issues, contact us at igorpaim8@gmail.com or comment in our github repository.