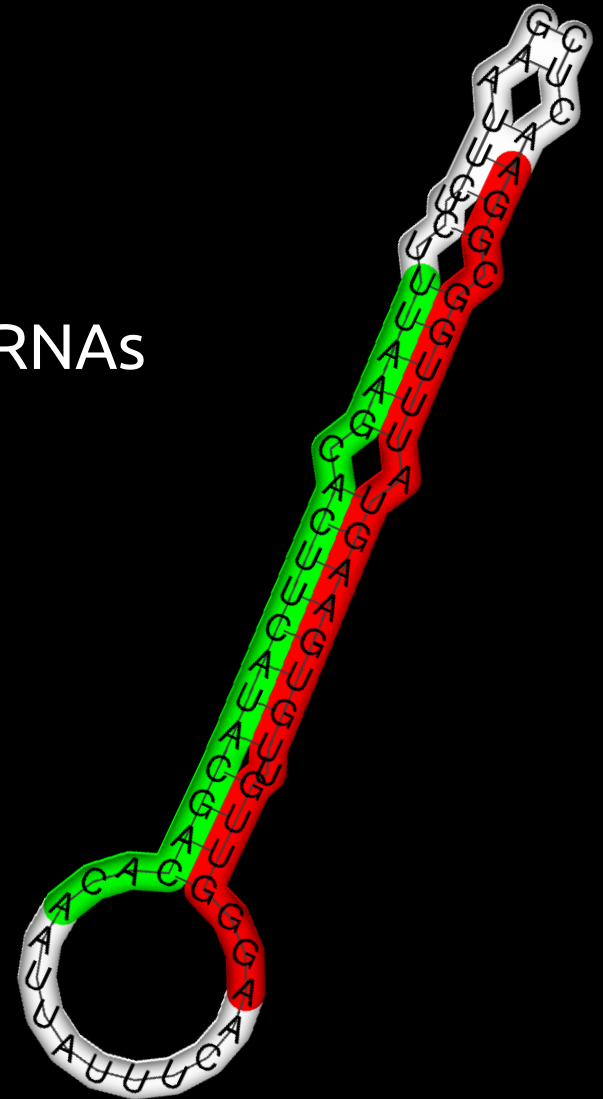


pre-miRNA-plot

quick and easy tool for generating images of pre-miRNAs

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1. Configuration

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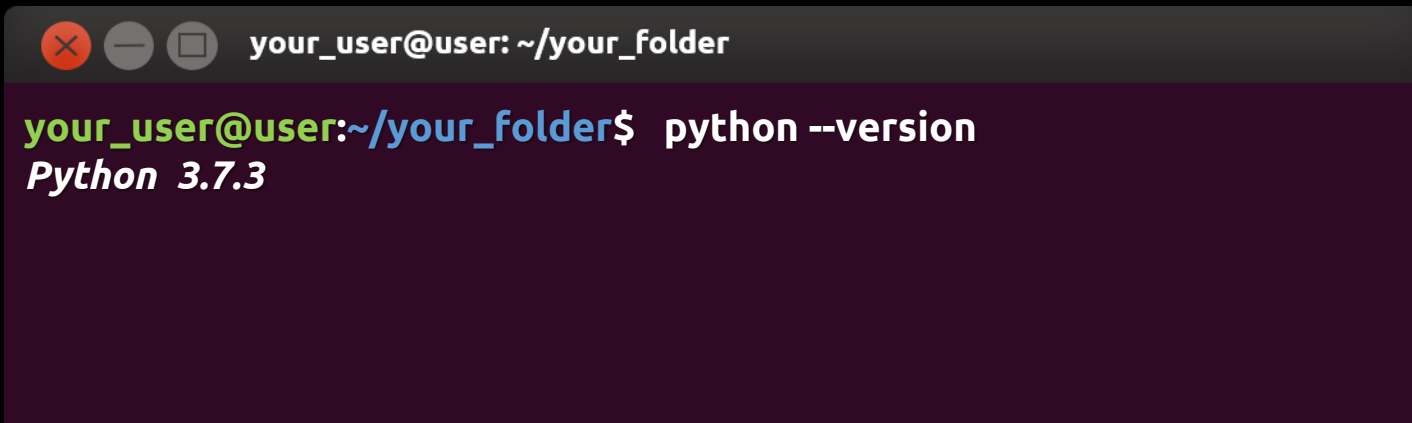
3.2 Installation

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.



A terminal window with a dark background and light text. The title bar shows 'your_user@user: ~/your_folder'. The prompt is 'your_user@user:~/your_folder\$' and the command entered is 'python --version'. The output is 'Python 3.7.3'. A red curved arrow points from the left towards the terminal window.

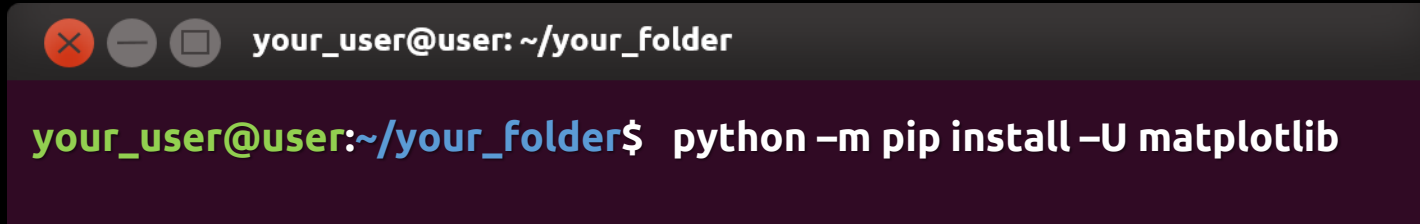
```
your_user@user: ~/your_folder
your_user@user:~/your_folder$ python --version
Python 3.7.3
```

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

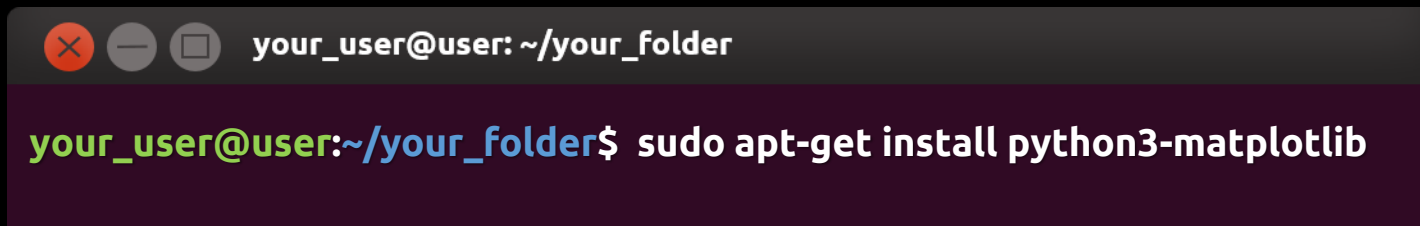
1.1 Matplotlib

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

A terminal window with a dark background. The title bar shows a red close button, a grey minimize button, and a grey maximize button, followed by the text 'your_user@user: ~/your_folder'. The terminal content shows a green prompt 'your_user@user:~/your_folder\$' followed by the command 'python -m pip install -U matplotlib' in white text.

```
your_user@user: ~/your_folder  
your_user@user:~/your_folder$ python -m pip install -U matplotlib
```

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

A terminal window with a dark background. The title bar shows a red close button, a grey minimize button, and a grey maximize button, followed by the text 'your_user@user: ~/your_folder'. The terminal content shows a green prompt 'your_user@user:~/your_folder\$' followed by the command 'sudo apt-get install python3-matplotlib' in white text.

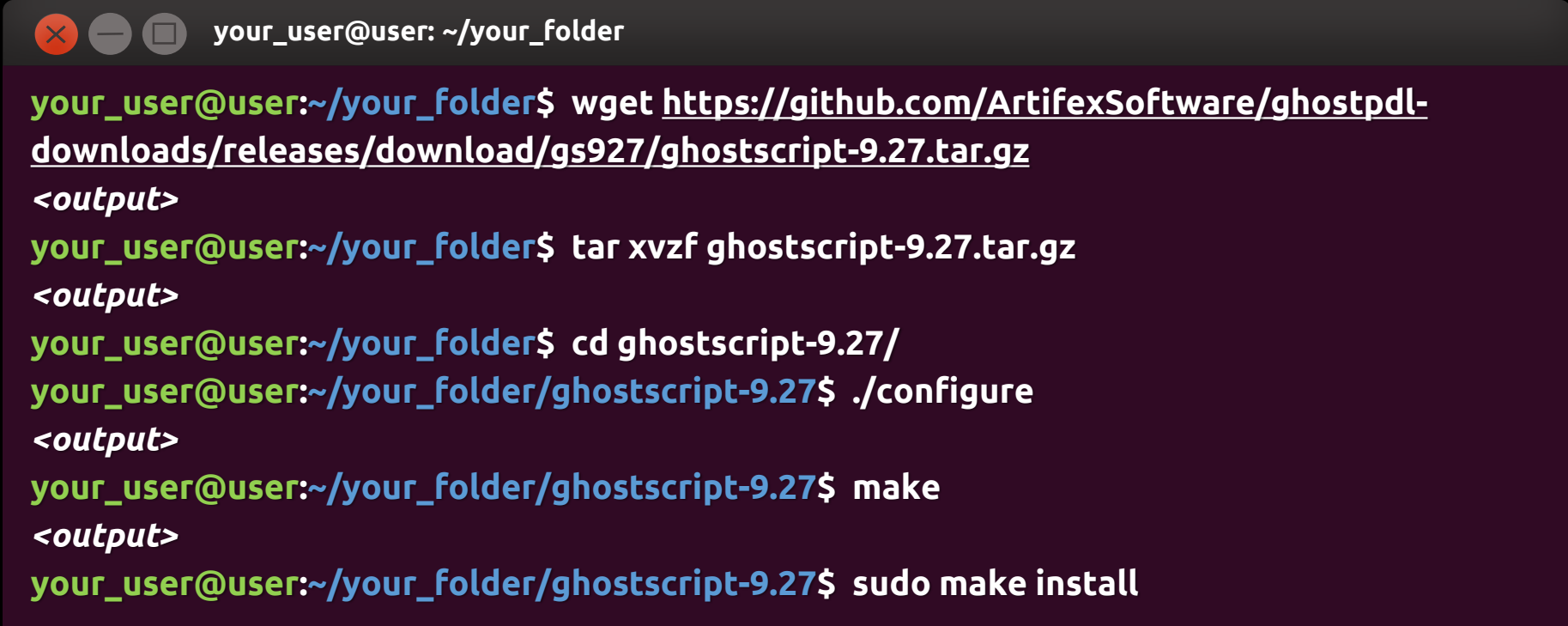
```
your_user@user: ~/your_folder  
your_user@user:~/your_folder$ sudo apt-get install python3-matplotlib
```

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.



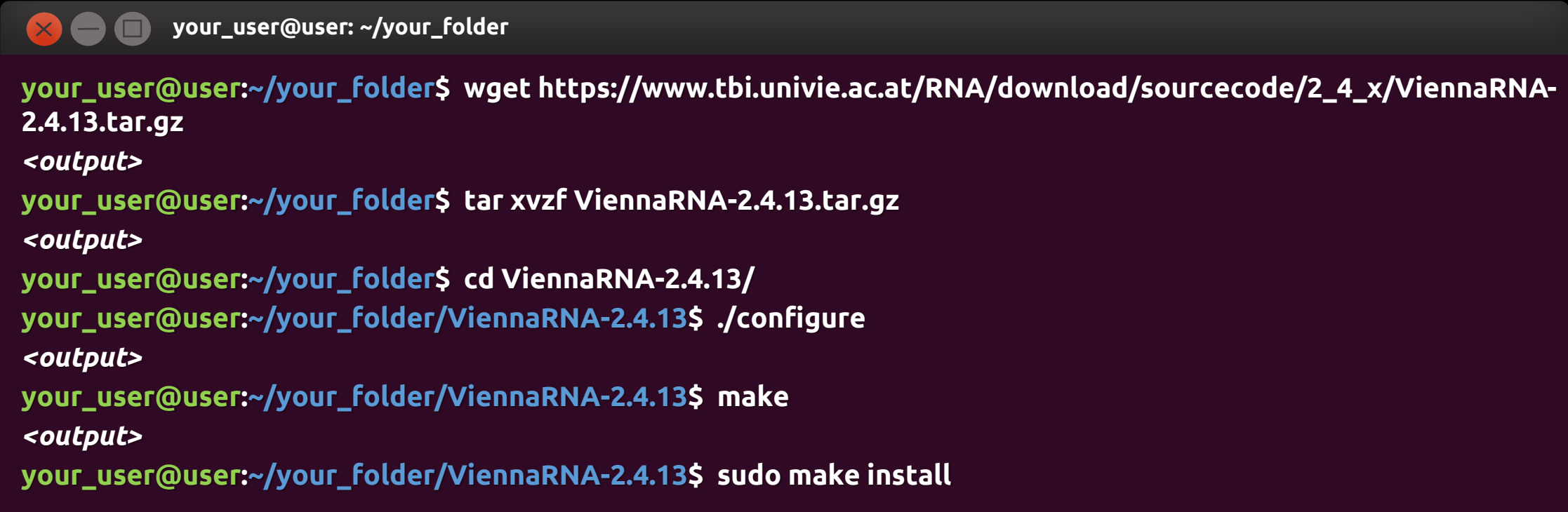
```
your_user@user: ~/your_folder

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 “customize” it, respectively. You can visit their [website](#) to have more details and get to know more about this amazing package.



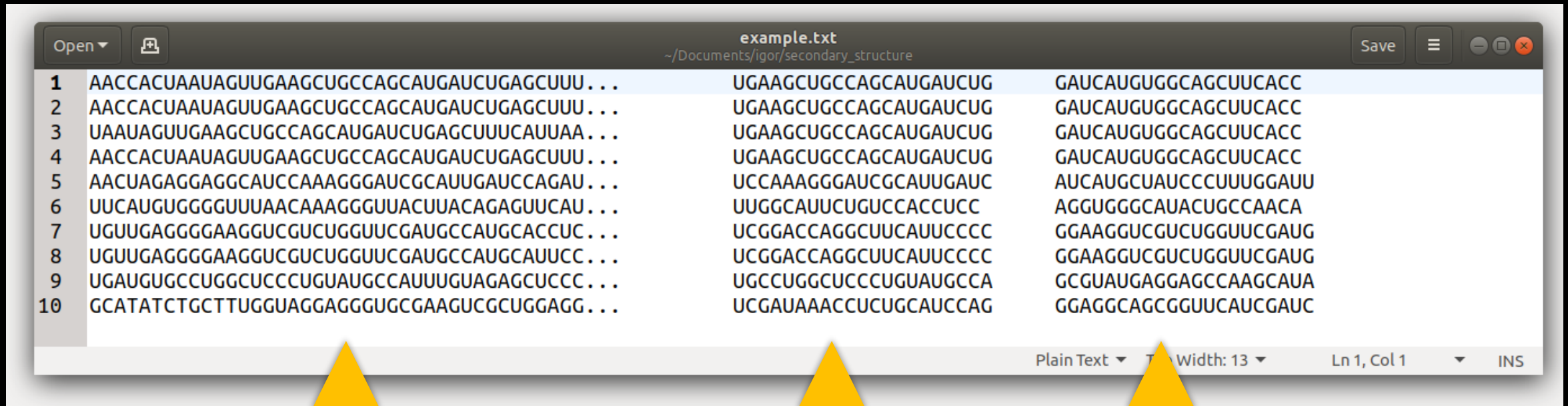
```
your_user@user: ~/your_folder

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:



```
example.txt
~/Documents/igor/secondary_structure

1 AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU... UGAAGCUGCCAGCAUGAUCUG GAUCAUGUGGCAGCUUCACC
2 AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU... UGAAGCUGCCAGCAUGAUCUG GAUCAUGUGGCAGCUUCACC
3 UAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUUUCAUUA... UGAAGCUGCCAGCAUGAUCUG GAUCAUGUGGCAGCUUCACC
4 AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU... UGAAGCUGCCAGCAUGAUCUG GAUCAUGUGGCAGCUUCACC
5 AACUAGAGGAGGCAUCCAAAGGGAUCGCAUUGAUCCAGAU... UCCAAAGGGAUCGCAUUGAUC AUCAUGCUAUCCCUUUGGAUU
6 UUCAUGUGGGGUUUAACAAAGGGUACUUCAGAGUUCAU... UUGGCAUUCUGUCCACCUC AGGUGGGCAUACUGCCAACA
7 UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACCUC... UCGGACCAGGCUUCAUUC CCC GGAAGGUCGUCUGGUUCGAUG
8 UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCAUUC... UCGGACCAGGCUUCAUUC CCC GGAAGGUCGUCUGGUUCGAUG
9 UGAUGUGCCUGGCUCUCCUGUAUGCCAUUUGUAGAGCUCCC... UGCCUGGCUCUCCUGUAUGCCA GCGUAUGAGGAGCCAAGCAUA
10 GCATATCTGCTTUGGUAGGAGGGUGCGAAGUCGCUGGAGG... UCGAUAAACCUCUGCAUCCAG GGAGGCAGCGGUUCAUCGAUC
```

pre-miRNA sequence

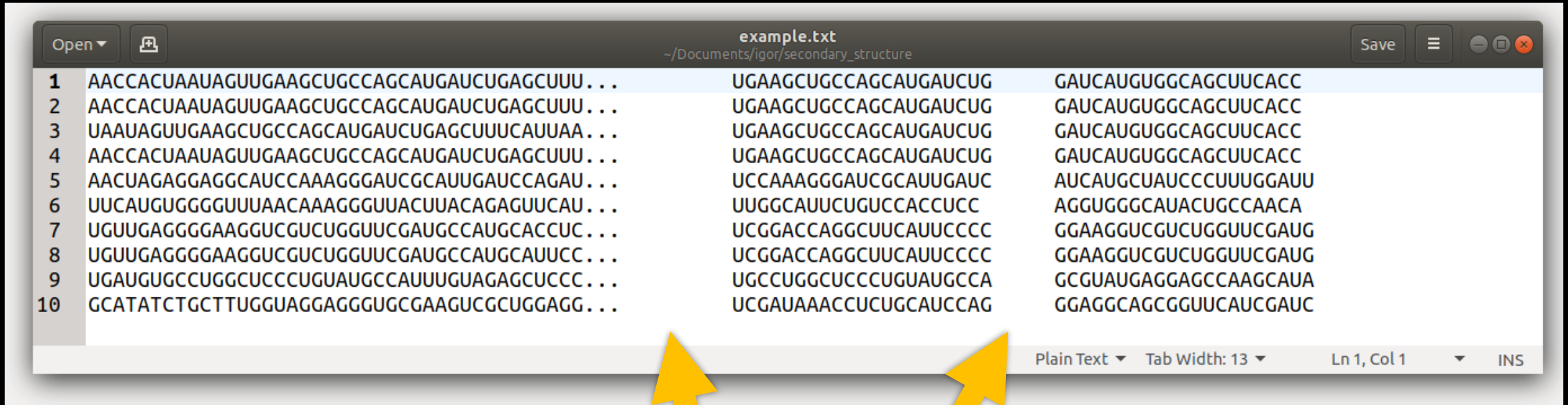
miRNA sequence

another miRNA seq.

2. How to use

2.1 Input files

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



The screenshot shows a text editor window titled "example.txt" with the path "~/Documents/igor/secondary_structure". The editor contains a table with 10 rows and 3 columns of RNA sequence data, separated by tabs. Two yellow arrows point to the tab characters between the columns. The status bar at the bottom indicates "Plain Text", "Tab Width: 13", and "Ln 1, Col 1".

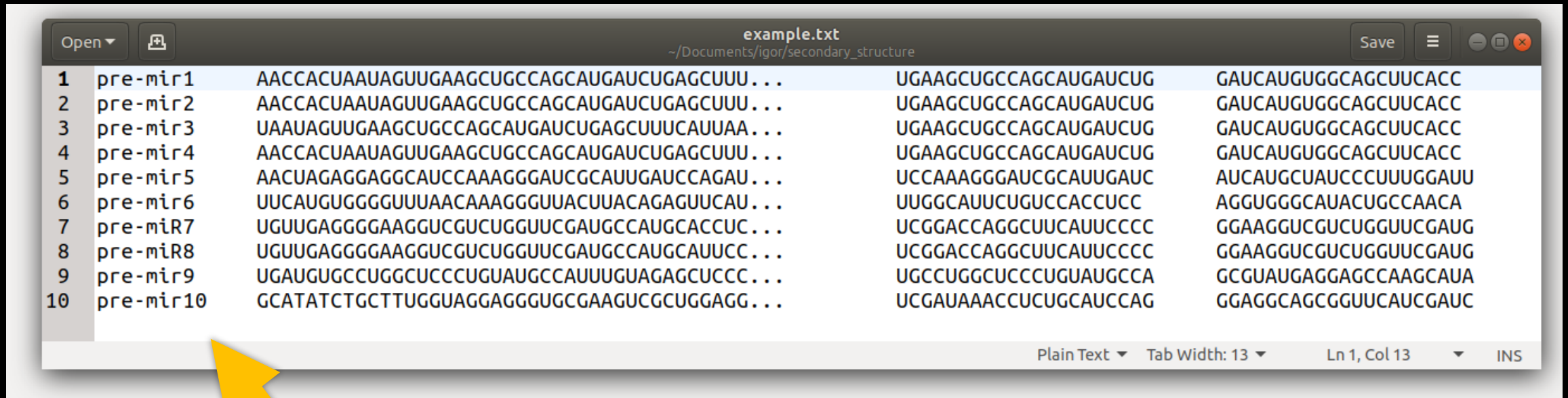
1	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
2	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
3	UAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUUUCAUUA...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
4	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
5	AACUAGAGGAGGCAUCCAAAGGGAUCGCAUUGAUCCAGAU...	UCCAAAGGGAUCGCAUUGAUC	AUCAUGCUAUCCCUUUGGAUU
6	UUCAUGUGGGGUUUAACAAAGGGUACUUCAGAGUUCAU...	UUGGCAUUCUGUCCACCUC	AGGUGGGCAUACUGCCAACA
7	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACCUC...	UCGGACCAGGCUUCAUUC	GGAAGGUCGUCUGGUUCGAUG
8	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCAUUC...	UCGGACCAGGCUUCAUUC	GGAAGGUCGUCUGGUUCGAUG
9	UGAUGUGCCUGGCUCUCCUGUAUGCCAUUUGUAGAGCUCCC...	UGCCUGGCUCUCCUGUAUGCCA	GCGUAUGAGGAGCCAAGCAUA
10	GCATATCTGCTTUGGUAGGAGGGUGCGAAGUCGCUGGAGG...	UCGAUAAACCUCUGCAUCCAG	GGAGGCAGCGGUUCAUCGAUC

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, necessarily on the first column



The screenshot shows a text editor window titled "example.txt" with a file path of "~/Documents/igor/secondary_structure". The window contains a table with 10 rows of pre-miRNA data. The first column contains line numbers (1-10), the second column contains labels (pre-mir1 to pre-mir10), and the subsequent columns contain nucleotide sequences. A yellow arrow points to the first column, highlighting the labels.

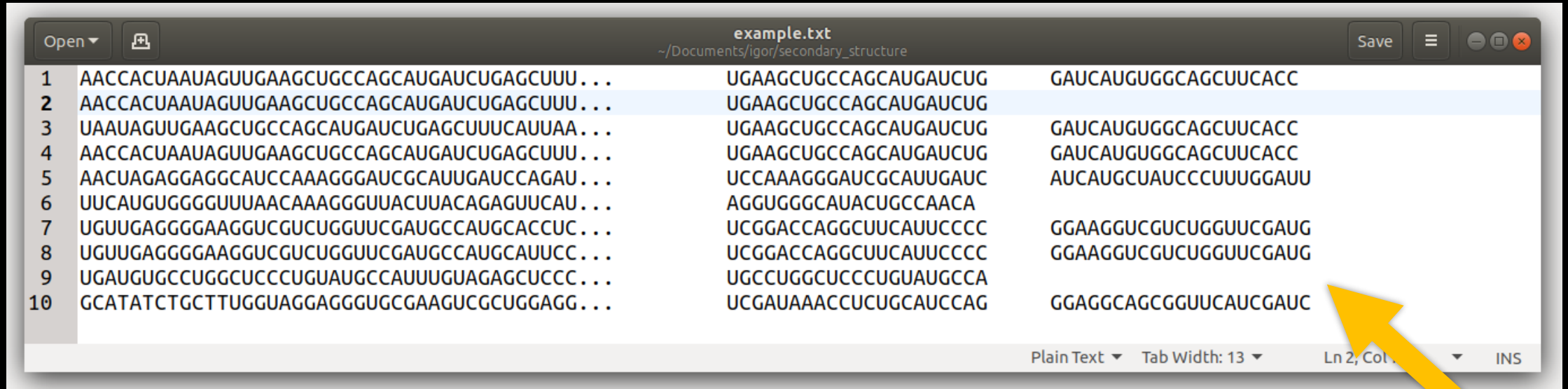
Line	Label/Annotation	Sequence 1	Sequence 2	Sequence 3
1	pre-mir1	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
2	pre-mir2	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
3	pre-mir3	UAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUUCAUUA...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
4	pre-mir4	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
5	pre-mir5	AACUAGAGGGAGGCAUCCAAAGGGAUCGCAUUGAUCCAGAU...	UCCAAAGGGAUCGCAUUGAUC	AUCAUGCUAUCCCUUUGGAUU
6	pre-mir6	UUCAUGUGGGGUUUAACAAAGGGUACUUACAGAGUUCAU...	UUGGCAUUCUGUCCACCUC	AGGUGGGCAUACUGCCAACA
7	pre-mir7	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACCUC...	UCGGACCAGGCUUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG
8	pre-mir8	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGC AUUCC...	UCGGACCAGGCUUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG
9	pre-mir9	UGAUGUGCCUGGCUCUCCUGUAUGCCA UUGUAGAGCUCCC...	UGCCUGGCUCUCCUGUAUGCCA	GCGUAUGAGGAGCCAAGCAUA
10	pre-mir10	GCATATCTGCTTUGGUAGGAGGGUGCGAAGUCGCUGGAGG...	UCGAUAAACCUCUGCAUCCAG	GGAGGCAGCGGUUCAUCGAUC

Label/annotation

2. How to use

2.1 Input files

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



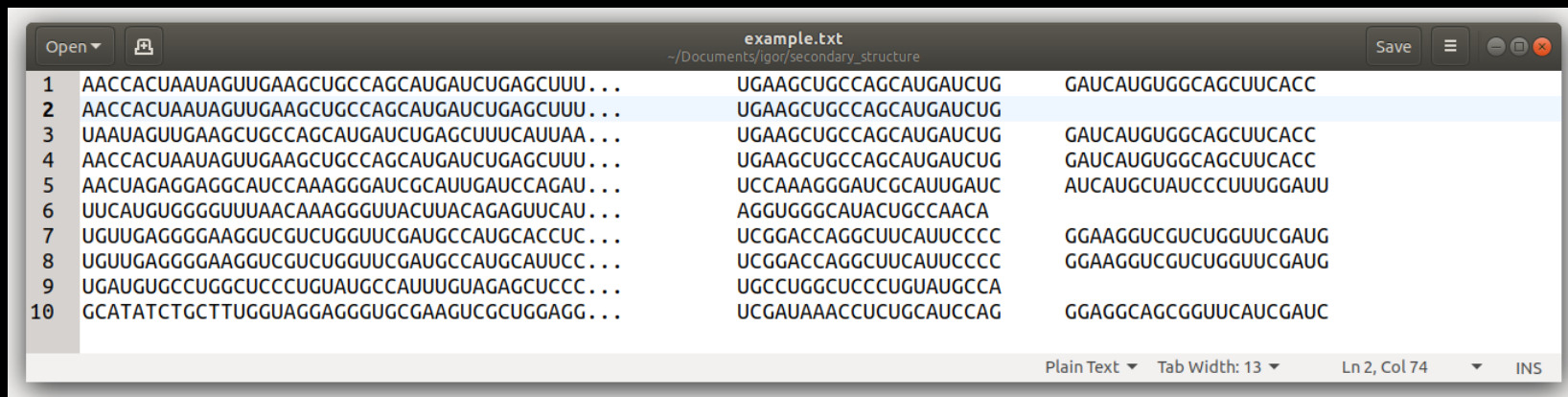
The screenshot shows a text editor window titled "example.txt" with the path "~/Documents/igor/secondary_structure". The editor contains a table with 10 rows and 3 columns of nucleotide sequences. A yellow arrow points to the third column of the table.

	Column 1	Column 2	Column 3
1	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
2	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	
3	UAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUUCAUUA...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
4	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC
5	AACUAGAGGAGGCAUCCAAAGGGAUUCGAUUGAUCCAGAU...	UCCAAAGGGAUUCGAUUGAUC	AUCAUGCUAUCCCUUUGGAUU
6	UUCAUGUGGGGUUUAACAAAGGGUACUACAGAGUUCAU...	AGGUGGGCAUACUGCCAACA	
7	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACCUC...	UCGGACCAGGCUUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG
8	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCAUUC...	UCGGACCAGGCUUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG
9	UGAUGUGCCUGGCUCCCUGUAUGCCAUUUGUAGAGCUCCC...	UGCCUGGCUCCCUGUAUGCCA	
10	GCATATCTGCTTUGGUAGGAGGGUGCGAAGUCGCUGGAGG...	UCGAUAAACCUCUGCAUCCAG	GGAGGCAGCGGUUCAUCGAUC

Plain Text ▾ Tab Width: 13 ▾ Ln 2, Col. 1 INS

2. How to use

2.1 Running



```
1  AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...  UGAAGCUGCCAGCAUGAUCUG  GAUCAUGUGGCAGCUUCACC
2  AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...  UGAAGCUGCCAGCAUGAUCUG
3  UAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUUCAUUA...  UGAAGCUGCCAGCAUGAUCUG  GAUCAUGUGGCAGCUUCACC
4  AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...  UGAAGCUGCCAGCAUGAUCUG  GAUCAUGUGGCAGCUUCACC
5  AACUAGAGGAGGCAUCCAAAGGGAUCGCAUUGAUCCAGAU...  UCCAAAGGGAUCGCAUUGAUC  AUCAUGCUAUCCCUUGGAUU
6  UUCAUGUGGGGUUUAACAAAGGGUACUACAGAGUUCAU...  AGGUGGGCAUACUGCCAACA
7  UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACCUC...  UCGGACCAGGCUUCAUUCCCC  GGAAGGUCGUCUGGUUCGAUG
8  UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCAUUC...  UCGGACCAGGCUUCAUUCCCC  GGAAGGUCGUCUGGUUCGAUG
9  UGAUGUGCCUGGCUCUCCUGUAUGCCAUUUUGUAGAGCUC...  UGCCUGGCUCUCCUGUAUGCCA
10 GCATATCTGCTTUGGUAGGAGGGUGCGAAGUCGCGUGGAG...  UCGAUAAACCUCUGCAUCCAG  GGAGGCAGCGGUUCAUCGAUC
```

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

```
python premirnaplot.py file1.txt
```

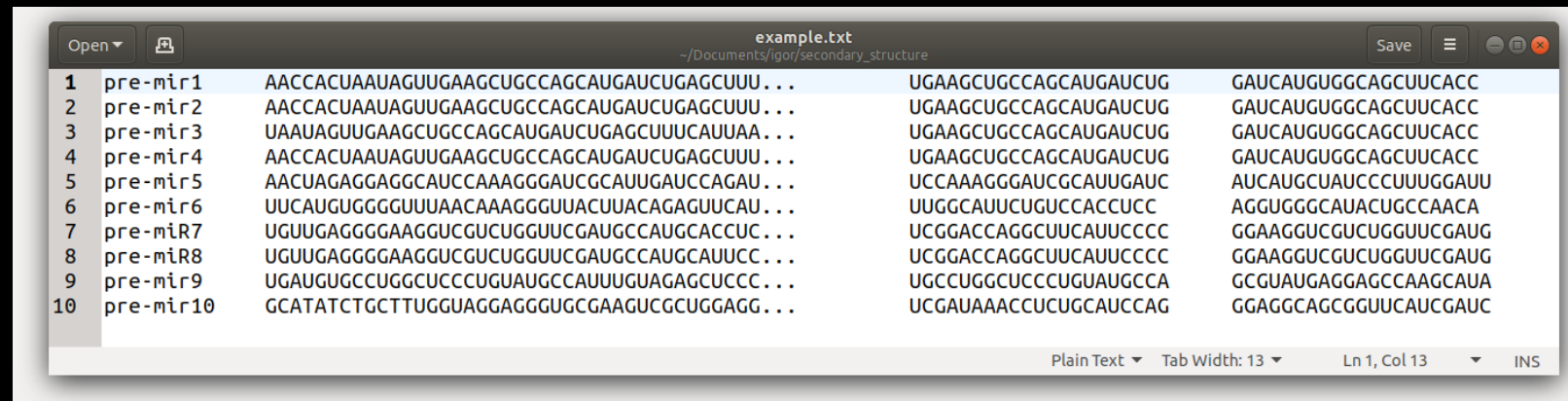
```
python premirnaplot.py file1.txt file2.txt file3.txt ...
```

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

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

2. How to use

2.1 Running



The screenshot shows a text editor window titled "example.txt" with a file path of "~/Documents/igor/secondary_structure". The editor contains a table with 10 rows, each representing a pre-miRNA. The first column lists the pre-miRNA names (pre-mir1 to pre-mir10). The second column contains the pre-miRNA sequences. The third and fourth columns contain the 5' and 3' flanking regions, respectively. The fifth column contains the mature miRNA sequence. The sixth column contains the mature miRNA sequence with its 5' and 3' flanking regions. The seventh column contains the mature miRNA sequence with its 5' and 3' flanking regions and the mature miRNA sequence. The eighth column contains the mature miRNA sequence with its 5' and 3' flanking regions and the mature miRNA sequence. The ninth column contains the mature miRNA sequence with its 5' and 3' flanking regions and the mature miRNA sequence. The tenth column contains the mature miRNA sequence with its 5' and 3' flanking regions and the mature miRNA sequence. The editor interface includes a menu bar with "Open", "Save", and "INS" buttons. The status bar at the bottom indicates "Plain Text", "Tab Width: 13", "Ln 1, Col 13", and "INS".

pre-miRNA	Sequence	5' Flanking	3' Flanking	Mature miRNA	Mature miRNA (5' Flanking)	Mature miRNA (3' Flanking)	Mature miRNA (5' Flanking)
pre-mir1	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC				
pre-mir2	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC				
pre-mir3	UAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUUCAUUAA...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC				
pre-mir4	AACCACUAAUAGUUGAAGCUGCCAGCAUGAUCUGAGCUUU...	UGAAGCUGCCAGCAUGAUCUG	GAUCAUGUGGCAGCUUCACC				
pre-mir5	AACUAGAGGAGGCAUCCAAAGGGAUCGCAUUGAUCAGAU...	UCCAAAGGGAUCGCAUUGAUC	AUCAUGCUAUCCUUUGGAUU				
pre-mir6	UUCAUGUGGGGUUUAACAAAGGGAUACUUACAGAGUUCAU...	UUGGCAUUCUGUCCACCUC	AGGUGGGAUACUGCCAACA				
pre-mir7	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACCUC...	UCGGACCAGGCUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG				
pre-mir8	UGUUGAGGGGAAGGUCGUCUGGUUCGAUGCCAUGCACUCC...	UCGGACCAGGCUCAUUCCCC	GGAAGGUCGUCUGGUUCGAUG				
pre-mir9	UGAUGUGCCUGGCUCUCCUGUAUGCCAUUUGUAGAGCUCCC...	UGCCUGGCUCUCCUGUAUGCCA	GCGUAUGAGGAGCCAAGCAUA				
pre-mir10	GCATATCTGCTTUGGUAGGAGGGUGCGAAGUCGUGGAGG...	UCGAUAAACCUCUGCAUCCAG	GGAGGCAGCGGUUCAUGAUC				

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

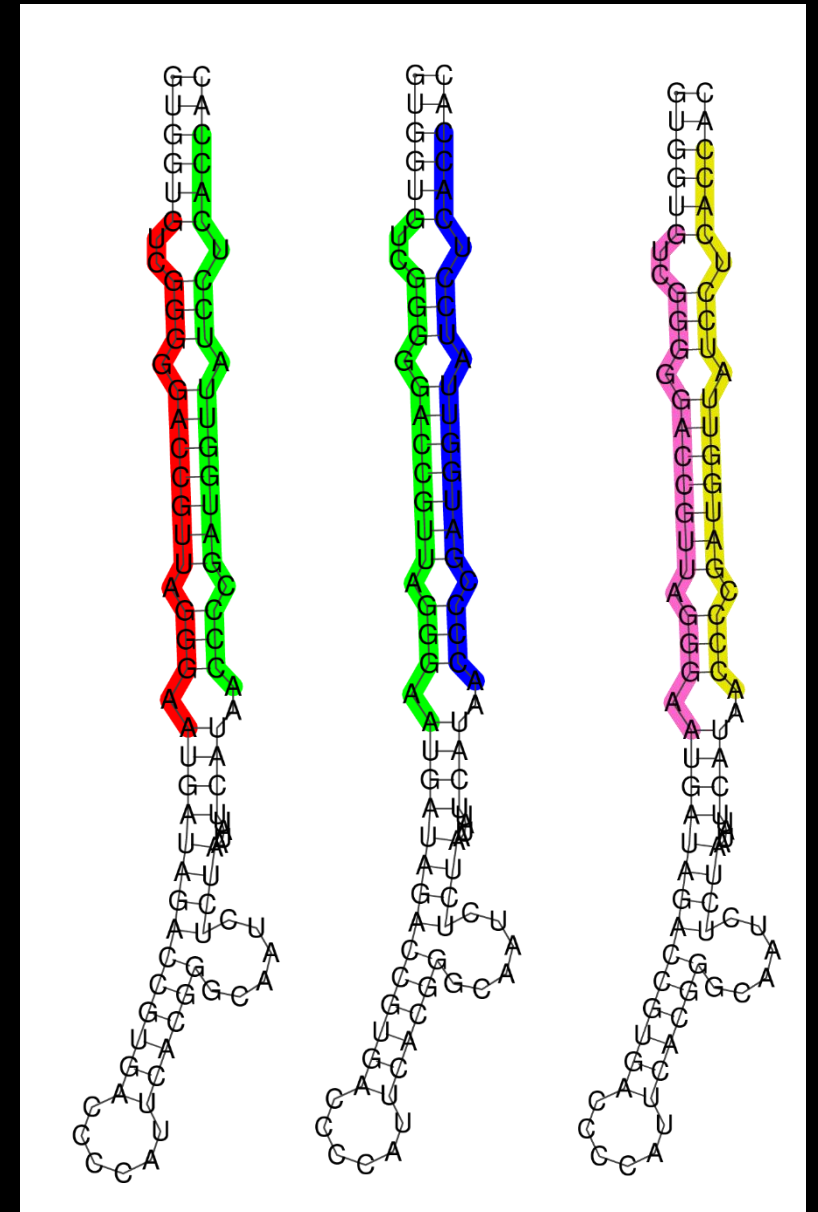
2.1 Exploring the parameters

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

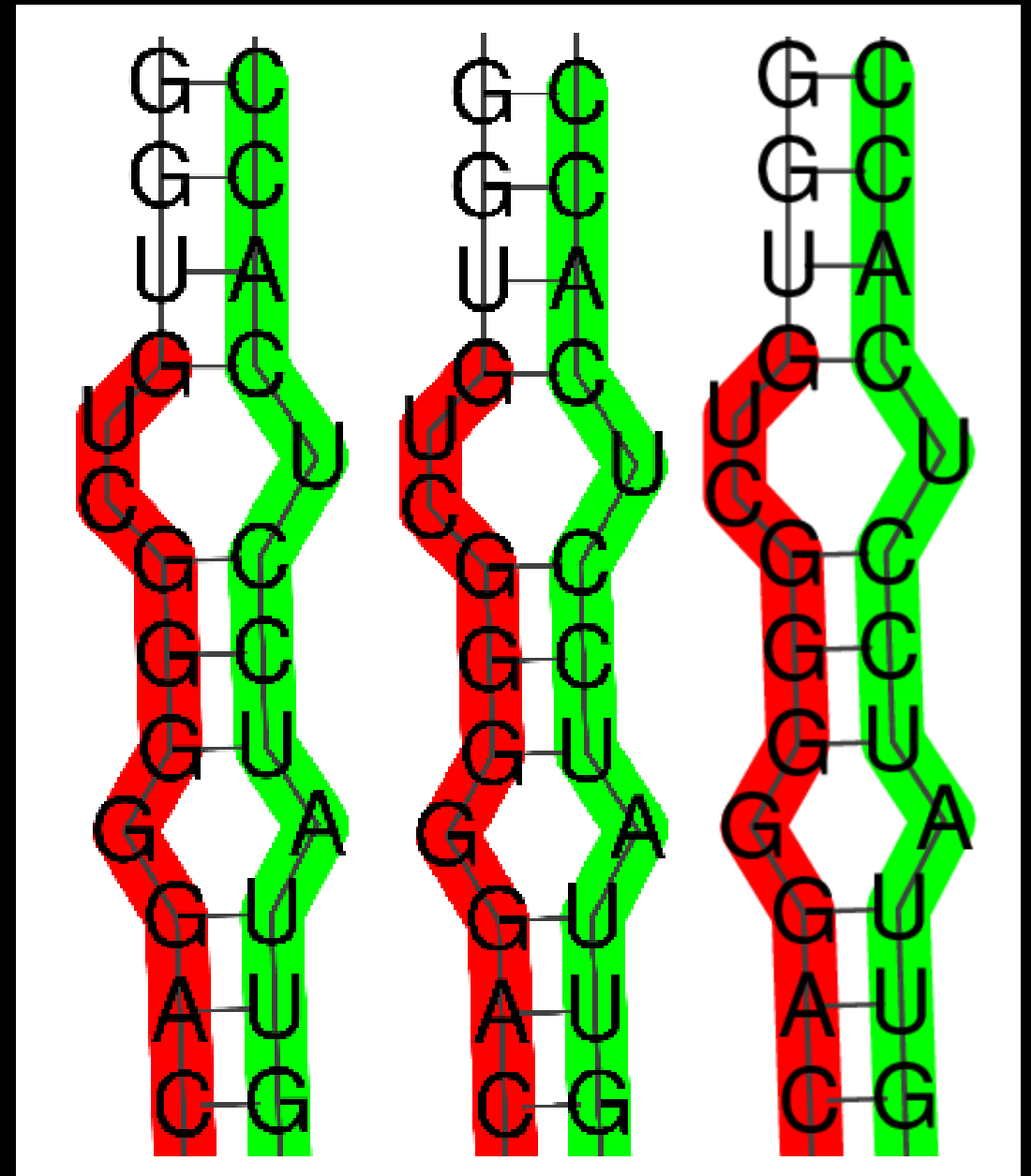
2. How to use

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](#).