

Chop up the gene into 58 fragments

Source code: chop_up.cpp

Example input file: Eya1_1.fna

Example output file: Eya1_1_chopped.txt

Instructions:

- 1) Open the terminal window and change the directory using the command “cd Desktop”
- 2) Copy the source file from the web to a text editor (I use TextWrangler) and name the file: CGR_v2.cpp Ensure that the file is on the Desktop.
- 3) Copy the test file from the web to a text editor and name the file: A_55_P2423586_Eya1_1.fna Ensure that the file is on the Desktop.
- 4) I assume that you have a GCC compiler on your computer (If not, you will have to download a compiler from the web).
- 5) Compile the source code to an application using the following line command in the terminal window:

```
g++ chop_up.cpp -o chop_up
```

This will create an application call CGR on the Desktop.

- 6) Run the program in the terminal window by invoking the following command:

```
./chop_up 53 Eya1_1.fna Eya1_1_fragments.txt
```

The fast file ‘Eya1_1.fna’ will be chopped into 53 nt fragments. For example:

```
AAACCAATAAGGTTAGGACAAGAGACTAGCTGTGGTTTGC GTTGCAAAAACAA
```

```
AACCAATAAGGTTAGGACAAGAGACTAGCTGTGGTTTGC GTTGCAAAAACAA
```

```
..
```

```
AATAAGGTTAGGACAAGAGACTAGCTGTGGTTTGC GTTGCAAAAACAAACAA
```

The fragments will be deposited in a file called ‘Eya1_1_fragments.txt.’