

Convert a gene sequence into x - and y - coordinates

Source code: `make_CGR.cpp`

Example input file: `Eya1_1.fna`

Example output file: `Eya1_1_CGR.txt`

Instructions:

1) Compile the source code to app called CGR using the line command:

```
g++ make_CGR.cpp -o make_CGR
```

2) Run the program by invoking the following line command in the terminal:

```
./make_CGR Eya1_1.fna
```

Result:

A file called `Eya1_1_CGR.txt` will contain 3 columns of data. The first column is the nucleotide in the sequence, the second column is the x -coordinate, and the third column is the y -coordinate.