

Determine the GC histogram of a metagenomic sample

Purpose: to determine the GC histogram of a metagenomic sample

Source code: gc_histogram.cpp

Example input file: test_GC.txt

Example output file: histogram_GC.txt

Instructions:

1) Compile source code to app called “GC_histo” using the line command:

```
g++ gc_histogram.cpp -o GC_histo
```

2) Run the “GC_histo” program by invoking the following line command:

```
./GC_histo test_GC.txt histogram_GC.txt
```