

Determine the GC content of each sequence in a metagenomic sample

Purpose: to determine the GC content of each sequence in a metagenomic sample

Source code: `determine_GC_each_seq.cpp`

Example input file: `text_insert.txt`

Example output file: `test_GC.txt`

Instructions:

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

```
g++ determine_GC_each_seq.cpp -o GC_each_seq
```

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

```
./GC_each_seq text_insert.txt test_GC.txt
```