

## **Determine the GC content of a metagenomic sample**

Purpose: to the GC content of a metagenomic sample

Source code: `determine_GC_MG_run.cpp`

Example input file: `text_insert.txt`

Example output file: `GC_sequences.txt`

### *Instructions:*

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

```
g++ determine_GC_MG_run.cpp -o GC_seq
```

2) Run the `GC_seq` program by invoking the following line command:

```
./GC_seq text_insert.txt GC_sequences.txt
```