

## Count a specific mer target (e.g., AAACCA) in a CGR plot

Source code: count\_CGR\_mer.cpp

Example input file: Eya1\_1\_CGR.txt

Example output file: AAACCA.txt

### *Instructions:*

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

```
g++ count_CGR_mer.cpp -o count_CGR_mer
```

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

```
./count_CGR_mer AAACCA Eya1_1_CGR.txt AAACCA.txt
```

The sequence AAACCA was found twice in the transcript of Eya1 (out of the 4348 possible). The outfile (AAACAA.txt) contains the mer length, the query mer, the number of identical mers in the transcript, and the total number of nucleotides in the transcript sequence.

Output:

```
6    AAACCA    2    4348
```