problem 1A

JobID	JobName	ReqMem	MaxRSS	ReqCPUS	UserCPU	Timelimit	Elapsed	State	JobEff
37473526	problemIA	19.5G	3.24G	1.	00:25.001	00:10:00	00:01:45	COMPLETED	17.04

<u>Fig. 1</u>

```
yg336@wind:~/inf503/homework2

The number of arguments passed: 4

The first argument is: main

The second argument is: problem1A

The third argument is: /common/contrib/classroom/inf503/hw_dataset.fa

The fourth argument is: /common/contrib/classroom/inf503/test_genome.fasta

time used for reading all the reads is: 9 s

memory released!
```

Fig. 2

problem 1B

```
FASTAreadset_LL::~FASTAreadset_LL()
{
    Node *temp1, *temp2;
    temp1 = head;
    temp2 = head;
    while(temp1 != NULL)
    {
        delete[] temp1->sequence;
        temp1 = temp1->next;
        delete[] temp2;
        temp2 = temp1;
    }
    cout << "memory released!" << endl;
}</pre>
```

From problem 1A we can see that the memories can be released by this destructor.

O(n). When releasing the memories, the program just deallocate the memories one by one.

problem 1C

```
FASTAreadset_LL::FASTAreadset_LL(const FASTAreadset_LL &obj)
{
    this->init();
    Node *temp1, *temp2;
    temp1 = obj.head;
    if(temp1 == NULL)
```

```
return;
    }
    this->head = new Node;
    temp2 = this->head;
    temp2->sequence = new char[51];
    strcpy(temp2->sequence, temp1->sequence);
    temp1 = temp1->next;
    while(temp1 != NULL)
    {
        temp2->next = new Node;
        temp2 = temp2 -> next;
        temp2->sequence = new char[51];
        strcpy(temp2->sequence, temp1->sequence);
        temp1 = temp1->next;
    }
}
```

```
The number of arguments passed: 4
The first argument is: ./main
The second argument is: problem1C
The third argument is: /common/contrib/classroom/inf503/hw dataset.fa
The fourth argument is: /common/contrib/classroom/inf503/test genome.fasta
first 10 segments from the file:
GTAACTGAACTGTTTGGTCAGCTCAGCGACTACAGACGACTTGTAGTAAT
AGGGGCAGGCGTACGGCCTTTTCTTCGCGCTCGCGCAACGACCGCGCG
AATGGCTTTTTTCCAAAGATAAACCGAATTTTTTAATATATTTACTGAC
GTGACCCAGAAACCCAACCGATCATGATGCGTCTGCAATCGGATCTGGTT
TTCCGAAAGCTGTACTAAGCCTTTCAGCAGTTGCTTTTGCTTGAGTGGGT
ACGAGAACTGATAGCCGGCCGTCACCGCGACGCGCTGCTCCGCCTGCGCG
TGTCGAAGGATGTCGGTAAATCGATATTCTGTGTCGAAACGTCGATATAA
AAACATGTTGATACAACTGAGTACATTAAACTAGACTATAGCTATTCATA
ACCATTAATTGATTTTGTTCAGATGCACATCCATTTGTGGGAATGGAATT
first 10 segments from the copied object:
GTAACTGAACTGTTTGGTCAGCTCAGCGACTACAGACGACTTGTAGTAAT
AGGGGCAGGCGTACGGCCTTTTCTTCGCGCTCGTCGCGAACGACCGCGCG
AATGGCTTTTTTCCAAAGATAAACCGAATTTTTTAATATATTTACTGAC
GTGACCCAGAACCCAACCGATCATGATGCGTCTGCAATCGGATCTGGTT
TTCCGAAAGCTGTACTAAGCCTTTCAGCAGTTGCTTTTGCTTGAGTGGGT
ACGAGAACTGATAGCCGGCCGTCACCGCGACGCGCTGCTCCGCCTGCGCG
TGTCGAAGGATGTCGGTAAATCGATATTCTGTGTCGAAACGTCGATATAA
AAACATGTTGATACAACTGAGTACATTAAACTAGACTATAGCTATTCATA
ACCATTAATTGATTTGTTCAGATGCACATCCATTTGTGGGAATGGAATT
memory released!
memory released!
```

<u>Fig. 3</u>

O(n). When copying all the elements from an object to another, the program copy them one by one.

problem 1D

<u>Fig. 4</u>

problem 2A

The number of 50-character fragments is 5227244.

```
yg336@wind:~/inf503/homework2

The number of arguments passed: 4

The first argument is: main

The second argument is: problem2A

The third argument is: /common/contrib/classroom/inf503/hw_dataset.fa

The fourth argument is: /common/contrib/classroom/inf503/test_genome.fasta

The number of 50-character fragments is: 5227244

memory released!
```

Fig. 5

problem 2B

1000 searches

yg336@wind:~/inf503/homework2

```
The number of arguments passed: 4

The first argument is: main

The second argument is: problem2B

The third argument is: /common/contrib/classroom/inf503/hw_dataset.fa

The fourth argument is: /common/contrib/classroom/inf503/test_genome.fasta

Reads in the read set: 36220412

segments in the genome file: 5227244

Found 797 50-character fragments in readset!

Time cost is: 256 s

memory released!

memory released!
```

Fig. 6

```
yg336@wind:~/inf503/homework2

The number of arguments passed: 4

The first argument is: main

The second argument is: problem2B

The third argument is: /common/contrib/classroom/inf503/hw_dataset.fa

The fourth argument is: /common/contrib/classroom/inf503/test_genome.fasta

Reads in the read set: 36220412
segments in the genome file: 5227244

Lound 8372 50-character fragments in readset!

Time cost is: 2373 s
memory released!
memory released!
memory released!
```

<u>Fig. 7</u>

100000 searches

```
The number of arguments passed: 4
The first argument is: main
The second argument is: problem2B
The third argument is: /common/contrib/classroom/inf503/hw_dataset.fa
The fourth argument is: /common/contrib/classroom/inf503/test_genome.fasta

Reads in the read set: 36220412
segments in the genome file: 5227244

Found 83188 50-character fragments in readset!
Time cost is: 21905 s
memory released!
memory released!
```

<u>Fig. 8</u>

From the results of 1000, 10000 and 100000 searches we can estimate that the total time consumption for 5227244 segments is about:

```
(5227244/100000)*21905 = 1145027 (s) = 401 (h)
```