

Created by Praphul Shivakoti for MW(2:00-3:15).

This handout is supposed to act as a guide for getting you started on this lab as many of you had questions about getting started, enums and command line args.

- Step 1:

Compiling through the command line:

Through your terminal or command prompt go to the directory with your DNAList file.

Compile your code using :

[javac DNAList.java] or [javac *.java] (if you have more than one java file to compile).

Running your code:

java DNAList 50 command.txt

(the arraySize(50) is an arbitrary number for the size of the Sequence array.

However, make sure it is a big enough number).

(make sure you move the command.txt to the source file before or instead of - command.txt pass in the path to command.txt as well).

- Step 2:

Data structures you need:

Since you are creating an array of sequences you want to enumerate the type of data for storage.

Declaring sequence enum:

```
enum Sequence{  
    DNA, RNA;  
}
```

You can take it a step further by setting enum type for what characters can be of type DNA or RNA which can help with avoiding setting the wrong character on the wrong sequence in the wrong sequence type but that is not required and makes the whole process harder.

The basic idea is to create a DNA or RNA (a linked list) which is then stored in the main sequence array.

- Step 3:

Getting the values from command line arguments:

You can assume that there are 2 commands being passed on while running the DNAList (arraySize and filename or path).

```
int size = Integer.valueOf(args[0]);
```

After this, you can create an array of type Sequence and of size [size].

```
Sequence[] mainSequenceArray = new Sequence[size];
```

```
File file = new File(args[1]);
```

- Step 4

The next step is to read the command file [file].

There are many ways of doing it, one good way for doing it would be to continue reading the file using a while loop until it has a new line. Splitting each line on space character and calling the commands based on that.

You might want to look at the main method we provided for the first 3 labs which implement a similar syntax for splitting lines.

If you need help with implementing specific methods, come to labs or email any of the lab TA's with any questions you have.

Also, you can post your questions on piazza which can be very helpful as all the TA's, instructor, and your classmates will help answer your questions quickly. Piazza is much faster than waiting for lab day or emailing your TA.

<https://piazza.com/class/jqr2pmbx8gq485?cid=4#>