Assignment 5

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# Description

The objective of this assignment is to generate mappability of 250 gene sequences in scope of HG19.chr1. There are 3 different applications made for this purpose and here is a step by step guidance on how to achieve the goal (Take note that all the files must be placed under Assignment4/io folder as this is the main io folder for both input and output):

1. Generate Reads with different length by running the following application: /Assignment5/src/com/bio/main/GenerateReadsApp.java
2. Use the read files (reads50.fa for example) one by one and generate BowTie outputs and place them in io folder (length 50 BT output is called final-BTout50-v2-m1 in this assignment. Same naming convention was used for the rest).
3. Generate the mappability files by running the following application: /Assignment5/src/com/bio/main/CheckMappabilityApp.java
4. Merge the 3 mappability files (for example: final-output-50) generated from step 3 by running the following application: /Assignment5/src/com/bio/main/MergeOutputApp.java
5. The final file which can be used by R application will be named: Mappability-output-250

## 

## Application specifications

**Programming language:** JAVA

**Other required installations:** JRE 1.8 to run the application,

JDK 1.8 to compile the application.

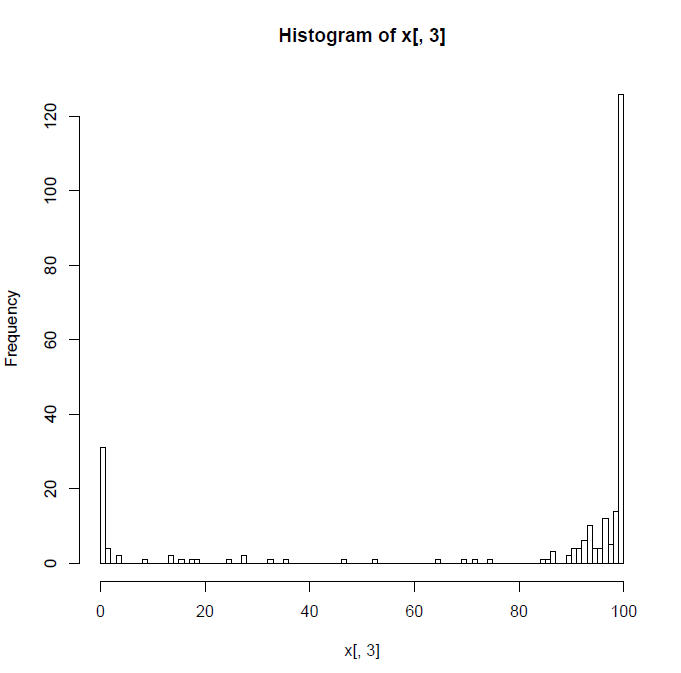
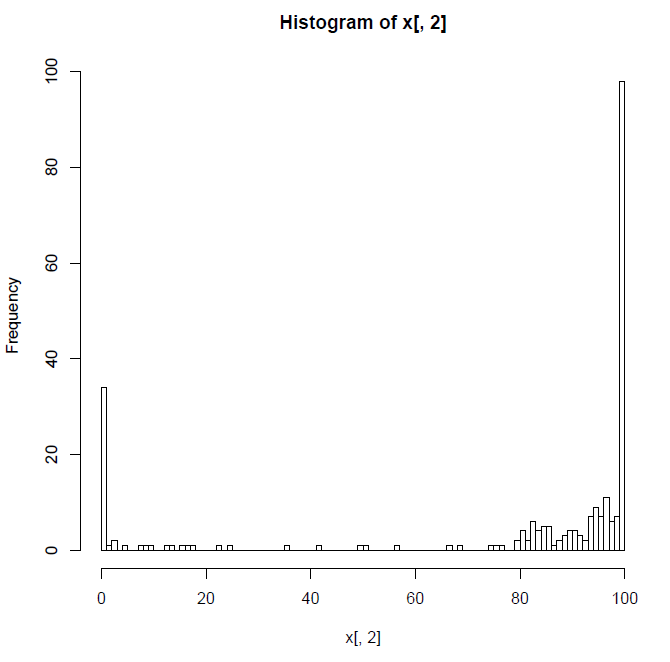
**Version Control:** Git (GitHub) - https://github.com/momazia/Bioinformatic/tree/master/Assignment5

**IDE:** Eclipse (Mars 4.5.1)

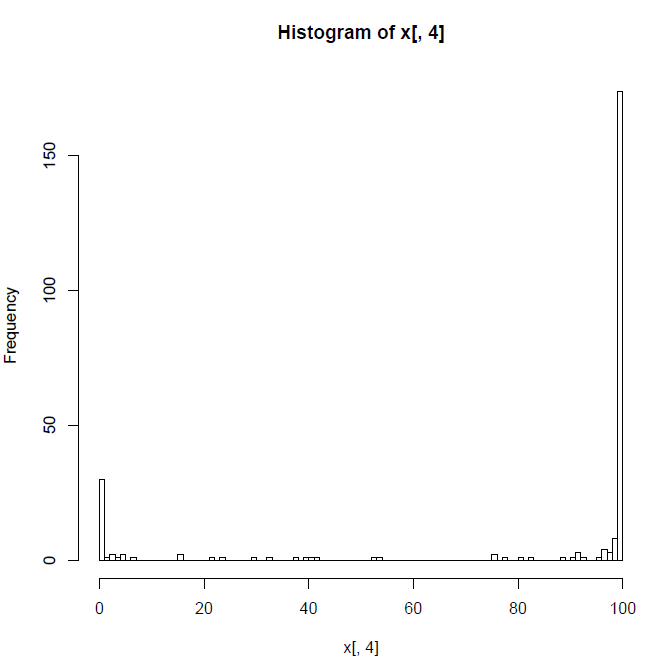
**Build automation tool:** Maven (Refer to /Assignment5/pom.xml for the list of the libraries used)

## Analysis of generated Graphs

As an individual study on each of mappabilities of the different lengths, by looking at their Histogram graphs, the most mappabilities are distributed on either 100 or zero percent. It also shows that 100% mappabilities in all 3 different lengths are having the most occurrences in the output.

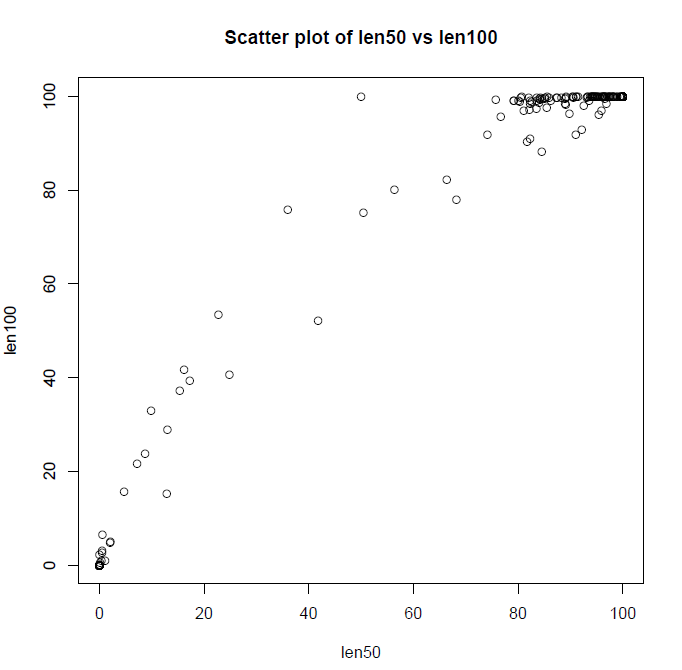
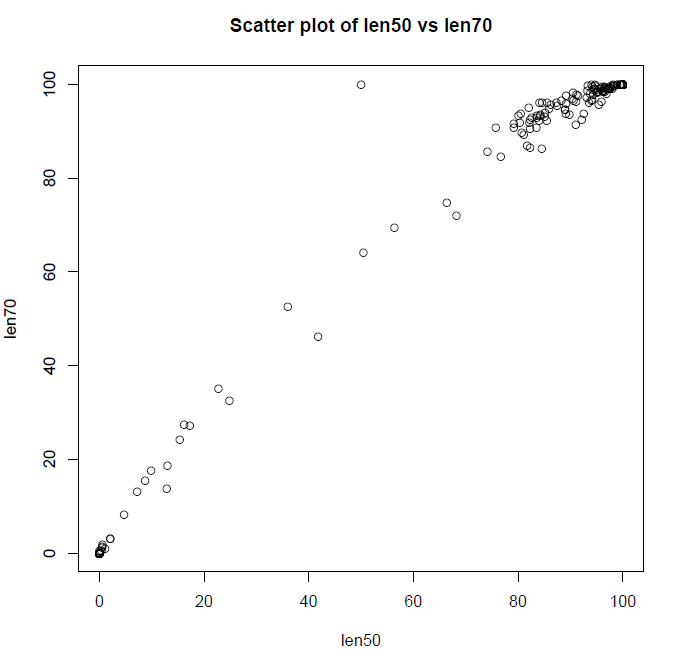


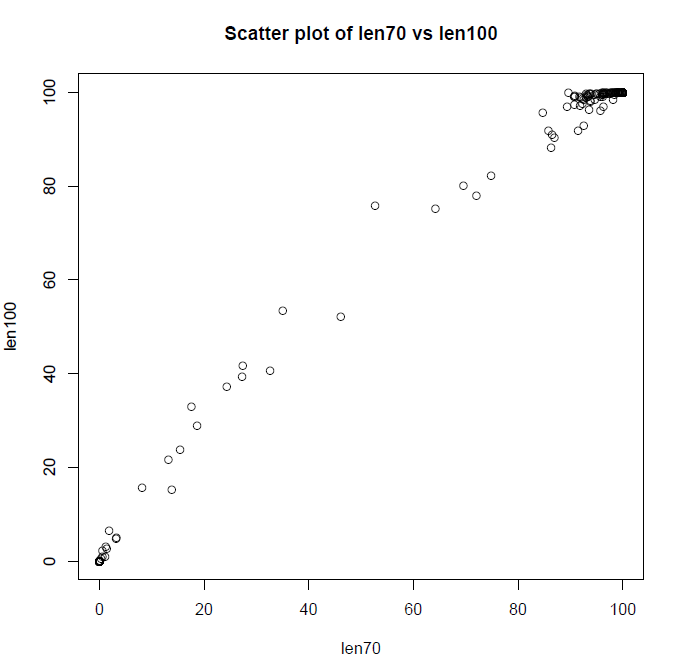
Length 50 Length 70



Length 100

By comparing scatter plot graphs of all the possible combinations between the 3 different read lengths, it is most obvious that the longer the length of a read, the higher the mappability of the read is. Because in none of the graphs below, we have a single dot under the line , where the smaller read length is presented on in all the graphs.





# Mappability-output-205

geneID readLen50 readLen70 readLen100

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# Source code