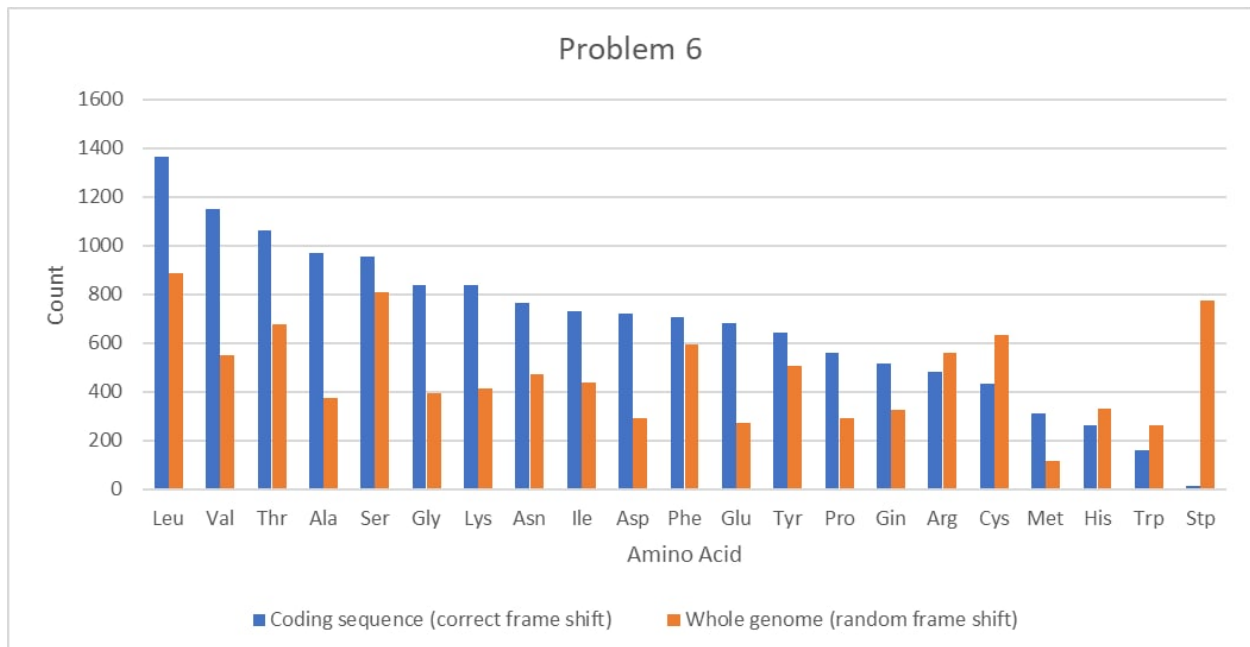
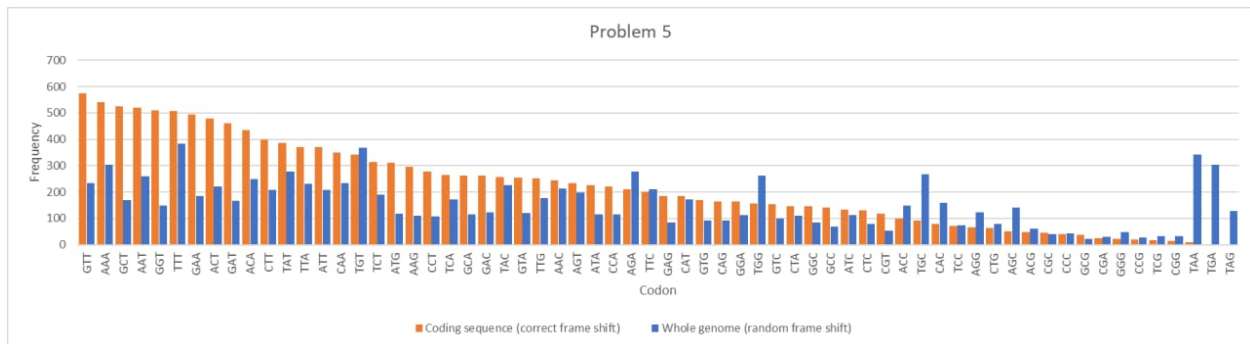


Homework 1 - Writeup

To run the file:

```
#compile file
javac count_codons.java

#run program
java count_codons [input-file] [output.csv]
```



Homework 3

The largest discrepancy happens to be in the stop codons. Mainly this is due to the fact that file with the separate codons contains the separate genes without the intergenic material that is usually in-between and can be found in the whole sequence. The intergenic material contain a lot of TAA TAG TGA so our stop codon counts increases. We see in the head of the skipped genome file we see that there were a lot of information skipped in between location=26245..26472 to location=27202..27387 , for example. This is is probably where the stop codons were in the separated one therefore there is a big discrepancy.