**Assignment #5 – Automatic identification of primers**

In this assignment your script will take in a DNA sequence file for the *C. elegans* genome, and a chromosome and position you want amplified.

The idea is that the user wants to genotype a SNP at a particular position. To do this they will need to amplify a sequence of DNA around 600-800 bp long. It is also important that the beginning and end of the PCR product is at least 100 bp away. A visual schematic is included below. The first primer should be chosen between 0-400. The second primer should be chosen between 600-1000. The total product size should be 600-800 bp long.

1000

600

400

0

You should use primer3 to choose the primers and report back the best choice. Some example output is included below. I have uploaded the fasta\_file for you to use as well.

[pmcgrath7@bioebb301301:~/Dropbox/NewGeneralWork/Teaching/BIOL48038803/Assignments]$python3 Assignment5\_Solution.py -h

usage: Assignment5\_Solution.py [-h] fasta\_file chromosome position

This program runs primer3 to identify the best two primers to amplify a given

sequence

positional arguments:

fasta\_file Enter a genome file containing DNA sequence

chromosome Enter the chromosome you want amplified

position Enter the position you want amplified

optional arguments:

-h, --help show this help message and exit

$ python3 Assignment5\_Solution.py c\_elegans.WS220.genomic.fa CHROMOSOME\_I 4564564

ttggcagttgggaccgttta

catcgagcagtgcaggaaga

$ python3 Assignment5\_Solution.py c\_elegans.WS220.genomic.fa CHROMOSOME\_V 4564564

tgcccaggaaaatgtgacgt

catcccccatgtcgattcga

$ python3 Assignment5\_Solution.py c\_elegans.WS220.genomic.fa CHROMOSOME\_V 45645

ggagccaaagataacgccct

cggtaaccggcaattttgga

$ python3 Assignment5\_Solution.py c\_elegans.WS220.genomic.fa CHROMOSOME\_III 456452

gtcctctaggagccgaggaa

ttggaaggagtggggaaacg

$ python3 Assignment5\_Solution.py c\_elegans.WS220.genomic.fa CHROMOSOME\_IV 456452

gacaggccgaggtatgtacg

ctgcaagttctcgggcagta