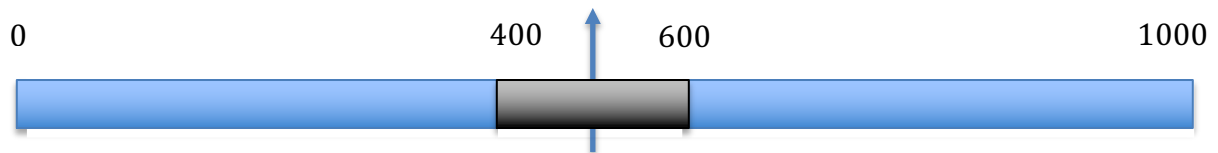


Assignment #5 – Automatic identification of primers

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.



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/Assignment
s]$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
catcgagcagtgagggaaga
$ python3 Assignment5_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_V 4564564
tgcccaggaaaatgtgacgt
catccccatgtcgattcga
$ python3 Assignment5_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_V 45645
ggagccaaagataacgccct
cggtaccggcaattttgga
$ python3 Assignment5_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_III
456452
gtcctctaggagccgaggaa
ttggaaggagtgggaaacg
$ python3 Assignment5_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_IV 456452
gacaggccgaggtatgtacg
ctgcaagttctcgggcagta
```