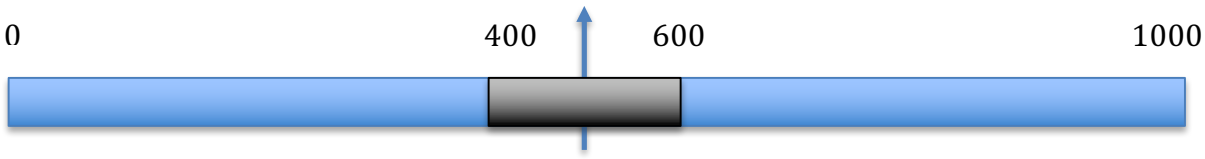
Assignment #5 – Automatic identification of primers

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.

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[pmcgrath7@bioebb301301:~/Dropbox/NewGeneralWork/Teaching/BIOL48038803/Assignments]$python3 Assignment7_Solution.py -h
usage: Assignment7_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 Assignment7_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_I 4564564
ttggcagttgggaccgttta
catcgagcagtgcaggaaga
$ python3 Assignment7_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_V 4564564
tgcccaggaaaatgtgacgt
catcccccatgtcgattcga
$ python3 Assignment7_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_V 45645
ggagccaaagataacgccct
cggtaaccggcaattttgga
$ python3 Assignment7_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_III
456452
gtcctctaggagccgaggaa
ttggaaggagtggggaaacg
$ python3 Assignment7_Solution.py c_elegans.WS220.genomic.fa CHROMOSOME_IV 456452
gacaggccgaggtatgtacg
ctgcaagttctcgggcagta
```