

REPORT

1-) Pseudo Code

PROBES(input.txt, probeLen)

1. subSeqDict = **dict**()
2. nuc = {'A', 'T', 'G', 'C'}
3. dnaSequences = **list**()
4. lengthOfValidSequence = 27000
5. **for** every line (i) **in** input.txt
6. i = i[:lengthOfValidSequence] #every i will have 27000 char
7. **if** every char in i is equal to one of the nuc's chars
8. add i to the dnaSequences
9. dnaSequences = **list**(**set**(dnaSequences)) #in order to eliminate same sequences, I use set()
10. **for** every dna sequence **in** dnaSequences
11. tempSet = **set**()
12. **for** every proper subsequence of current dna sequence
13. **if** current subsequence is already in subSeqDict and **not in** tempSet
14. increase value of this subsequence in subSeqDict by 1
15. **else**
16. add current subsequence as key into subSeqDict and assign it's value as 1
17. add current subsequence to the tempSet
18. maxKeyValue = 1
19. **for** key, result **in** subSeqDict.items()
21. find maxKeyValue
22. resultList = **list**()
23. **for** key, result **in** subSeqDict.items()
24. add key to the resultList which has value that equal to maxKeyValue
25. write number of valid sequences, maximum number sequences that the probes are found,
26. length of the returning list of the probes function and resultList to the output.txt file

NOTE: I use set() at line 9. Thus, if you run this algorithm for a limited number(10,500,1000, etc.) of valid DNA sequences instead of whole valid DNA sequences, this limited number of selected valid DNA sequences will be random. As a result, the result of the output.txt file can vary for each run. However, if you run for whole valid DNA sequences, the result will be always the same.

2-)Results Table

The number of valid sequences	The number of sequences probe is found	Probe length	Time in seconds
10	22823	90	10.49
50	12839	90	7.18
100	7334	90	7.77
250	1865	90	13.05
500	466	90	22.86
1000	53	90	42.21
10	22393	100	8.74
50	11835	100	6.75
100	6407	100	7.47
250	1467	100	13.51
500	323	100	23.41
1000	42	100	43.69