# Extra Credit

I have answered **(a)** and **(b)** from the extra credit section.

a.There is a very seductive but INCORRECT algorithm for shuffling that, historically, many students have used, despite our warnings. Read the blog post about it, linked from slide 48. Does it correctly shuffle a 2 card deck? Explain why or why not.

The naïve shuffle is correctly shuffling a 2 card deck.

The random call sequence is as follows :

|  |  |
| --- | --- |
| Naïve shuffle | Knuth-Fisher-Yates shuffle |
| rand.Next(2)  rand.Next(2) | rand.Next(2) |

|  |  |
| --- | --- |
| Knuth-Fisher-Yates shuffle | |
| Rand.Next(2) possibilities | Final combination in deck |
| 0 | 2 1 |
| 1 | 1 2 |

From above we see that Naïve shuffle results in 22 possibilities though there are only 2 possible combinations, but if we list down the possibilities for (1 2) by running through the algorithm we see that in Naïve shuffle the deck combinations appear evenly. Also, mathematically 22 is divisible by 2

|  |  |
| --- | --- |
| Naïve shuffle | |
| Rand.Next(2) possibilities | Final combination in deck |
| 0 0 | 2 1 |
| 0 1 | 1 2 |
| 1 0 | 1 2 |
| 1 1 | 2 1 |

Also, when each of naïve and fisher were run for 1000000 runs, each combination was seen almost equally~500000. (Attached code in submission for reference)

b. Implement the global (Needleman-Wunsch) alignment algorithm, run it on the same examples, and compare/contrast results.

Implemented Needleman-Wunsch algorithm in the same solution as localSequenceAlgorithm.

Comparing the scores for global vs local sequence alignment, it is seen that in the global sequence algorithm can have score as good as local sequence algorithm in the best case(ex: P10085 and P15172) else lower. It cannot be better than local sequence alignment as it tries to align the entire sequence increasing the cost paid on gap penalty hence lower score.

Scores for Global sequence alignment

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | P15172 | P17542 | P10085 | P16075 | P13904 | Q90477 | Q8IU24 | P22816 | Q10574 | O95363 |
| P15172 |  | -28 | 1500 | 1020 | 978 | 880 | 234 | 220 | -420 | -227 |
| P17542 |  |  | -24 | -22 | -47 | -47 | -126 | 77 | -422 | -153 |
| P10085 |  |  |  | 1043 | 1002 | 909 | 246 | 235 | -409 | -234 |
| P16075 |  |  |  |  | 1146 | 1072 | 283 | 235 | -344 | -233 |
| P13904 |  |  |  |  |  | 1073 | 299 | 211 | -299 | -240 |
| Q90477 |  |  |  |  |  |  | 321 | 196 | -277 | -291 |
| Q8IU24 |  |  |  |  |  |  |  | 147 | -105 | -452 |
| P22816 |  |  |  |  |  |  |  |  | -383 | -112 |
| Q10574 |  |  |  |  |  |  |  |  |  | -810 |
| O95363 |  |  |  |  |  |  |  |  |  |  |

Scores for Local sequence alignment

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | P15172 | P17542 | P10085 | P16075 | P13904 | Q90477 | Q8IU24 | P22816 | Q10574 | O95363 |
| P15172 |  | 143 | 1500 | 1020 | 978 | 893 | 428 | 368 | 118 | 56 |
| P17542 |  |  | 128 | 129 | 128 | 112 | 144 | 123 | 156 | 66 |
| P10085 |  |  |  | 1043 | 1002 | 925 | 440 | 367 | 118 | 52 |
| P16075 |  |  |  |  | 1147 | 1093 | 448 | 414 | 120 | 61 |
| P13904 |  |  |  |  |  | 1104 | 450 | 410 | 120 | 72 |
| Q90477 |  |  |  |  |  |  | 449 | 410 | 117 | 62 |
| Q8IU24 |  |  |  |  |  |  |  | 446 | 125 | 45 |
| P22816 |  |  |  |  |  |  |  |  | 124 | 74 |
| Q10574 |  |  |  |  |  |  |  |  |  | 67 |
| O95363 |  |  |  |  |  |  |  |  |  |  |