Homework Assignment

Computational Gene Finding

02-17-2023

Task A

```
# Accession number for SARS Coronavirus MA15 ExoN1
accession_number <- "FJ882953"

# Query
q <- query("q", paste("AC=", accession_number, sep = ""))
```

```
## [1] "Retrieved 1 sequence(s) for Accession Number: FJ882953"
```

```
## [1] "Length of the sequence: 29648"
```

```
## 29648-letter DNAString object
## seq: CTCGATCTCTTGTAGATCTGTTCTCTAAACGAACTT...GGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGT
```

Task B

```
# Reverse complement of the sequence
reverse_comp_seq <- reverseComplement(seq_str)
print(reverse_comp_seq)
```

```
## 29648-letter DNAString object
## seq: ACTACTAAAATTAATTTTACACATTAGGGCTCTTCC...AAGTTCGTTTAGAGAACAGATCTACAAGAGATCGAG
```

```
# Print all the potential ORFs in the reverse complement of
# the sequence
orfs_rev_comp <- findORFs(as.character(reverse_comp_seq))
print(orfs_rev_comp[, c("start", "end", "length")])
```

```
##        start   end     length
##   [1,] "98"    "145"   "48"
##   [2,] "132"   "149"   "18"
##   [3,] "158"   "163"   "6"
##   [4,] "231"   "308"   "78"
##   [5,] "301"   "462"   "162"
##   [6,] "333"   "344"   "12"
##   [7,] "366"   "428"   "63"
##   [8,] "478"   "516"   "39"
##   [9,] "495"   "566"   "72"
##  [10,] "563"   "613"   "51"
##  [11,] "577"   "594"   "18"
##  [12,] "600"   "674"   "75"
##  [13,] "625"   "690"   "66"
##  [14,] "665"   "694"   "30"
##  [15,] "745"   "756"   "12"
```

```
##  [16,] "802"   "825"   "24"
##  [17,] "1003"  "1113"  "111"
##  [18,] "1128"  "1199"  "72"
##  [19,] "1388"  "1432"  "45"
##  [20,] "1516"  "1521"  "6"
##  [21,] "1521"  "1589"  "69"
##  [22,] "1610"  "1651"  "42"
##  [23,] "1632"  "1742"  "111"
##  [24,] "1706"  "1720"  "15"
##  [25,] "1822"  "1875"  "54"
##  [26,] "1836"  "1898"  "63"
##  [27,] "1862"  "1918"  "57"
##  [28,] "2065"  "2124"  "60"
##  [29,] "2152"  "2190"  "39"
##  [30,] "2196"  "2249"  "54"
##  [31,] "2279"  "2344"  "66"
##  [32,] "2375"  "2380"  "6"
##  [33,] "2390"  "2407"  "18"
##  [34,] "2413"  "2436"  "24"
##  [35,] "2424"  "2444"  "21"
##  [36,] "2561"  "2608"  "48"
##  [37,] "2605"  "2781"  "177"
##  [38,] "2811"  "2852"  "42"
##  [39,] "2859"  "3011"  "153"
##  [40,] "2959"  "2994"  "36"
##  [41,] "3150"  "3179"  "30"
##  [42,] "3288"  "3386"  "99"
##  [43,] "3298"  "3321"  "24"
##  [44,] "3473"  "3634"  "162"
##  [45,] "3561"  "3572"  "12"
##  [46,] "3725"  "3787"  "63"
##  [47,] "3732"  "3737"  "6"
##  [48,] "3808"  "3837"  "30"
##  [49,] "3896"  "3955"  "60"
##  [50,] "3942"  "4049"  "108"
##  [51,] "3964"  "4005"  "42"
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##  [54,] "4141"  "4146"  "6"
##  [55,] "4151"  "4201"  "51"
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##  [59,] "4437"  "4442"  "6"
##  [60,] "4508"  "4519"  "12"
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##  [62,] "4657"  "4713"  "57"
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```

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## [284,] "20959" "20979" "21"
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## [381,] "28245" "28262" "18"
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## [388,] "28501" "28536" "36"
## [389,] "28533" "28571" "39"
## [390,] "28572" "28679" "108"
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```
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## [395,] "28962" "28997" "36"
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## [400,] "29211" "29222" "12"
## [401,] "29458" "29544" "87"
```
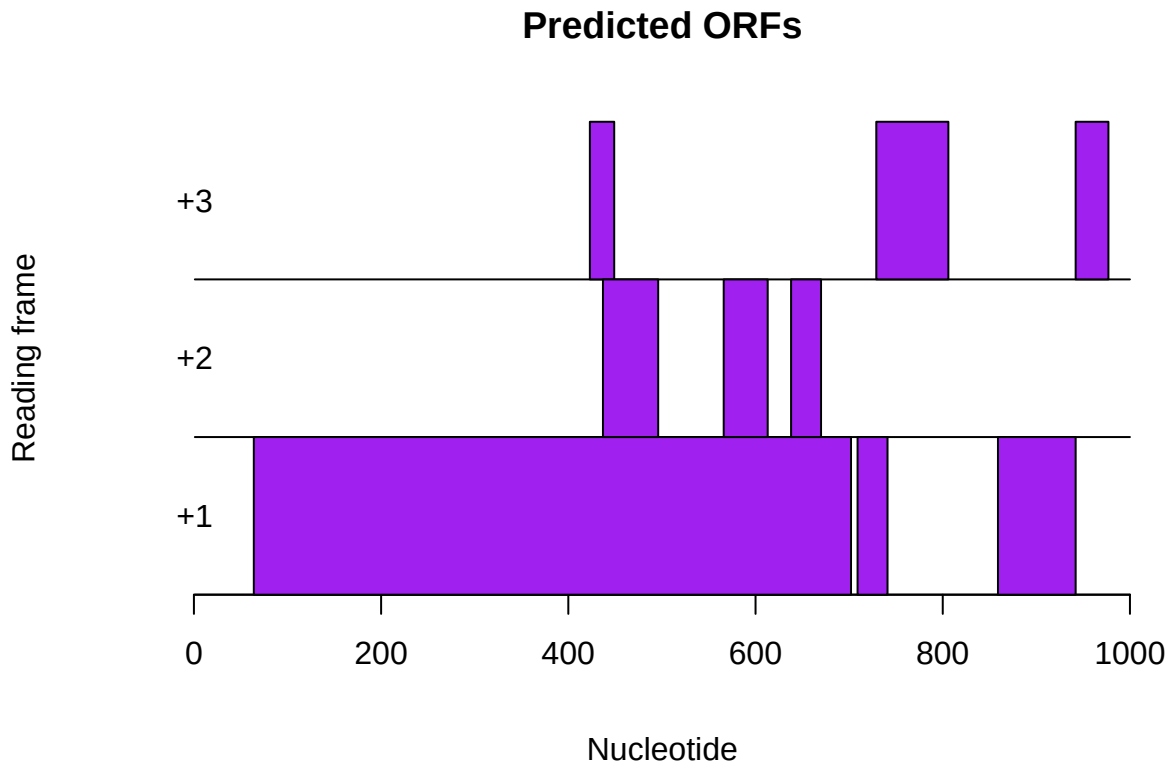

Task C

```
# Plot potential ORFs in the last 1000 bases
plotORFsinSeq(c2s(tail(seq_vector, 1000)))
```



Task D

```
# Extract, translate and print the longest potential gene
potential_orfs <- findORFs(as.character(seq_str))
longest_gene <- potential_orfs[as.numeric(potential_orfs[, "length"]) ==
    max(as.numeric(potential_orfs[, "length"]))]
print(paste("The longest gene starts at index", longest_gene[1],
    "and ends at index", longest_gene[2]))
```

```
## [1] "The longest gene starts at index 227 and ends at index 13375"
```

```
print(paste("Length of the longest gene:", longest_gene[3]))
```

```
## [1] "Length of the longest gene: 13149"
```

```
print("The longest gene:")
```

```
## [1] "The longest gene:"
```

```
print(DNAString(longest_gene[4]))
```

```
## 13149-letter DNAString object
## seq: ATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA...GATGCATCAACGTTTTTAAACGGGTTTGCGGTGTAA
```

```
protein <- translate(DNAString(longest_gene[4]))
print(paste("The resulting protein sequence of length:", length(protein)))
```

```
## [1] "The resulting protein sequence of length: 4383"
```

```
print(protein)
```

```
## 4383-letter AAString object
## seq: MESLVLGVNEKTHVQLSLPVLQVRDVLVRGFGDSVE...TVCGMWKGYGCSCDQLREPLMQSADASTFLNGFAV*
```

Task E and F

```
# Identify the significant ORFs using the 95th percentile
# as the threshold value.
random_seqs <- generateSeqsWithMultinomialModel(c2s(seq_vector),
    30)
random_orfs <- lapply(random_seqs, findORFs)

length_vector <- sapply(random_orfs, get_max_seq_vector)

threshold <- quantile(length_vector, 0.95)
print(threshold)
```

```
##    95%
## 395.55
```

```
significant_orfs <- potential_orfs[as.numeric(potential_orfs[,
    "length"]) > threshold, ]

print("Significant ORFs:")
```

```
## [1] "Significant ORFs:"
```

```
print(significant_orfs[, c("start", "end", "length")])
```

```
##      start   end     length
## [1,] "227"   "13375" "13149"
## [2,] "696"   "1187"  "492"
## [3,] "13561" "21447" "7887"
## [4,] "21454" "25221" "3768"
## [5,] "25230" "26054" "825"
## [6,] "25651" "26115" "465"
## [7,] "26360" "27025" "666"
## [8,] "28082" "29350" "1269"
```

Not all of the ORFs found in a DNA sequence correspond to real genes. Some of them occur by chance. To extract the actual genes, lab experimentation is necessary along with bioinformatics. As computer scientists, we can make predictions to extract genes from a sequence. The length of the ORF can be used as a measure, as long ORFs cannot happen by chance. Small ORFs have a high probability of occurring by chance, so we can eliminate those using a threshold. We could have used the 100th percentile (or the largest value) of the ORF length as the threshold, but by reducing the threshold slightly (5% in this case), we improve our chances of finding the actual genes in the sequence.