## CSCI 451/551 Fall 2023 Homework 1 Due: Thu, Sept 7, start of class

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## **Problem 1 (5 pts)** Exercise 5 (textbook section 1.9, pg 27)

5. For the following mRNA sequence, can you extract its 5' UTR, 3' UTR and the protein sequence?

ACTTGTCATGGTAACTCCGTCGTACCAGTAGGTCATG

**Clarification:** this is actually a DNA sequence; you should look for the DNA versions of start and stop codons rather than the RNA version.

Answer: The Start codon is ATG. The stop codon is TAG. Starting from ATG but not including ATG, we convert each three characters into the DNA sequence to RNA, then its protein sequence using <a href="https://biomodel.uah.es/en/lab/cybertory/analysis/trans.htm">https://biomodel.uah.es/en/lab/cybertory/analysis/trans.htm</a>. The Protein sequence is VTPQYQ

**Problem 2 (10 pts)** Implement the *Z-algorithm* in the language of your choice. Also, code up the *Exact Pattern Matching* algorithm that makes use of the Z algorithm.

Demonstrate both algorithms on some test strings (use screen shots to show runs). Include your source code at the end of the PDF.

```
Concatenated Pattern and sequence to match: caabxaaabaaab
Pattern Length: 3
Pattern found at 0
Pattern found at 5
Pattern found at 9
PS C:\Users\haedt\Desktop\Computational Biology\Z Algorithm>
```

```
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Concatenated Pattern and sequence to match: abcdeaabdfaabbfg
Pattern Length: 4
Pattern found at 9
PS C:\Users\haedt\Desktop\Computational Biology\Z Algorithm>
```

```
def test():
    string = "caabxaaabaaab"
    pattern = "aab"
    conStr = pattern + "#" + string
    strlength = len(conStr)
    z = [0] * strlength
    print(conStr)
    print(strlength)
    1 = 0
    r = 0
    for index in range (strlength):
        if index > r:
            l,r = index,index
            while r < strlength and conStr[r-1]==conStr[r]:</pre>
            z[index] = r -1
            r-=1
        else:
            k = index - 1
            if z[k] < r - index + 1:
                z[index] = z[k]
            else:
                1 = index
                while r < strlength and conStr[r-1] == conStr[r]:</pre>
                z[index] = r - 1
                r-=1
    for i in range(0, strlength-1):
        if z[i] == len(pattern):
            print(i - len(pattern) - 2)
def book():
    string = "abcdeaabdfaabbfg"
    k = 1
    pattern = "aabb"
    conStr = pattern + "#" + string
    strlength = len(conStr)
    patL = len(pattern)
    z = [0] * strlength
    print(strlength)
    1 = 0
    r = 0
    for i in range (strlength):
```

```
if i > r:
            r=i
            1= r
            while conStr[r-1] == conStr[r] and r < strlength:</pre>
            z[i] = r-1
            r-=1
        else:
            k = i - 1
            if z[k] < r - i + 1:
                z[i] = z[k]
            else:
                1 = i
                while r < strlength and conStr[r-1] == conStr[r]:</pre>
                    r+=1
                z[i] = r - 1
                r-=1
    print("Concatenated Pattern and sequence to match: ", string)
    print("Pattern Length: ", str(patL))
    for i in range(strlength):
        if z[i] == patL:
            print("Pattern found at", i - patL - 2)
def main():
    book()
main()
```