William Kelley
Lab16-ITE315

```
$ python3 lab16.py
['GTG', 'TGA', 'GAC', 'TAT', 'ACA', 'GTC', 'TTC', 'GTC', 'TTT', 'CAA']
-TC
$ python3 lab16.py
['CTC', 'TAT', 'TTG', 'GAT', 'GGC', 'ACG', 'CCG', 'GCG', 'ACT', 'GAG']
GCG
$ python3 lab16.py
['TAT', 'CTG', 'TTG', 'AAT', 'GGC', 'TTA', 'GCG', 'TCG', 'GTC', 'ACG']
TTG
```

```python
#!/usr/bin/python

import random

def frequencyTable(dnaList):
  n = max([len(dna) for dna in dnaList])
  frequency_matrix = {
    'A': [0]*n,
    'C': [0]*n,
    'G': [0]*n,
    'T': [0]*n
  }
  for dna in dnaList:
    for index, base in enumerate(dna):
      frequency_matrix[base][index] += 1

  return frequency_matrix

def generateString(N, alphabet=list('ATGC')):
  dna = [random.choice(alphabet) for i in range(N)]
  dna = ''.join(dna)
  return dna

def findConsensus(freqMatrix):
  consensus = ''
  dnaLength = len(freqMatrix['A'])

  for i in range(dnaLength):
    maxFreq = -1
    maxFreqBase = None
    for base in 'ATGC':
      l = freqMatrix[base]
      if l[i] > maxFreq:
        maxFreq = freqMatrix[base][i]
        maxFreqBase = base
      elif l[i] == maxFreq:
        maxFreqBase = '-'
    consensus += maxFreqBase
  return consensus

def main():
```

```python
    listDna=list()
    for _ in range(10):
        listDna.append((generateString(3)))
    print(listDna)
    print(findConsensus(frequencyTable(listDna)))


if __name__ == '__main__':
    main()
```