

TP DNA

1- Given the following:

DNA1 =

'agcgccttgaattcggcaccaggcaaattctcaaggagaagttccggggagaagggtgaagattagggttt'

DNA2 = 'cggggagtggggagttgagtcgcaagatgagcgagcggatgtccactatgagcgataataagt'

Each above-mentioned string contains the DNA sequence of a person. Using Spyder, write the necessary instructions that:

- Display the length of each DNA chain.
- Display the bigger DNA length.
- Find out how many base “n” contains each DNA
- Find out how many base “a” contains each DNA
- Find the percentage of each base in each string.
- Display the Genetic codes included in each DNA (a genetic code is a sequence of three bases).
- Given that EcoRI = 'GAATTC' and BamHI = 'GGATCC' are two patterns; verify if the aforementioned DNAs contain these patterns.
- Calculate the number of occurrences of each base in each chain
- Calculate the percentage of each base in the sequence.

2- Write a function `count_nucleic_acids (dna)` which takes as argument a string of characters representing a DNA sequence and which in a single run of this string determines the number of occurrences of each base a, c, g, t present in the sequence. Do not use the `count ()` method, but use a for loop. This function must return a dictionary associating with each nucleic acid, its number of appearances in the sequence. Your main program simply needs browse the dictionary (for loop) and properly display the values associated with the keys.