

BIF Assignment 1

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import Bio

from Bio.Seq import Seq

from Bio.SeqUtils import gc_fraction

#Providing DNA Sequences

dna_sequence =
"AGTCAGTAGACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGC
TAGCTAGCTAGCTA"

#Creating object for Seq

seq = Seq(dna_sequence)

def find_motifs(sequence, motif):

    positions = [i for i in range(len(sequence) - len(motif) + 1) if sequence[i:i + len(motif)] == motif]

    return positions

# Function to identify coding regions

def identify_coding_regions(sequence):

    start_codon = "ATG"

    stop_codons = ["TAA", "TAG", "TGA"]

    coding_regions = []

    i = 0

    while i < len(sequence):

        if sequence[i:i + 3] == start_codon:

            start_index = i

            i += 3

            while i < len(sequence):

                if sequence[i:i + 3] in stop_codons:

                    stop_index = i + 3

                    coding_regions.append((start_index, stop_index))

                    break

                i += 3
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else:

    i += 1

return coding_regions

motif1 = "AGCTAGCTA"
motif2 = "CTAGCTAGC"
motif1_positions = find_motifs(seq, motif1)
motif2_positions = find_motifs(seq, motif2)
# Calculating GC content
gc_content = gc_fraction(seq)

# Identifying coding regions
coding_regions = identify_coding_regions(seq)
report = "DNA Sequence Analysis Report\n\n"
report += f"Provided DNA Sequence:\n{seq}\n\n"
report += "Analysis 1: Finding Motifs\n"
report += f"Motif 1 ({motif1}) found at positions: {motif1_positions}\n"
report += f"Motif 2 ({motif2}) found at positions: {motif2_positions}\n\n"
report += "Analysis 2: Calculating GC Content\n"
report += f"GC Content: {gc_content:.2%}\n\n"
report += "Analysis 3: Identifying Coding Regions\n"
if len(coding_regions) > 0:
    report += "Coding regions found:\n"
    for start, stop in coding_regions:
        report += f"Start: {start} Stop: {stop}\n"
else:
    report += "No coding regions found in the sequence."

with open("DNA_SEQUENCE_ANALYSIS.txt", "w") as report_file:
    report_file.write(report)

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print("Analysis report generated as 'DNA_SEQUENCE_ANALYSIS.txt'.")
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