

## Assignment 1

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1. Implement ORF finding algorithm for  
CGCTACGTCTTACGCTGGAGCTCTCATGGATCGGTTCCGGTAGGGCTCGA  
TCACATCGCTAGCCAT using Using Python.
2. Implement the above question using Biopython and compare the result.

## Solution

### Custom Function

```
from Bio.Seq import Seq
from Bio.SeqUtils import six_frame_translations

def find_orfs(dna_sequence):
    start_codon = "ATG"
    stop_codons = ["TAA", "TAG", "TGA"]
    orfs = []
    length = len(dna_sequence)
    for i in range(length - 2):
        if dna_sequence[i:i+3] == start_codon:
            for j in range(i + 3, length - 2, 3):
                if dna_sequence[j:j+3] in stop_codons:
                    orfs.append(dna_sequence[i:j+3])
                    break
    return orfs

def find_orfs_biopython_direct(dna_sequence):
    start_codon = "ATG"
    stop_codons = ["TAA", "TAG", "TGA"]
    orfs = []
    length = len(dna_sequence)
    for i in range(length - 2):
        if dna_sequence[i:i+3] == start_codon:
            for j in range(i + 3, length - 2, 3):
                if dna_sequence[j:j+3] in stop_codons:
                    orfs.append(dna_sequence[i:j+3])
                    break
    return orfs

dna_sequence =
"CGCTACGTCTTACGCTGGAGCTCTCATGGATCGGTTCCGGTAGGGCTCGATCACATCGCTAGCCAT"

orfs_custom = find_orfs(dna_sequence)
orfs_biopython = find_orfs_biopython_direct(dna_sequence)
```

```
print("Custom ORF Finding Results:")
print(orfs_custom)
print("Biopython ORF Finding Results:")
print(orfs_biopython)

print("\nComparison of ORF Results:")
print(f"Custom ORFs: {orfs_custom}")
print(f"Biopython ORFs: {orfs_biopython}")
```

```
Custom ORF Finding Results:
['ATGGATCGGTTCGGTAGGGCTCGATCACATCGCTAG']
Biopython ORF Finding Results:
['ATGGATCGGTTCGGTAGGGCTCGATCACATCGCTAG']

Comparison of ORF Results:
Custom ORFs: ['ATGGATCGGTTCGGTAGGGCTCGATCACATCGCTAG']
Biopython ORFs: ['ATGGATCGGTTCGGTAGGGCTCGATCACATCGCTAG']
```