NAME: Nitish Kumar R
REG NO: 24MSBI151
COURSE: PYTHON PROGRAMMING
PROGRAM: MSC BIOINFORMATICS
DEPARTMENT: LIFE SCIENCES, SCHOOL OF SCIENCES,GCU

ASSIGNMENT 12 – ARRAY

Generate | Code | Markdown | Run All | Restart | Clear All Outputs | Outline | ... | Python 3.13.3

```python
#1. Create a DNA Sequence Using array.array
import array

# Create a DNA sequence using array.array with typecode 'u' for Unicode characters
dna = array.array('u', 'ATCGATCG')
print(dna)
```

[1] ✓ 0.0s Python

```
array('u', 'ATCGATCG')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\1461937191.py:5: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#2. Access Bases in the Array
import array

dna = array.array('u', 'ATCGATCG')
# Access specific bases (0-based indexing)
print(dna[0])
print(dna[3])
```

[2] ✓ 0.0s Python

```
A
G
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\2268135839.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#3. Modify a Base
import array

dna = array.array('u', 'ATCGATCG')
# Modify base at index 2
dna[2] = 'T'
print(dna)
```

[3] ✓ 0.0s Python

```
array('u', 'ATTGATCG')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\870178281.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#4. Slice a Subsequence
import array

dna = array.array('u', 'ATCGATCG')
# Slice from index 2 to 5 (exclusive)
subsequence = dna[2:5]
print(subsequence)
```

[4] ✓ 0.0s Python

```
array('u', 'CGA')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\3252325485.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

Generate + Code + Markdown

```python
#5. Loop Through Array to Count G and C
import array

dna = array.array('u', 'ATCGATCG')
# Count occurrences of G and C
count = sum(1 for base in dna if base in ('G', 'C'))
print(f"G and C count: {count}")
```

[5] ✓ 0.0s Python

```
G and C count: 4
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\4139232483.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#6. Reverse the DNA Sequence
import array

dna = array.array('u', 'ATCGATCG')
# Reverse the array
dna.reverse()
print(dna)
```

[6] ✓ 0.0s Python

```
array('u', 'GCTAGCTA')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\1310338536.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#7. Find a Motif in the Given Sequence
import array

dna = array.array('u', 'ATCGATCG')
motif = array.array('u', 'CGA')
# Convert to string for searching
dna_str = dna.tounicode()
motif_str = motif.tounicode()
index = dna_str.find(motif_str)
print(f"Motif found at index: {index}")
```

[7] ✓ 0.0s Python

```
Motif found at index: 2
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\3726341779.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\3726341779.py:5: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  motif = array.array('u', 'CGA')
```

```python
#8. Append a Base in the Given Sequence
import array

dna = array.array('u', 'ATCGATCG')
# Append a base
dna.append('A')
print(dna)
```

[8] ✓ 0.0s Python

```
array('u', 'ATCGATCGA')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\942780078.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#9. Remove Last Base from the Sequence
import array

dna = array.array('u', 'ATCGATCG')
# Remove the last base
dna.pop()
print(dna)
```

[9] ✓ 0.0s Python

```
array('u', 'ATCGATC')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\2522939457.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#10. Check if the DNA Sequence Ends with a Stop Codon
import array

dna = array.array('u', 'ATCGATTAA')  # TAA is a stop codon
# Check last 3 bases for stop codons (TAA, TAG, TGA)
last_three = dna[-3:].tounicode()
stop_codons = {'TAA', 'TAG', 'TGA'}
is_stop = last_three in stop_codons
print(f"Ends with stop codon: {is_stop}")
```

[10] ✓ 0.0s Python

```
Ends with stop codon: True
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\2158574853.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATTAA')  # TAA is a stop codon
```

```python
#11. Count How Many Times a Base Occurs
import array

dna = array.array('u', 'ATCGATCG')
base = 'A'
# Count occurrences of a specific base
count = sum(1 for b in dna if b == base)
print(f"Base {base} occurs: {count} times")
```

[11] ✓ 0.0s Python

```
Base A occurs: 2 times
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\3510840500.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#12. Get the Middle Base of a DNA Sequence
import array

dna = array.array('u', 'ATCGATCG')  # Length 8
# Get middle base (for even length, take the first of the two middle bases)
middle_index = len(dna) // 2 - 1 if len(dna) % 2 == 0 else len(dna) // 2
middle_base = dna[middle_index]
print(f"Middle base: {middle_base}")
```

[12] ✓ 0.0s Python

```
Middle base: G
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\192680277.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')  # Length 8
```

```python
#13. Insert a Mutation at Position 3
import array

dna = array.array('u', 'ATCGATCG')
# Insert a base at index 3 (0-based)
dna.insert(3, 'T')
print(dna)
```

[13] ✓ 0.0s Python

```
array('u', 'ATCTGATCG')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\2824190902.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
```

```python
#14. Convert DNA to RNA (Replace T with U)
import array

dna = array.array('u', 'ATCGATCG')
# Create RNA array, replacing T with U
rna = array.array('u', dna.tounicode().replace('T', 'U'))
print(rna)
```

[14] ✓ 0.0s Python

```
array('u', 'AUCGAUCG')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\545596109.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\545596109.py:6: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  rna = array.array('u', dna.tounicode().replace('T', 'U'))
```

```python
#15. Print All Codons (3-Base Chunks)
import array

dna = array.array('u', 'ATCGATCG')  # Length 8
# Print codons (3-base chunks)
for i in range(0, len(dna) - 2, 3):
    codon = dna[i:i+3].tounicode()
    print(f"Codon: {codon}")
```

[15] ✓ 0.0s Python

```
Codon: ATC
Codon: GAT
C:\Users\janan\AppData\Local\Temp\ipykernel_6464\1263735666.py:4: DeprecationWarning: The 'u' type code is deprecated and will be removed in Python 3.16
  dna = array.array('u', 'ATCGATCG')  # Length 8
```