loop

Example_04

Problem Statement:

In a laboratory experiment, a culture of bacteria doubles in number every hour. If you start with a single bacterium, how many bacteria will be in the culture after a certain number of hours? Write a program to calculate the number of bacteria after each hour up to 10 hours.

```
n = 1  # starting with one bacterium
hours = 0  # initial hour

while hours < 10:
    print(f"Hour {hours}: {n} bacteria")
    n = n * 2  # double the number of bacteria each hour
    hours = hours + 1

print("Experiment concluded after 10 hours")
```

(class work)

```
# Total number of growth stages of a plant
total_stages = 5

# Loop through each growth stage
for stage in range(total_stages):
    print(f"Current stage: {stage}")

    # Make a comment when the plant reaches an advanced growth stage
    if stage > 2:
        print(f"Plant is in an advanced growth stage: {stage}")

print("Monitoring complete.")
```

assignment

```
mammals = ["cat", "dog", "elephant", "whale", "human"]
birds = ["sparrow", "eagle", "parrot", "penguin", "owl"]

while True:
    animal = input("Enter the name of an animal: ").lower()

    if animal in mammals:
        print(f"{animal} is a mammal.")
        continue  # Skip to the next iteration for mammals

    if animal in birds:
        print(f"{animal} is a bird.")
        continue  # Skip to the next iteration for birds

    print(f"{animal} is neither a mammal nor a bird.")
    break  # Break out of the loop if the animal is neither a mammal nor a bird
```

Example: 11

Problem Statement: Average Protein Length in a Cell

Background:

Proteins, composed of long chains of amino acids, are essential molecules in all living organisms. They perform a vast array of functions within organisms, including catalyzing metabolic reactions, DNA replication, and responding to stimuli. The length of a protein, measured in the number of amino acids, can vary significantly and is crucial for its function.

Task:

Create a Python program that calculates the average length of a set of proteins. The program should take a list of tuples as input, with each tuple containing the name of a protein and the number of amino acids it comprises. The program should then calculate and display the average length of these proteins in terms of amino acids.

```
Sample Data:
protein_lengths = [
    ("Hemoglobin", 574),
    ("Insulin", 51),
    ("Myc", 439),
    ("P53", 393),
    ("Lysozyme", 129)
]
Expected Output:
The average protein length is 317.2 amino acids.
```

```python
# Sample data: list of tuples with protein names and their lengths
protein_lengths = [
    ("Hemoglobin", 574),
    ("Insulin", 51),
    ("Myc", 439),
    ("P53", 393),
    ("Lysozyme", 129)
]

# Initialize total length and count of proteins
total_length = 0
protein_count = 0

# Iterate through each tuple in the list
for protein, length in protein_lengths:
    total_length += length
    protein_count += 1

# Calculate the average length
average_length = total_length / protein_count

# Output the result
print(f"The average protein length is {average_length:.1f} amino acids.")
```

Example: 12

Problem Statement: DNA Sequence Motif Filtering

Background:

In molecular biology, DNA sequences are made up of four types of nucleotides: adenine (A), thymine (T), cytosine (C), and guanine (G). Certain short sequences or motifs within these longer DNA sequences can be of significant interest, as they might indicate important biological functions, such as binding sites for proteins or regulatory elements.

Task:

Create a Python program that filters a list of DNA sequences to find those that contain a specific nucleotide motif. The program should take two inputs: a list of DNA sequences and a DNA motif to search for. The program should then display only those DNA sequences that contain the specified motif.

```
# Sample Data:
dna_sequences = [
    "ATGCGTACGTAG",
    "CCGTAAGTCTAC",
    "TTAGCGTATCGA",
    "CGTAGCTAGCTA",
    "GTACGATCGTCA"
]
# Expected Output
DNA sequences containing the motif 'CGTA':
- ATGCGTACGTAG
- CCGTAAGTCTAC
- GTACGATCGTCA
```

```
# Sample data: list of DNA sequences
dna_sequences = [
    "ATGCGTACGTAG",
    "CCGTAAGTCTAC",
    "TTAGCGTATCGA",
    "CGTAGCTAGCTA",
    "GTACGATCGTCA"
]

# User input for DNA motif
dna_motif = input("Enter a DNA motif to search for: ").upper()

print(f"DNA sequences containing the motif '{dna_motif}':")

# Loop through the list and check if each sequence contains the motif
for sequence in dna_sequences:
    if dna_motif in sequence:
        print(f"- {sequence}")
```