Homework on Command Line

Task: Counting the frequency of individual letters in DNA sequences
Due date: 2025-05-25

Write a python script that counts how many times each letter (e.g., A, C, G, T) appears in a given text file containing DNA sequences.

The solution should be provided in two parts:

1. A Python script (`hw_count_freq.py`) that reads from `stdin` and prints the frequency of each letter.

2. A Bash script (`hw_count_all.sh`) that processes all files in the `qwerty-dna/` directory, and for each file outputs the letter frequencies. The Bash script should find all `.txt` files in the `qwerty-dna/` directory, run the Python script for each file

Note: Follow the examples and procedures shown in notes.ipynb and associated examples from our last session.

Submission: Send the solution by email with Subject 'Homework on Command Line', attach the two scripts.

Ad 1

Example usage:

```
cat qwerty-dna/ASDF13.txt | ./hw_count_freq.py
```
Should output:

```
g 32
c 21
a 26
t 21
```

Ad 2

Running the script `hw_count_all.sh` should process all files in the `qwerty-dna/` directory and output the frequencies for each file.

```
./hw_count_all.sh
```
Should output the frequencies for each file in the directory, similar to:

```
processing qwerty-dna/ASDF13.txt
g 32
```

```
c 21
a 26
t 21
processing qwerty-dna/CVBN21.txt
a 24
c 26
t 30
g 20
processing qwerty-dna/DFGH15.txt
c 31
g 22
a 26
t 21
```