2H   Implement DistanceBetweenPattern ndStrings

Distance Between Pattern and Strings Problem
Compute DistanceBetweenPattern ndStrings.

Input: A DNA string *Pattern* and a collection of DNA strings *Dna*.
Output: Distance D(*Pattern*, *Dna*) between *Pattern* and *Dna*.

$$d(\text{AAA}, \begin{matrix} \text{CTTAAC} \\ \text{GATATC} \\ \text{ACGGCG} \\ \text{CTAAAG} \end{matrix}) = 4$$

Formatting

Input: A DNA string *Pattern*, followed by a space-separated collection of DNA strings *Dna*.
Output: An integer representing the output of DISTANCEBETWEENPATTERNANDSTRINGS(*Pattern*, *Dna*).

Constraints

- The length of *Pattern* will be between 1 and 10^1.

- The number of strings in *Dna* will be between 1 and 10^2.

- The length of each string in *Dna* will be between 1 and 10^2.

- *Pattern* and each string in *Dna* will be DNA strings.

Test Cases

Case 1

Description: This dataset checks that you are able to identify mismatches between *Pattern* and individual sequences in *Dna* when the mismatch occurs in the beginning, middle, and end of the sequence.

Input:

```
  T   C   G
```

Output:
3

Case 2

Description: This dataset checks that you are able to identify perfect matches of *Pattern* within individual sequences of *Dna* when *Pattern* occurs in the beginning, middle, and end of the sequence.

Input:
```
G
G TT CG T TTG
```

Output:
0

Case 3

Description: This dataset checks your solution works on a standard input.

Input:
```
 CG
GTG CC TTT CG   C CC
```

Output:
2

Case 4

Description: This dataset checks your solution works on a standard input.

Input:
```
GGGG
GGGCTC C  GGGTT C  GG GT C T G GGT T C
```

Output:
```
4
```

Case 5

Description: A larger dataset of the same size as that provided by the randomized autograder.