

### 433. Minimum Genetic Mutation

A gene string can be represented by an 8-character long string, with choices from 'A', 'C', 'G', and 'T'.

Suppose we need to investigate a mutation from a gene string `startGene` to a gene string `endGene` where one mutation is defined as one single character changed in the gene string.

- For example, "AACCGGTT" --> "AACCGGTA" is one mutation.

There is also a gene bank `bank` that records all the valid gene mutations. A gene must be in bank to make it a valid gene string.

Given the two gene strings `startGene` and `endGene` and the gene bank `bank`, return the minimum number of mutations needed to mutate from `startGene` to `endGene`. If there is no such a mutation, return -1.

Note that the starting point is assumed to be valid, so it might not be included in the bank.

#### Example 1:

- **Input:** `startGene = "AACCGGTT", endGene = "AACCGGTA", bank = ["AACCGGTA"]`
- **Output:** 1

#### Example 2:

- **Input:** `startGene="AACCGGTT",endGene="AAACGGTA",bank=["AACCGGTA","AACCGCTA","AAACGGTA"]`
- **Output:** 2

#### Constraints:

- $0 \leq \text{bank.length} \leq 10$
- `startGene.length == endGene.length == bank[i].length == 8`
- `startGene`, `endGene`, and `bank[i]` consist of only the characters ['A', 'C', 'G', 'T'].