

433. Minimum Genetic Mutation

Description

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 <= bank.length <= 10`
- `startGene.length == endGene.length == bank[i].length == 8`
- `startGene`, `endGene`, and `bank[i]` consist of only the characters `['A', 'C', 'G', 'T']`.

