Unimum Genetic Mutation

This problem is a shortest path search in an unweighted graph:

· Usdes: Gene strings (1-char)

· Edges: Your modes are commected of they differ by exactly one character.

· 4901: Find the minimum mutations (edges) to reach and gene from start Gene sewing only volid genes from bank.

Key Thights:

1. Bank as allowed modes.

· If end Gene is not in bank, return -1 (no valid patts).

L. One-character mutation rule;

· Two genes are neighbors if they differ by exactly one character.

3. Un BFS (Breadth-Fint Search):

· BES ensures munimum steps in an enroweighted graph.

At each step, mutato one character and check if it is in bank and not visited.

[Algorithm Item:

I but bank into a set for O(e) bookeys.

2. Initialize BTS quare with start Gene

3. At each step:

For each gene in the queue, generate all valid 1-chan mutations.

If mutation is end Gene seteer consent steps + 1.

· Mark visited to avoid bogs.

4. If BFS ends without fending end gave return -1.

(Complexity: 1

Time: up to bank length & gene length \$ 4- O(10*8*4) - O(320) woult-case (vey small).

Space: O(Vank. length) for visited ut.