```
Індивідуальна робота 4
Завірюха Еліна, МП-21
#include <iostream>
#include <vector>
#include <queue>
#include <unordered set>
using namespace std;
int minMutation(string startGene, string endGene, vector<string>& bank) {
  // Convert bank to an unordered set for faster lookup
  unordered_set<string> bankSet(bank.begin(), bank.end());
  // Check if endGene is not in the bank, return -1
  if (bankSet.find(endGene) == bankSet.end()) {
     return -1;
  }
  // Define possible mutations for each character
  char mutations[] = {'A', 'C', 'G', 'T'};
  // Initialize queue for BFS
  queue<pair<string, int>> q;
  q.push({startGene, 0});
  while (!q.empty()) {
     string currentGene = q.front().first;
     int mutationsCount = q.front().second;
     q.pop();
     // Check if we reached the endGene
     if (currentGene == endGene) {
       return mutationsCount;
     }
     // Try all possible mutations
     for (int i = 0; i < 8; ++i) {
       char originalChar = currentGene[i];
       for (char mutation : mutations) {
          if (mutation != originalChar) {
            currentGene[i] = mutation;
            // Check if the mutated gene is in the bank
            if (bankSet.find(currentGene) != bankSet.end()) {
               q.push({currentGene, mutationsCount + 1});
               bankSet.erase(currentGene); // Mark as visited to avoid duplicates
            }
          }
       }
       // Revert the gene back to the original state for the next mutation
       currentGene[i] = originalChar;
```

```
return -1; // No valid mutation found

int main() {
    // Example 1
    string startGene1 = "AACCGGTT";
    string endGene1 = "AACCGGTA";
    vector<string> bank1 = {"AACCGGTA"};
    cout << "Example 1: " << minMutation(startGene1, endGene1, bank1) << endl;

// Example 2
    string startGene2 = "AACCGGTT";
    string endGene2 = "AAACGGTA";
    vector<string> bank2 = {"AACCGGTA", "AACCGCTA", "AAACGGTA"};
    cout << "Example 2: " << minMutation(startGene2, endGene2, bank2) << endl;
    return 0;
}
```