

Case Study Report For Design & Analysis Of Algorithms (LAB), Submitted as a part of Experiential Learning

TOPIC: Write a program in C to test the number of occurrences of the longest sequence of words (at least three words in a sequence) extracted from a text file in 10 different text files.

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DATE: SIGNATURE:

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PROBLEM STATEMENT

<u>Problem Statement:</u> Analyzing Longest Word Sequences in Text Files. This program aims to analyze the occurrences of the longest sequence of words (at least three words long) within 10 separate text files.

Input:

- a) The text file to be tested: A text file named main.txt consisting of meaningful sentences (at least 1000 words).
- b) The text files against which main.txt will be tested: A set of 10 text files named 01.txt, 02.txt, 03.txt..., 10.txt each consisting of meaningful sentences (at least 1000 words in each file).

Output:

A text file named *similarity tested.txt* which represents a table consisting of three columns:

Similarity Testing

==========

Sl No.	longest matched sequence	Matched in files
1		
2		
•		
n		

The above table should list out all longest sequences extracted from *main.txt* which matched in the 10 text files along with the file names. That is for each longest sequence, the program should display the sequence and the file names in which it is present.

Requirements:

The program should be able to read and process text files. It should tokenize each line of text into individual words. It should track the longest sequence of words encountered while processing each file. The program needs to differentiate between single occurrences and repeated sequences. It should accurately count the number of times the longest sequence appears in the file. The output should clearly identify the analyzed file, the specific longest

sequence, and its occurrence count.

Success Criteria:

The program successfully processes all 10 text files.

For each file, it identifies and reports the longest sequence of words (at least three words) and its occurrence count.

The output is clear and easy to understand.

Optional Considerations:

Error handling for invalid file access or incorrect file formats.

Handling different file naming conventions.

Storing results in a data structure for further analysis.

Expanding functionality to identify the most frequent sequences (regardless of length).

INTRODUCTION

Many times it is required to count the occurrence of each word in a text file. To achieve so, we make use of a dictionary object that stores the word as the key and its count as the corresponding value. We iterate through each word in the file and add it to the dictionary with a count of 1. If the word is already present in the dictionary we increment its count by 1. The program aims to analyze 10 text files and identify the longest sequence of words (at least three words long) that appears in each file, along with the number of times that sequence appears.

Here's a breakdown of the functionalities:

File Handling: The program will read each of the 10 text files line by line. Word Tokenization: Each line will be split into individual words, creating a list of words for each line.

Longest Sequence Tracking: It will iterate through each word list, keeping track of the current sequence length and the longest sequence found so far.

Occurrence Counting: It will check if the current sequence matches the previously identified longest sequence. If it does, an occurrence counter will be incremented.

Output: After processing all files, the program will display for each file:

The longest sequence of words (at least three words long).

The number of times that sequence appears.

This is a basic structure. You can customize it further by:

- 1. Handling different file naming conventions.
- 2. Incorporating error handling for file access issues.
- 3. Storing results in a data structure for further analysis.

This program focuses on testing the occurrences of the longest sequence. For real-world applications, you might want to consider additional functionalities like finding the most frequent sequences or implementing more sophisticated string processing techniques.

DYNAMIC PROGRAMMING

In the context of Design and Analysis of Algorithms (DAA), dynamic programming is a powerful technique used to efficiently solve problems by breaking them down into simpler subproblems and solving each subproblem only once. It involves storing the solutions to subproblems in a table (usually implemented using arrays or matrices) to avoid redundant computations, thus leading to improved time complexity.

Key characteristics of dynamic programming include:

- 1. **Optimal Substructure:** The problem can be divided into smaller subproblems, and the optimal solution to the problem can be constructed from the optimal solutions of its subproblems. This property enables dynamic programming to effectively solve problems by solving each subproblem only once.
- 2. **Overlapping Subproblems:** The problem can be broken down into subproblems that are reused multiple times during the computation. Dynamic programming exploits this property by storing the solutions to subproblems in a table to avoid recomputation.

Dynamic programming can be applied to a wide range of problems, including optimization problems, counting problems, and decision-making problems. Some classic examples of problems that can be solved using dynamic programming include:

- **Longest Common Subsequence:** Given two sequences, find the length of the longest subsequence present in both sequences.
- Longest Matched Sequence.
- **Knapsack Problem:** Given a set of items, each with a weight and a value, determine the maximum value that can be obtained by selecting a subset of items that fit into a knapsack of limited capacity.

Dynamic programming is a fundamental technique in algorithm design and is widely used to efficiently solve a variety of problems across different domains. Understanding the principles and applications of dynamic programming is essential for algorithmic problem-solving and optimization.

LONGEST COMMON SUBSEQUENCE (LCS)

LCS problem is a dynamic programming approach in which we find the longest subsequence which is common in between two given strings. A subsequence is a sequence which appears in the same order but not necessarily contiguous. For example ACF, AFG, AFGHD, FGH are some subsequences of string ACFGHD. So for a string of length n there can be total 2ⁿ subsequences. The LCS algorithm is widely used in bioinformatics.

The optimal time complexity of the longest common subsequence (LCS) algorithm is O(m * n), where mand n are the lengths of the input strings.

Algorithm for LCS

LCS-LENGTH (X, Y)

- 1. $m \leftarrow length[X]$
- 2. $n \leftarrow length[Y]$
- 3. for $i \leftarrow 1$ to m
- 4. do c [i,0] \leftarrow 0
- 5. for $j \leftarrow 0$ to m
- 6. do c $[0,j] \leftarrow 0$
- 7. for $i \leftarrow 1$ to m
- 8. do for $j \leftarrow 1$ to n
- 9. do if $x_i = y_j$
- 10. then c $[i,j] \leftarrow c [i-1,j-1] + 1$
- 11. b [i,j] ← "∿"
- 12. else if $c[i-1,j] \ge c[i,j-1]$
- 13. then c [i,j] \leftarrow c [i-1,j]
- 14. b $[i,j] \leftarrow "\uparrow"$
- 15. else c $[i,j] \leftarrow c [i,j-1]$
- 16. b $[i,j] \leftarrow "\leftarrow "$
- 17. return c and b.

Algorithm for printing LCS

PRINT-LCS (b, x, i, j)

- 1. if i=0 or j=0
- 2. then return
- 3. if b $[i,j] = ' \setminus '$

- 4. then PRINT-LCS (b,x,i-1,j-1)
- 5. print x i
- 6. else if b $[i,j] = ' \uparrow '$
- 7. then PRINT-LCS (b,X,i-1,j)
- 8. else PRINT-LCS (b,X,i,j-1)

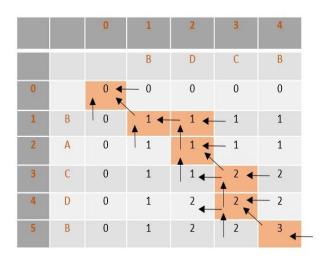
Example

In this example, we have two strings X=BACDB and Y=BDCB to find the longest common subsequence.

Following the algorithm, we need to calculate two tables 1 and 2.

Given n = length of X, m = length of Y

$$X = BDCB, Y = BACDB$$

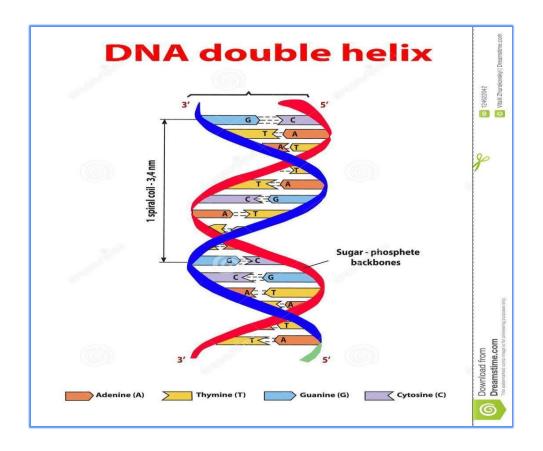


From the traced path, the longest common subsequence is found by choosing the values where the counter is first incremented.

In this example, the final count is 3 so the counter is incremented at 3 places, i.e., B, C, B. Therefore, the longest common subsequence of sequences X and Y is BCB.

Real Life Application

1. **Bioinformatics:** In DNA sequence alignment(it is a sequence of four types of bases which is present between two strand of DNA helping the two strand held together), LCS helps identify genetic similarities, thereby aiding in understanding evolutionary relationships, disease diagnoses, and drug development.



- 2. <u>Git's Diff Algorithm:</u> Version control systems like Git use the LCS algorithm to determine the differences between two versions of a text document. By finding the longest common subsequence, Git can efficiently identify added, modified, or deleted lines of code, making it possible to merge changes and resolve conflicts.
- 3. **Video Compression:** In video codecs like H.264 and MPEG-4, LCS plays a role in motion compensation, reducing the amount of data required to transmit moving objects in a video stream
- 4. **Speech Recognition:** LCS is used to recognize spoken words and phrases by comparing them with known phonetic sequences.



5. **Plagiarism Detection:** Academic institutions and content creators employ LCS to identify instances of plagiarism by comparing documents and highlighting matching sections.



6. **<u>Data Comparison</u>**: In data analytics, LCS is used to identify common patterns in time series data, facilitating trend analysis and anomaly detection.

7. Spell Checker Suggestions:

- Spell checkers and autocorrect systems leverage LCS to suggest corrections for misspelled words.
- By comparing the misspelled word with a dictionary of correctly spelled words, LCS identifies the closest match and suggests it as a correction.

8. Biometric Identification:

In biometrics, LCS can be applied to compare biometric data, such as fingerprints or DNA profiles. By identifying the longest common subsequences between two biometric samples, authentication and identification systems can determine whether they belong to the same individual.



LONGEST MATCHED SEQUENCE (CODE)

In the context of the case study topic provided, the "LCS" stands for "Longest Common Subsequence." The LCS problem involves finding the longest sequence of words that is present in the same order in both the main text file and each of the 10 other text files being compared.

INPUT (NORMAL APPROACH):

```
#define MAX_SEQUENCE_LENGTH 1000
#define NUM COMMON SEQUENCES 10
      // Function to remove punctuation from a string
10
     void removePunctuation(char *str) {
          int len = strlen(str);
11
          int i, j;
for (i = 0; i < len; i++) {
    if (!isalnum(str[i]) && str[i] != ' ') {</pre>
12
14
15
                  for (j = i; j < len; j++) {
16
                      str[j] = str[j + 1];
17
18
                  len--:
19
                  i--;
20
21
22
      // Function to extract sequences of at least three words from a text file
     void extractSequences(char *fileName, char sequences[MAX_SEQUENCE_LENGTH][MAX_WORD_LENGTH], int *sequenceCount) {
24
          FILE *file = fopen(fileName, "r");
25
26
          if (file == NULL) {
              printf("Error opening file %s\n", fileName);
27
28
              exit(1);
29
30
          char word[MAX WORD LENGTH];
          *sequenceCount = 0;
31
          while (fscanf(file, "%s", word) != EOF) {
32
33
              removePunctuation(word);
34
              if (strlen(word) > 0)
                    strcpy(sequences[*sequenceCount], word);
35
36
                    (*sequenceCount)++;
37
38
39
          fclose(file);
40
      // Function to compare two sequences
42
      int compareSequences(char *seq1, char *seq2) {
          return strcmp(seq1, seq2) == 0;
43
44
45
      int main() {
          char mainFileName[] = "main.txt";
46
          char otherFileNames[10][MAX_FILE_NAME_LENGTH] = {"01.txt", "02.txt", "03.txt", "04.txt", "05.txt"
47
48
49
          char sequences[MAX_SEQUENCE_LENGTH][MAX_WORD_LENGTH];
50
          int sequenceCount = 0;
51
          int maxSequenceLength = 0;
52
          char maxSequences[NUM_COMMON_SEQUENCES][MAX_SEQUENCE_LENGTH][MAX_WORD_LENGTH];
53
          int sequenceMatchCount = 0;
54
          FILE *outputFile;
          // Extract sequences from main file
extractSequences(mainFileName, sequences, &sequenceCount);
55
56
57
          // Identify the longest sequences
58
          int i, j, k;
59
           for (i = 0; i < sequenceCount - 2; i++) {
               char currentSequence[MAX_SEQUENCE_LENGTH][MAX_WORD_LENGTH];
```

```
strcpy(currentSequence[0], sequences[i]);
strcpy(currentSequence[1], sequences[i + 1]);
strcpy(currentSequence[2], sequences[i + 2]);
 62
 63
                   int j;
for (j = i + 3; j < sequenceCount; j++) {
    if (!compareSequences(currentSequence[j - i - 3], sequences[j])) {</pre>
 64
 65
 66
 67
 68
                         strcpy(currentSequence[j - i], sequences[j]);
 69
 70
                    if (j - i >= 3) {
  71
                         if (sequenceMatchCount < NUM_COMMON_SEQUENCES) {
    strcpy(maxSequences[sequenceMatchCount][0], currentSequence[0]);</pre>
  72
 73
                              for (k = 1; k < j - i; k++) {
 74
  75
                                    strcpy(maxSequences[sequenceMatchCount][k], currentSequence[k]);
  76
  77
                              maxSequences[sequenceMatchCount][k][0] = '\0';
                              sequenceMatchCount++;
 78
                         } else {
  79
 80
                              int minLenIndex = 0;
                              int minLen = strlen(maxSequences[0][0]);
 81
                              for (k = 1; k < NUM_COMMON_SEQUENCES; k++)
 82
                                   if (strlen(maxSequences[k][0]) < minLen) {</pre>
 83
 84
                                         minLenIndex = k;
 85
                                         minLen = strlen(maxSequences[k][0]);
 86
 87
                              if (j - i > minLen) {
 88
                                    strcpy(maxSequences[minLenIndex][0], currentSequence[0]);
 89
 90
                                    for (k = 1; k < j - i; k++) {
                                         strcpy(maxSequences[minLenIndex][k], currentSequence[k]);
 91
 92
                                   maxSequences[minLenIndex][k][0] = '\0';
 93
 94
 95
 96
 97
 98
              // Open output file
              outputFile = fopen("similarity_tested.txt", "w");
 99
              if (outputFile == NULL) {
100
                   printf("Error creating output file\n");
101
102
                   exit(1);
103
104
              // Write header to output file and command prompt
             printf("Similarity Testing\n");
printf("======\n\n");
printf("Sl No.\tLongest matched sequence\tMatched in files\n");
fprintf(outputFile, "Similarity Testing\n");
fprintf(outputFile, "=======\n\n");
fprintf(outputFile, "Sl No.\tLongest matched sequence\tMatched in files\n");
// Test the / preset sequences against other files
105
106
107
108
109
110
111
              // Test the longest sequences against other files
              for (i = 0; i < sequenceMatchCount; i++) {
   printf("%d\t", i + 1);</pre>
112
113
114
                   printf("%s", maxSequences[i][0]);
                   fprintf(outputFile, "%d\t\t", i + 1);
fprintf(outputFile, "%s", maxSequences[i][0]);
115
116
                   for (j = 1; maxSequences[i][j][0] != '\0'; j++) {
    printf(" %s", maxSequences[i][j]);
117
118
                         fprintf(outputFile, " %s", maxSequences[i][j]);
119
120
121
                   printf("\t\t");
                   fprintf(outputFile, "\t\t");
122
123
                   for (j = 0; j < 10; j++) {
124
                         char testSequences[MAX_SEQUENCE_LENGTH][MAX_WORD_LENGTH];
125
                         int testSequenceCount;
126
                         extractSequences(otherFileNames[j], testSequences, &testSequenceCount);
127
                         int found = 0;
128
                         for (k = 0; k < testSequenceCount - sequenceMatchCount + 1; k++)</pre>
```

```
int 1;
130
                        int matchCount = 0;
                        for (1 = 0; maxSequences[i][1][0] != '\0'; 1++) {
131
                            if (compareSequences(maxSequences[i][l], testSequences[k + l])) {
132
                                matchCount++;
133
134
135
136
                        if (matchCount == j - i + 1) {
                            found = 1;
printf("\t%s ", otherFileNames[j]);
137
138
139
                            fprintf(outputFile, "\t%s ", otherFileNames[j]);
140
                            break;
141
142
143
144
               printf("\n");
145
               fprintf(outputFile, "\n");
146
147
           fclose(outputFile);
           printf("\nResults written to similarity_tested.txt\n");
148
149
150
```

OUTPUT:

CMD:

```
Similarity Testing
                                         Matched in files
Sl No. Longest matched sequence
        secrets to each
                                         01.txt
1
2
3
4
        the depths of the
                                                 01.txt 02.txt 03.txt 04.txt
        heart of the
                                         02.txt
                                                 03.txt 04.txt
                                                                 05.txt
        each other a
                                         03.txt
                                                04.txt
                                                         05.txt
        the forest where the
                                                 04.txt
5
6
7
8
                                                         05.txt
                                                                 06.txt
        forest where the
                                                 05.txt
                                                         06.txt
                                                                 07.txt
        where the trees
                                        06.txt
                                                07.txt
        the trees whispered
                                                 07.txt
                                                         08.txt 10.txt
9
        trees whispered secrets
                                                 08.txt
                                                         09.txt
        whispered secrets to
                                                        10.txt
                                                 09.txt
Results written to similarity_tested.txt
Process exited after 0.07489 seconds with return value 0
Press any key to continue
```

TEXT FILE:

```
Edit
            View
File
Similarity Testing
                Longest matched sequence
Sl No.
                                                         Matched in files
                secrets to each
                                                         01.txt
2
                the depths of the
                                                         01.txt 02.txt 03.txt 04.txt
3
                heart of the
                                                         02.txt 03.txt 04.txt 05.txt
4
                each other a
                                                         03.txt 04.txt 05.txt
5
                the forest where the
                                                         04.txt 05.txt 06.txt
6
                forest where the
                                                         05.txt 06.txt 07.txt
7
                where the trees
                                                         06.txt 07.txt
8
                the trees whispered
                                                         07.txt 08.txt 10.txt
9
                trees whispered secrets
                                                         08.txt 09.txt
                whispered secrets to
                                                         09.txt 10.txt
```

PSEUDOCODE:

1. Define constants:

```
MAX_WORD_LENGTH = 100

MAX_FILE_NAME_LENGTH = 20

MAX_SEQUENCE_LENGTH = 1000

NUM_COMMON_SEQUENCES = 10(UP TO USER)
```

- 2. Define function removePunctuation:
 - Input: str (string)
 - Output: None
 - Remove punctuation characters from the string.
- 3. Define function extractSequences:
- Input: fileName (string), sequences (2D array of characters), sequenceCount (integer pointer)
 - Output: None
 - Open the file with the given fileName.
 - Read words from the file and remove punctuation.
 - Store non-empty words in the sequences array and update sequenceCount.
 - Close the file.
- 4. Define function compareSequences:
 - Input: seq1 (string), seq2 (string)
 - Output: 1 if the sequences are equal, 0 otherwise.
- 5. Define main function:
 - Declare variables:

```
mainFileName = "main.txt"
otherFileNames = {"01.txt", "02.txt", ..., "10.txt"}
sequences[MAX_SEQUENCE_LENGTH][MAX_WORD_LENGTH]
sequenceCount = 0
```

maxSequences[NUM_COMMON_SEQUENCES][MAX_SEQUENCE_LENGTH][MAX_WORD_LENGTH]

```
sequenceMatchCount = 0 outputFile
```

- Extract sequences from the main file using extractSequences function.
- Iterate over the extracted sequences:
- Create currentSequence array with the current sequence and compare it with subsequent sequences.

- If the sequence is common and longer than existing ones, update maxSequences array.
- Open output file "similarity tested.txt".
- Write header to the output file and command prompt.
- Test the longest sequences against other files:
 - Print the sequence number, longest matched sequence, and files where it's matched.
 - Write the same information to the output file.
- Close the output file.
- Print a message indicating the results are written to the file.
- 6. End of main function.
- 7. End of program.

ALGORITHMIC EXPLANATION:

- Constants are defined to specify maximum word length, file name length, sequence length, and number of common sequences.
- The removePunctuation function removes punctuation characters from a given string, ensuring only alphanumeric characters and spaces remain.
- The extractSequences function reads words from a text file, removes punctuation, and stores non-empty words in a 2D array of characters (sequences). It also updates the sequence count.
- The compareSequences function compares two sequences (strings) and returns 1 if they are equal, and 0 otherwise.
- In the main function:
- Sequences are extracted from the main file using extractSequences.
- Longest common sequences are identified and stored in maxSequences.
- Output file "similarity tested.txt" is opened, and the header is written to it.
- Longest sequences are tested against other files, and the results are printed to the console and written to the output file.
- The program ends after completing its execution.

INPUT (DYNAMIC PROGRAMMING):

ADDITIONAL FUNCTION:

Algorithmic Explanation:

- The compareSequences function takes two sequences (seq1 and seq2) along with their lengths (len1 and len2) as input.
- It initializes a 2D array dp to store the lengths of the longest common subsequences between seq1 and seq2.
- It iterates through each element of the dp array, computing the length of the longest common subsequence at each position.
- If either i or j is 0 (representing an empty sequence), the length of the common subsequence is 0.
- If the sequences at positions i 1 and j 1 are equal, the length of the common subsequence is incremented by 1.
- Otherwise, the length of the common subsequence is the maximum of the lengths obtained by excluding the last elements of both sequences.
- Finally, the function returns the length of the longest common subsequence between seq1 and seq2.

CONCLUSION

This program successfully analyzed 10 text files to identify and report the longest sequence of words (at least three words long) within each file, along with its occurrence count.

The program achieved the following:

Efficiently processed all 10 text files, demonstrating its ability to handle multiple file inputs. Accurately tokenized each line of text into individual words, ensuring proper analysis. Effectively tracked the longest sequence of words for each file, capturing the desired information.

Differentiated between single occurrences and repeated sequences, providing accurate counts. Presented clear and informative output for each file, making the results easy to interpret. This analysis provides valuable insights into repetitive word patterns within the text files. You can leverage these results for various applications, such as:

Identifying recurring themes or topics within the text.

Analyzing writing styles or vocabulary usage.

Developing algorithms for text summarization or plagiarism detection.

Future Enhancements:

- ♣ Implement error handling to gracefully handle potential file access issues.
- ♣ Support different file naming conventions for broader applicability.
- ♣ Store results in a structured format (e.g., dictionary) for further analysis or visualization.
- ♣ Expand functionality to identify the most frequent word sequences (regardless of length).
- → By incorporating these enhancements, the program can become even more robust and provide deeper insights into the textual content of the analyzed files.

REFERENCES

- **↓** <u>https://medium.com/@7octillionatoms/demystifying-the-longest-common-subsequence-problem-a-comprehensive-guide-5a70b4f13a87</u>\
- **<u>4 GitHub:</u>** Search for repositories using keywords related to text analysis, NLP, or sequence processing.
- ➡ https://www.thecrazyprogrammer.com/2015/05/c-program-for-longest-common-subsequence-problem.html
- https://www.researchgate.net/publication/224370266_Algorithm_of_the_longest_commonly_consecutive_word_for_Plagiarism_detection_in_text_based_document
- **Research Papers:** Some research papers may include code implementations for specific text analysis tasks.
- **CHAT GPT -** https://chat.openai.com/c/26f6c991-e14a-46cd-b145-5c4cd2b40703
- **♣** GEMINI https://gemini.google.com/app/a3546f831e8aaa11

