Algorithms and Complexity. Exercise session 3+4

Dynamic Programming

Longest Common Substring The string `ALGORITHM` and the string `PLÅGORIS` have the common substring `GORI`. The *longest common substring* of these strings has thus length 4. The letters in a substring must form a coherent sequence.

Construct an efficient algorithm that given two strings $a_1a_2\dots a_m$ and $b_1b_2\dots b_n$ calculates the length of the longest common substring. The algorithm uses dynamic programming and runs in time $O(nm)$.

Solution to Longest Common Substring
Let $M[i,j]$ be the number of letters to the left of (and including) a_i which comply with the same number of letters to the left (and including) b_j. The length of the longest common string is the largest number in matrix M.

M can be defined recursively as follows:

$$M[i,j] = \begin{cases} 0 & \text{if } i = 0 \text{ or } j = 0, \\ M[i-1,j-1]+1 & \text{if } a_i = b_j, \\ 0 & \text{otherwise.} \end{cases}$$

The following algorithm computes M and returns the largest number in M.

```
$max \leftarrow 0$
for $j \leftarrow 0$ to $n$
  $M[0,j] \leftarrow 0$
for $i \leftarrow 1$ to $m$
  $M[i,0] \leftarrow 0$
  for $j \leftarrow 1$ to $n$
    if $a_i = b_j$ then
      $M[i,j] \leftarrow M[i-1,j-1]+1$
      if $M[i,j] > max$ then $max \leftarrow M[i,j]$
    else $M[i,j] \leftarrow 0$
return $max$
```

The running time is dominated by the nested *for* loops and therefore is $\Theta(nm)$. □

Sequences You are given two sequences of positive integers $a_1, a_2, \dots, a_n$ and $b_1, b_2, \dots, b_n$, where all numbers are less than n^2, and a positive integer B, such that $B \le n^3$. The problem is to determine if there is a sequence $c_1, c_2, \dots, c_n$ such that $\sum_{i=1}^{n} c_i = B$ and $c_i = a_i$ or $c_i = b_i$ for $1 \le i \le n$.

Describe and analyze an algorithm that solves this problem by using dynamic programming. Moreover, describe how to extend the algorithm to construct the solution, where $c_i = a_i$ or $c_i = b_i$ for $1 \le i \le n$.

Solution to Sequences
We create a boolean $n \times B$-matrix M that is initially contains only zeros. A one in $M[k,s]$ means that there is a choice of $c_1, \dots, c_k$ such that $\sum_{i=1}^{k} c_i = s$.

The recursive equation for $M[k, s]$ becomes:

$$M[k,s] = \begin{cases} 1 & \text{if } k = 1 \text{ and } (s = a_1 \text{ or } s = b_1), \\ 1 & \text{if } k > 1 \text{ and } (M[k-1, s-a_k] = 1 \text{ or } M[k-1, s-b_k] = 1), \\ 0 & \text{otherwise.} \end{cases}$$

The calculation begins with $M[1, a_1]$ and $M[1, b_1]$ set to 1. Then we put ones in $M[2, a_1 + a_2]$, $M[2, a_1 + b_2]$, $M[2, b_1 + a_2]$ and $M[2, b_1 + b_2]$ in the second row of the matrix, then we put it ones in the third row and so on. If there is a one in $M[n, B]$, the answer to the problem is yes.

The algorithm may look like this in C:

```
int ExistsC(int n, int a[], int b[], int B)
{ char M[n + 1][B + 1]; /* Dynamc arrays are an extension of gcc */
  int i, j;
  for (i = 1; i <= n; i++)
    for (j = 1; j <= B; j++) M[i][j] = 0;
  M[1][a[1]] = M[1][b[1]] = 1;
  for (i = 2; i <= n; i++)
    for (j = 1; j <= B; j++) {
      if (j - a[i] > 0 && M[i - 1][j - a[i]]) M[i][j] = 1;
      if (j - b[i] > 0 && M[i - 1][j - b[i]]) M[i][j] = 1;
    }
  return M[n][B];
}
```

The nested *for* loop runs $(n-1)B$ times and each time it performs more than four comparisons and two assignments, ie a constant number. The whole running time of the algorithm is therefore in $O(n^2) + O((n-1)B) = O(n^2 + nB) \subseteq O(n^4)$. You can construct the solution by starting from the end (from the n-th row and up) and looking for positions where there is a one. The one in $M[n, B]$ must be there because of a one in either $M[n-1, B-a_n]$ or $M[n-1, B-b_n]$. Remember which of these it is. If a one occurs in two positions, just pick one (as only one solution is requested) and continue in this way from the selected position. Implementation in C is as follows.

```
void WriteC(int n, int a[], int b[], int B)
{ int c[n + 1], pos;

  /* Procedure ExistsC goes here*/

  pos = B;
  for (i = n; i > 1; i++) {
    if (pos - a[i] > 0 && M[i - 1][pos - a[i]]) c[i] = a[i];
    else c[i] = b[i];
    pos -= c[i];
  }
  c[1] = pos;
  printf("The answer is %d", c[1]);
  for (i = 2; i <= n; i++) printf(" + %d", c[i]);
}
```

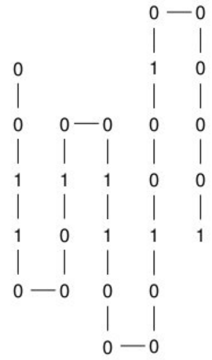
□

Protein Folding A protein is a long chain of aminoacids. The protein chain is not straight but it is folded in a way that minimizes the potential energy. Our goal is to calculate how the protein will fold itself. In this exercise we will therefore consider a simple model of protein folding in which aminoacids are either *hydrophobic* or *hydrophilic*. Hydrophobic aminoacids tend to clump together.

For simplicity, we can see the protein as a binary string in which ones correspond to hydrophobic aminoacids and zeros hydrophilic aminoacids. The string (protein) should then be folded into a two-dimensional square grid. The goal is to make the hydrophobic aminoacids stick together, i.e., to get as many ones as possible to be close to each other. Hence we have an optimization problem where the objective function is the number of pairs of ones that are next to each other in the grid (vertically or horizontally) without being next to each other in the string.

You should design an algorithm using dynamic programming to construct an optimal *accordion fold* of a given protein string of length n. An *accordion fold* is a fold where the first string goes straight down, then goes straight up, then goes straight down, and so on. In such a fold, it can be observed that the vertical pairs of adjacent ones will always result in the string, so it's only horizontal pair of ones that contribute to the objective function.

The following figure shows the string 001100010011000001001000001 of accordion fold in such a way that the objective function is 4.



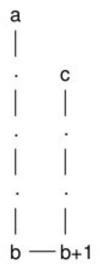
Problem definition PROTEIN ACCORDION FOLD:

INPUT A binary string of n characters.
PROBLEM: Find the accordion fold of input string that provides the greatest value to the objective function, ie the largest number of pairs of ones located next to each other, but not consecutive to each other in the string.

Construct and analyze the time complexity of an algorithm that solves protein accordion folding problem with dynamic programming.

Use the following algorithm which calculates the number of pairs of ones in a row (ie between two lines) lying next to each other (but not next to each other in the string). Suppose the protein is stored in an array `p[1..n]`. The parameters `a` and `b` indicate the index in the array for the first trait endpoints. The parameter `c` indicates the index for the second trait endpoint as dipicted in the figure below on the right.

```
profit(a,b,c) =
shortest←min(b-a,c-(b+1));
s←0;
for i←1 to shortest do
if p[b-i]=1 and p[b+1+i]=1 then
s←s+1;
return s;
```



Note: Protein folding is an important algorithmic problem studied in bioinformatics. Similar problems are studied in the *Algoritmisk bioinformatik* course.

Solution to Protein folding
Let $q_{a,b}$ be the maximum value of the objective function obtained for the folding of part $p[a..n]$

of the protein, where the first trait of the folding has endpoints a and b. We can express $q_{a,b}$ recursively as follows:

$$q_{a,b} = \max_{b+1<c\leq n} (\texttt{profit}(a,b,c) + q_{b+1,c}).$$

The base case is $q_{a,n} = 0$ if $1 \leq a < n$. Then, the answer consists of $\max\limits_{1<b\leq n} q_{1,b}$.
Now it only remains to calculate these formulas in the right order:

```
for a←1 to n-1 do q[a,n]←0;
for b←n-1 downto 2 do
    for a←1 to b-1 do
        t←-1;
        for c←b+2 to n do
            v←profit(a,b,c)+q[b+1,c];
            if v>t then t←v;
        q[a,b]←t;
max←0;
for b←2 to n do
    if q[1,b]>max then max←q[1,b];
return max;
```

Since we mostly have three nested `for`-loops and a call to `profit` takes time $O(n)$, the time complexity is $O(n^4)$. □

Analyzer for context-free grammars A context-free grammar is usually used to describe the syntax of a particular programming language. A context-free grammar in *Chomsky Normal Form* is described by

- a set of final symbols T (usually written in small letters),
- a set of non-final symbols N (usually written in capital letters),
- the initial symbol S (a non-final symbol in N),
- a set of rewrite rules of type $A \rightarrow BC$ or $A \rightarrow a$, for $A, B, C \in N$ and $a \in T$.

If $A \in N$ we define $\mathcal{L}(A)$ as

$$\mathcal{L}(A) = \{bc : b \in \mathcal{L}(B) \text{ and } c \in \mathcal{L}(C) \text{ where} A \rightarrow BC\} \cup \{a : A \rightarrow a\}.$$

The language generated by the grammar is then defined as $\mathcal{L}(S)$, ie. the set of all strings of the final symbols that can be formed by a rewriting chain from symbol S.

Example: Consider the grammar $T = \{a, b\}$, $N = \{S, A, B, R\}$, start symbol S and rules $S \rightarrow AR$, $S \rightarrow AB$, $A \rightarrow a$, $B \rightarrow b$, $R \rightarrow SB$. We can see that string $aabb$ is in the language generated by the grammar using the following chain of rewritings:

$$S \rightarrow AR \rightarrow aR \rightarrow aSB \rightarrow aSb \rightarrow aABb \rightarrow aaBb \rightarrow aabb.$$

In fact, one can show that the language generated by the grammar is the set of all strings consisting of k symbols a followed by k symbols b, where k is a positive integer.

Your task is to *design* and *analyze* an efficient algorithm that determines if a string is in the language generated by a given grammar. The input is a context-free grammar in Chomsky Normal Form, and a string of final symbols. The output is true or false depending on whether the string can be generated by the grammar or not. Calculate the time complexity of your algorithm in terms of number of rules m of the grammar and length n of the string.

You can read more on grammars in the course *Artificiella språk och syntaxanalys*.

Solution to Analyzer for context-free grammars

We use dynamic programming to solve this problem. We determine the order and the substring rules to apply.

The input is a set of rules R and a vector `w[1..n]`, indexed from 1 to n. Let us build a matrix `M[1..n,1..n]`, where the elements of `M[i,j]` indicate the set of non-final symbols from which one can derive the substring `w[i..j]` from a chain of rewriting rules. `M[i,j]` is recursively defined as:

$$\mathtt{M}[i,j] = \begin{cases} \{X : (X \rightarrow \mathtt{w}[i]) \in R\} & \text{if } i = j \\ \{X : (X \rightarrow AB) \in R \wedge \exists k : A \in \mathtt{M}[i,k-1] \wedge B \in \mathtt{M}[k,j]\} & \text{if } i < j \end{cases}$$

Since each position in the array is a set of non-final symbols, we must choose an appropriate data structure for this. We represent the set of non-final symbols as a bit vector indexed by non-final symbols. A 1 means that the symbol is in the set and a 0 means that the symbol is not in the set. Example: If `M[i,j]`[B]$= 1$, the non-final symbol B is in the set `M[i,j]`, namely, there is a chain of rewrite rules from B to the substring `w[i..j]`.

The algorithm computes the matrix `M[i,j]` and returns true if the string belongs to the language generated by the grammar:

```
for i←1 to n do
    M[i,i]←0; /* all bits are reset */
    for each rule $X$ →w[i] do
        M[i,i][$X$]←1;
for len←2 to n do
    for i←1 to n-len+1 do
        j←i+len-1;
        M[i,j]←0;
        for k←i+1 to j do
            for each rule $X \rightarrow AB$ do
                if M[i,k-1][$A$]=1 and M[k,j][$B$]=1 then
                    M[i,j][$X$]←1;
return M[1,n][$S$]= 1;
```

Time complexity: $O(n^3 m)$. Memory: $O(n^2 m)$ (because m is an upper bound on the number of non-final symbols). □