Bioinformatics Algorithms

Dynamic Programming

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Outline

- Dynamic programming basics
 - o recursion
 - o approaches
- Example problems
 - o Fibonacci numbers
 - o matrix product
 - o longest common subsequence

Sources

- Animations
 - o AIViE suite https://sites.google.com/site/alviehomepage/

Recursion

- Method where the **solution** to a problem **is built** from solution of **smaller instances** of the same problem
- Usually recursive problem is solved by a parameterized function which calls itself with parameter reflecting smaller instance(recursion)
- Examples
 - o factorial
 - $n! = n(n-1)! \to F(n) = nF(n-1)$
 - o Fibonacci numbers
 - o greatest common divisor
 - o binary search
 - O ...

Dynamic Programming (DP)

Algorithm design technique/concept

Conditions

- the optimal solutions to a problem is composed of optimal solutions to subproblems
- o if there are several optimal solutions, we don't care which one we get

Approaches

- o Top-down
 - retains standard recursive top-down structure but stores
- o Bottom-up
 - higher levels share results from the lower levels
 - DP solutions are often considered only those using bottom-up approach
- o see Fibonacci for an example

Dynamic Programming and Dimension

 Dynamic programming solves problems by dividing problem into subproblems and using their results later

Memoization

- o to store results of the subproblems n-dimensional array is usually used
- Usually, we talk about dynamic programming when $n \ge 2$
 - o e.g., algorithm for computation of Fibonacci numbers fulfills the conditions of DP solution but n < 2

Fibonacci Numbers (FN)

Definition

$$\circ F(n) = \begin{cases} n & n \leq 1 \\ F(n-1) + F(n-1) & n > 1 \end{cases}$$

o F(0) = 0, F(1) = 1, F(2) = 1, F(3) = 2, F(4) = 3, F(5) = 5, F(6) = 8, ...

- Task
 - o Given n compute F(n)



high redundancy

```
FN – DP – Top-Down
```

```
{
    if (n <= 1) return n;
    else if (f[n] == 0)
    {
        f[n] = FibDPTD_rec(n - 1, f) + FibDPTD_rec(n - 2, f);
    }
    return f[n];
}
static int FibDPTD(int n)
{
    //f ... dynamic programming array
    int[] f = new int[n];
    Array.Clear(f, 0, f.Length);
    return FibDPTD_rec(n, f);
}</pre>
```

requires O(n) time and space

FN - DP - Bottom-Up static int FibDP(int n) { //f ... dynamic programming array f[0] = 0; f[1] = 1; for (int k = 2; k < n; k++) f[k] = f[k - 1] + f[k - 2]; return f[n]; }</pre>

- one-dimensional dynamic programming array
- no redundant computations
- for computation of the solution, the subsolutions are used
- requires O(n) time and space (can be done in O(1))

Matrix Product Ordering (MPO) At a matrixAt a matrix<td

- Matrix multiplication
 - 0
 - and produces matrix $C[p \times r]$ \bigcirc

 $x_{12} = (a_{11}, a_{12}) \cdot (b_{12}, b_{22}) = a_{11}b_{12} + a_{12}b_{22}$ $x_{33} = (a_{31}, a_{32}) \cdot (b_{13}, b_{23}) = a_{31}b_{13} + a_{32}b_{23}.$

- associative \bigcirc
 - A(BC) = (AB)C
 - ABCD = ((AB)C)D = (A(BC)D) = A((BC)D) = A(B(CD)) = (AB)(CD)

Task

- Given *n* matrixes $A_1, A_2, \dots A_n$ find such a parenthesization minimizing Ο number of multiplications of the matrixes' items
 - order of multiplication in the chain is important
 - $n = 3, A_1[2 \times 3], A_2[3 \times 2], A_3[2 \times 5]$
 - o $A_1A_2 = 12$ multiplications, $(A_1A_2)A_3 = 20$ multiplications $\rightarrow 32$ in total o $A_2A_3 = 30$ multiplications, $A_1(A_2A_3) = 30$ multiplications $\rightarrow 60$ in total

MPO - Recursion

- MPORec returns minimum number of multiplications needed to multiply matrices $A_{ixFrom+1}, A_{ixTo+1}$ (+1 because C# arrays go from 0)
- scan the array of matrices
- at each position take the best result from left, right and add their product cost
- parenthesization can be stored in an auxiliary structure

MPO - DP

- DP matrix M will store in M[i, j] minimum number of multiplications needed to multiply *i* consequent matrices starting at position *j* $(A_j, A_{j+1}, \dots, A_{j+i-1}) \rightarrow M[n, 1]$ contains the **result** (indexing from 1 for sake of clarity) runs starting A_1 , at position 3
- M[i, j] can be computed by increasing i
 - $\circ \quad M[1,j] = 0$
 - $M[i,j] = \min(M[k,j] + M[i-k,j+k] + p[j-1] \times p[j+k-1] \times p[j+i-1])$



MPO – DP (cont.)

```
static int MPO()
    //n ... # matrices
   //m ... dynamic programming matrix
   //m[i][j] = minimum number of operations needed to multiply A i, ..., A i+j
   //p ... matrices dimenstions
    for (int i = 1; i <= n; i++) m[1][i] = 0; //indexing from 1 for sake of clarity
    for (int i = 1; i <= n; i++)</pre>
        for (int j = 1; j \le n - i + 1; j++)
            cntMin = Int32.MaxValue:
            for (int k = 1; k < i - 1; k++)
                int cntMult = m[k][j] + m[i - k][j + k] + p[j - 1] * p[j + k - 1] * p[j + i - 1];
                if (cntMult < cntMin) cntMin = cntMult;
            3
            m[i][j] = cntMin;
        3
    return cntMin;
```

• Runs in $O(n^3)$ time and $O(n^2)$ space

Longest Common Subsequences (LCS)

- Task
 - Given two sequence $S_1[1 \dots m]$ and $S_2[1 \dots n]$, find a longest common subsequence (not substring) common to both.
 - Sequence **S** of length |S| is a **subsequence** of sequence **A** of length |A| if there exists indeces $1 \le i_1 < i_2 < ... < i_{|S|} <= |A|$ in A such that $S[j] = A[i_j]$, j = 0, 1, ..., |S|
 - **S** is a **common subsequence** of S_1 and S_2 only if it is subsequence of both S_1 and S_2 .



Particularly important in computational biology

LCS – Brute-Force

- Check every subsequence of S_{1 in} S₂
 - o for each subsequence ss_1 in s_1 we can test whether it is present in s_2 in O(n) time
 - scanning s_2 linearly and checking whether first letter in s_2 corresponds to the first letter in ss_1
 - if so, let us continue in the same fashion with the second letter from that position
 - when we run out of letters of ss_1 , ss_1 is present in s_2
 - o the are $O(2^m)$ subsequences \rightarrow complexity of the brute-force algorithm is $O(n2^m)$
 - OK for short sequences but not for, e.g., DNA sequences

LCS – DP

- DP solution is based on computing LCS for prefixes of S_1 and S_2 (subproblems in DP)
- Let us denote LCS(i, j) LCS of i and j long prefixes of S₁ and S₂

• $LCS(|S_1|, |S_2|) =$ solution of LCS

Recursive rule

$$\circ \ \ LCS(i,j) \begin{cases} 0 & i = 0 \ or \ j = 0 \\ L(i,-1\ j-1) + 1 & S_1[i] = S_2[j] \\ max\{L(i,j-1),L(i-1,j)\} & S_1[i] \neq S_2[j] \end{cases}$$

$$LCS - DP(cont.)$$
• $L(i,j) \begin{cases} 0 & i = 0 \text{ or } j = 0 & (1) \\ L(i,-1j-1)+1 & S_1[i] = S_2[j] & (2) \\ max\{L(i,j-1),L(i-1,j)\} & S_1[i] \neq S_2[j] & (3) \end{cases}$

- 1. If there is only one sequence, LCS = 0
- 2. If $LCS(A_1, A_2) = n$ then $LCS(A_1x, A_2x) = n + 1$
 - because if two sequences have the same 1-letter suffix then their LCS will contain it, otherwise it wouldn't be LCS



3. If two sequences A_1x and A_2y differ at last position then their LCS is identical to either LCS(A_1x, A_2) or LCS(A_1, A_2y)



LCS – DP (cont.)

```
1 LCS( a, b )
      FOR (i = 0; i \le m; i = i+1)
 2
 3
       length[i][0] = 0;
      FOR (j = 0; j \le n; j = j + 1)
 4
        length[0][j] = 0;
 5
      FOR (i = 1; i \le m; i = i+1)
 6
 7
        FOR (j = 1; j \le n; j = j+1) {
 8
          IF (a[i-1] == b[j-1]) {
            length[i][j] = length[i-1][j-1] + 1;
 9
          } ELSE IF (length[i][j-1] > length[i-1][j]) {
10
11
            length[i][j] = length[i][j-1];
          } ELSE {
12
            length[i][j] = length[i-1][j];
13
14
          }
15
        }
16
      RETURN length[m][n];
```

 The alignment itself can be identified easily by backtracking

LCS Matrix

		В	D	С	Α	В	Α
	0	0	0	0	0	0	0
Α	0	0	0	0	1	1	1
В	0	1	1	1	1	2	2
С	0	1	1	2	2	2	2
В	0	1	1	2	2	3	3
D	0	1	2	2	2	3	3
A	0	1	2	2	3	3	4
В	0	1	2	2	3	4	4

LCS Backtracking

В

B

Α

A

А

		В	D	С	Α	B	Α
	0	0	0	0	0	0	0
Α	0	0	0	0	1	1	1
В	0	1	1	1	1	2	2
С	0	1	1	2	2	2	2
В	0	1	1	2	2	3	3
D	0	1	2	2	2	3	3
Α	0	1	2	2	3	3	4
B	0	1	2	2	3	4	4

В

В

А

D

C

C

В

D

		В	D	С	Α	В	Α
	0	0	0	0	0	0	0
Α	0	0	0	0	1	1	1
В	0	1	1	1	1	2	2
С	0	1	1	2	2	2	2
В	0	1	1	2	2	3	3
D	0	1	2	2	2	3	3
Α	0	1	2	2	3	3	4
B	0	1	2	2	3	4	4



LCS - example

AlVie

- Practise
 - o LCS (HUMAN, CHIMPANZEE)