COMP 355 Advanced Algorithms Dynamic Programming: Knapsack & LCS Section 6.4 (KT)



Knapsack Problem

There are two versions of the problem: (1) "0-1 knapsack problem" and (2) "Fractional knapsack problem"

 (1) Items are indivisible; you either take an item or not. Solved with *dynamic programming* (2) Items are divisible: you can take any fraction of an item. Solved with a *greedy algorithm*.

Knapsack Problem

Knapsack problem.

- Given *n* objects and a "knapsack."
- Item *i* weighs $w_i > 0$ kilograms and has value $v_i > 0$.
- Knapsack has capacity of W kilograms.
- Goal: fill knapsack so as to maximize total value.

Ex: { 3, 4 } has value 40.

Value Weight Item 1 1 1 2 2 6 3 18 5 22 4 6 5 28 7

Greedy: repeatedly add item with maximum ratio v_i / w_i . Ex: { 5, 2, 1 } achieves only value = 35 \Rightarrow greedy not optimal.

Knapsack Problem: Bottom-Up

Knapsack. Fill up an n-by-W array.

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Input: n, \mathbf{w}_1, \dots, \mathbf{w}_N, \mathbf{v}_1, \dots, \mathbf{v}_N
for w = 0 to W
   M[0, w] = 0
for i = 1 to n
    for w = 1 to W
        if (w_i > w)
            M[i, w] = M[i-1, w]
        else
            M[i, w] = \max \{M[i-1, w], v_i + M[i-1, w-w_i]\}
```

return M[n, W]

Knapsack Algorithm

							W + 1						
		0	1	2	3	4	5	6	7	8	9	10	11
n + 1	φ	0	0	0	0	0	0	0	0	0	0	0	0
	{1}	0	1	1	1	1	1	1	1	1	1	1	1
	{ 1, 2 }	0	1	6	7	7	7	7	7	7	7	7	7
	{ 1, 2, 3 }	0	1	6	7	7	18	19	24	25	25	25	25
	{ 1, 2, 3, 4 }	0	1	6	7	7	18	22	24	28	29	29	40
	{ 1, 2, 3, 4, 5 }	0	1	6	7	7	18	22	28	29	34	34	40

OPT: { 4, 3 }	
value = 22 + 18 = 40	

W = 11

Item	Value	Weight
1	1	1
2	6	2
3	18	5
4	22	6
5	28	7

Knapsack Problem: Running Time

Running time. $\Theta(n W)$.

- Not polynomial in input size!
- "Pseudo-polynomial."
- Decision version of Knapsack is NP-complete.

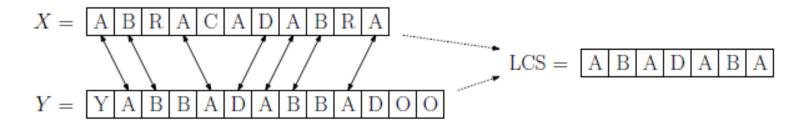
Knapsack approximation algorithm. There exists a polynomial algorithm that produces a feasible solution that has value within 0.01% of optimum.

Using DP to compare strings

- Determining the degree of similarity between two strings
 - Applications in computational biology (sequence alignment)
 - Applications in document processing and retrieval
- One common measure of similarity between two strings is the lengths of their longest common subsequence.

Longest Common Subsequence (LCS)

Given two sequences $X = \langle x_1, x_2, \ldots, x_m \rangle$ and $Z = \langle z_1, z_2, \ldots, z_k \rangle$, we say that Z is a subsequence of X if there is a strictly increasing sequence of k indices $\langle i_1, i_2, \ldots, i_k \rangle$ ($1 \leq i_1 < i_2 < \ldots < i_k \leq n$) such that $Z = \langle x_{i_1}, x_{i_2}, \ldots, x_{i_k} \rangle$. For example, let X = $\langle ABRACADABRA \rangle$ and let Z = $\langle AADAA \rangle$, then Z is a subsequence of X.



LCS Problem: Given two sequences $X = \langle x_1, \ldots, x_m \rangle$ and $Y = \langle y_1, \ldots, y_n \rangle$ determine the length of their longest common subsequence, and more generally the sequence itself.