

Objectives

- Dynamic Programming
 - Knapsacks
 - RNA Substructure

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Knapsack Problem

- Given n objects and a "knapsack"
- Item i weighs $w_i > 0$ kilograms and has value $v_i > 0$
 - Example: jobs require w_i time
- Knapsack has capacity of W kilograms
 - Example: W is time interval that resource is available

Goal: fill knapsack so as to maximize total value

$W = 11$

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

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Towards a Recurrence...

- What do we know about the knapsack with respect to item i ?

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Towards a Recurrence...

- What do we know about the knapsack with respect to item i ?
 - Either select item i or not
 - If don't select
 - Pick optimum solution of remaining items
 - Otherwise
 - What happens?
 - How does problem change?

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Dynamic Programming: False Start

- **Def.** $OPT(i)$ = max profit subset of items 1, ..., i
 - Case 1: OPT does not select item i
 - OPT selects best of $\{1, 2, \dots, i-1\}$
 - Case 2: OPT selects item i
 - Accepting item i does not immediately imply that we will have to reject other items
 - No known conflicts
 - Without knowing what other items were selected before i , we don't even know if we have enough room for i

➡ Need more sub-problems!

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Dynamic Programming: Adding a New Variable

- **Def.** $OPT(i, w)$ = max profit subset of items 1, ..., i with weight limit w
 - Case 1: OPT does not select item i
 - OPT selects best of $\{1, 2, \dots, i-1\}$ using weight limit w
 - Case 2: OPT selects item i
 - new weight limit = $w - w_i$
 - OPT selects best of $\{1, 2, \dots, i-1\}$ using new weight limit, $w - w_i$

$$OPT(i, w) = \begin{cases} 0 & \text{if } i = 0 \\ OPT(i-1, w) & \text{if } w_i > w \\ \max\{OPT(i-1, w), v_i + OPT(i-1, w - w_i)\} & \text{otherwise} \end{cases}$$

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Knapsack Problem: Bottom-Up

- Fill up an n-by-W array

```

Input: N, w1, ..., wN, v1, ..., vN
for w = 0 to W
    M[0, w] = 0
for i = 1 to N # for all items
    for w = 1 to W # for all possible weights
        if wi > w : # item's weight is more than available
            M[i, w] = M[i-1, w]
        else
            M[i, w] = max{ M[i-1, w], vi + M[i-1, w-wi] }
return M[n, W]
    
```

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Knapsack Algorithm

		W											
		0	1	2	3	4	5	6	7	8	9	10	11
i	φ	0	0	0	0	0	0	0	0	0	0	0	0
	{1}	0											
	{1,2}	0											
	{1,2,3}	0											
	{1,2,3,4}	0											
n + 1	{1,2,3,4,5}	0											

OPT:
Value=

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

W = 11

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Knapsack Algorithm

		W + 1											
		0	1	2	3	4	5	6	7	8	9	10	11
i = 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											
	{1,2,3}	0											
	{1,2,3,4}	0											
n + 1	{1,2,3,4,5}	0											

OPT:
Value=

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

W = 11

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Knapsack Algorithm

		W + 1											
		0	1	2	3	4	5	6	7	8	9	10	11
i = 2	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											
	{1,2,3,4}	0											
n + 1	{1,2,3,4,5}	0											

OPT:
Value=

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

W = 11

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Knapsack Algorithm

		W + 1											
		0	1	2	3	4	5	6	7	8	9	10	11
i = 3	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											
n + 1	{1,2,3,4,5}	0											

OPT:
Value=

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

W = 11

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Knapsack Algorithm

		W + 1											
		0	1	2	3	4	5	6	7	8	9	10	11
i = 4	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
n + 1	{1,2,3,4,5}	0											

OPT:
Value=

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

W = 11

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Knapsack Algorithm

$i = 5$

		$w + 1$											
		0	1	2	3	4	5	6	7	8	9	10	11
ϕ	0	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
{1,2}	0	1	6	7	7	7	7	7	7	7	7	7	7
{1,2,3}	0	1	6	7	7	18	19	24	25	25	25	25	25
{1,2,3,4}	0	1	6	7	7	18	22	24	28	29	29	40	40
{1,2,3,4,5}	0	1	6	7	7	18	22	28	29	34	35	40	40

OPT: Value=

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

W = 11

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Knapsack Algorithm

$i = 5$

		$w + 1$											
		0	1	2	3	4	5	6	7	8	9	10	11
ϕ	0	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
{1,2}	0	1	6	7	7	7	7	7	7	7	7	7	7
{1,2,3}	0	1	6	7	7	18	19	24	25	25	25	25	25
{1,2,3,4}	0	1	6	7	7	18	22	24	28	29	29	40	40
{1,2,3,4,5}	0	1	6	7	7	18	22	28	29	34	35	40	40

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

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

W = 11

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Analyzing Solution

How do we figure out the optimal solution?

```

Input: N, w1, ..., wn, v1, ..., vn
for w = 0 to W
  M[0, w] = 0
for i = 1 to N # for all items
  for w = 1 to W # for all possible weights
    if wi > w: # item's weight is more than available
      M[i, w] = M[i-1, w]
    else
      M[i, w] = max{ M[i-1, w], vi + M[i-1, w-wi] }
return M[n, W]
    
```

Costs?

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Analyzing Solution

- Costs?
 - $O(W)$
 - $O(NW)$

```

Input: N, w1, ..., wn, v1, ..., vn
for w = 0 to W
  M[0, w] = 0
for i = 1 to N # for all items
  for w = 1 to W # for all possible weights
    if wi > w: # item's weight is more than available
      M[i, w] = M[i-1, w]
    else
      M[i, w] = max{ M[i-1, w], vi + M[i-1, w-wi] }
return M[n, W]
    
```

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Knapsack Problem: Running Time

- Running time. $\Theta(nW)$
 - Not polynomial in input size!
 - "Pseudo-polynomial"
 - Reasonably efficient when W is reasonably small
 - Decision version of Knapsack is NP-complete [Chapter 8]
- Knapsack approximation algorithm. There exists a polynomial algorithm that produces a feasible solution that has value within 0.01% of optimum. [Section 11.8]

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Review: Dynamic Programming

- What is the key idea?
- What is our approach to solve a problem using dynamic programming?

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Review: Dynamic Programming

- What is the key idea?
 - Memoization: remember the answer for subproblems
 - Improves running time
 - Tradeoff in space
- What is our approach to solve a problem using dynamic programming?
 - Figure out what we're optimizing
 - Figure out how to break the problem into subproblems
 - Figure out how to compute solution from subproblems
 - Define the recurrence relation between the problems

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What was the Key to Solving each of these Problems?

- Weighted interval scheduling
- Segmented least squares
- Knapsack

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What was the Key to Solving each of these Problems?

- Weighted interval scheduling
 - Binary decision: job was in or wasn't
 - Know conflicts → reduce problem
- Segmented least squares
 - Knew last point was definitely in one segment
 - Could reduce
 - Multiway decision → many possibilities for segment starting point
- Knapsack
 - If select an item, reduce available size by item's size
 - Find opt solution for smaller weight, remaining items

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Applications of Dynamic Programming to Computational Biology

RNA SECONDARY STRUCTURE

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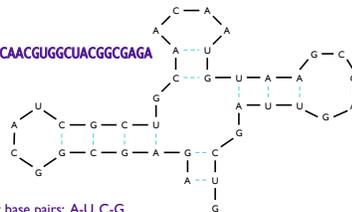
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RNA Secondary Structure

- RNA. String $B = b_1b_2\dots b_n$ over alphabet $\{A, C, G, U\}$
- Secondary structure. RNA is *single-stranded* so it tends to loop back and form base pairs with itself
 - This structure is essential for understanding behavior of a molecule.

Ex: GUCGAUUGAGCGAAUGUAACAACGUGGCUACGGCGAGA



complementary base pairs: A-U, C-G

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RNA Secondary Structure: Which Pairs Can We Combine?

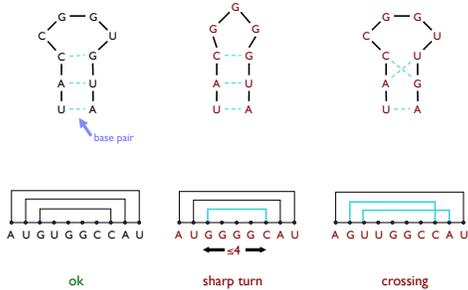
- A set of pairs $S = \{(b_i, b_j)\}$ that satisfy:
 - [Watson-Crick] S is a *matching* and each pair in S is a Watson-Crick complement: A-U, U-A, C-G, or G-C
 - [No sharp turns] The ends of each pair are separated by *at least 4* intervening bases. If $(b_i, b_j) \in S$, then $i < j - 4$
 - [Non-crossing] If (b_i, b_j) and (b_k, b_l) are two pairs in S , then we cannot have $i < k < j < l$

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Examples of RNA Secondary Structure



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RNA Secondary Structure

- A set of pairs $S = \{ (b_i, b_j) \}$ that satisfy:
 - [Watson-Crick] S is a *matching* and each pair in S is a Watson-Crick complement: A-U, U-A, C-G, or G-C
 - [No sharp turns] The ends of each pair are separated by at least 4 intervening bases. If $(b_i, b_j) \in S$, then $i < j - 4$
 - [Non-crossing] If (b_i, b_j) and (b_k, b_l) are two pairs in S , then we cannot have $i < k < j < l$
- Free energy.** Usual hypothesis is that an RNA molecule will form the secondary structure with the *optimum total free energy*. ← approximate by number of base pairs
- Goal.** Given an RNA molecule $B = b_1 b_2 \dots b_n$, find a secondary structure S that *maximizes the number of base pairs*

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Toward a Solution: First Attempt

- $OPT(j)$ = maximum number of base pairs in a secondary structure of the substring $b_1 b_2 \dots b_j$



- Towards a recurrence relation...
 - What are the possibilities?
 - What does b_j match with?
 - What are the subproblems?

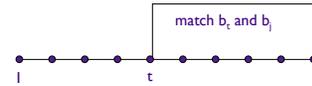
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Toward a Solution: First Attempt

- $OPT(j)$ = maximum number of base pairs in a secondary structure of the substring $b_1 b_2 \dots b_j$



- Relation:
 - If j isn't involved in a pair
 - If j is involved, results in two sub-problems

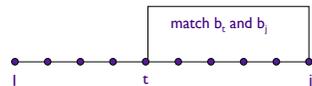
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Toward a Solution: First Attempt

- $OPT(j)$ = maximum number of base pairs in a secondary structure of the substring $b_1 b_2 \dots b_j$



- Relation:
 - If j isn't involved in a pair: $OPT(j-1)$
 - If j is involved, results in two sub-problems
 - Finding secondary structure in: $b_1 b_2 \dots b_{t-1}$ ← $OPT(t-1)$
 - Finding secondary structure in: $b_{t+1} b_{t+2} \dots b_{j-1}$ ← need more subproblems
- Doesn't match our subproblem (doesn't start at 1)
Need to start anywhere

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Dynamic Programming Over Intervals

- $OPT(i, j)$ = maximum number of base pairs in a secondary structure of the substring $b_i b_{i+1} \dots b_j$
 - What are the different cases?
 - How does it affect the recurrence relation?
 - For example, when will we know that there isn't a pair?

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Dynamic Programming Over Intervals

- $OPT(i, j)$ = maximum number of base pairs in a secondary structure of the substring $b_i b_{i+1} \dots b_j$
 - Case 1. If $i \geq j - 4$
 - $OPT(i, j) = 0$ by *no-sharp turns* condition
 - Case 2. Base b_j is not involved in a pair
 - $OPT(i, j) = OPT(i, j-1)$
 - Case 3. Base b_j pairs with b_t for some $i \leq t < j - 4$
 - *non-crossing* constraint decouples resulting sub-problems
 - $OPT(i, j) = 1 + \max_t \{ OPT(i, t-1) + OPT(t+1, j-1) \}$
 - take max over t such that $i \leq t < j-4$ and b_t and b_j are Watson-Crick complements

Mar 14, 2011 pairing CSCI211 b_t and b_j are Watson-Crick complements

Recurrence Relation

- Putting it all together...
 - j not in a base pair in optimal solution
 - $Opt(i, j) = \max(Opt(i, j-1), \max_t(1+Opt(i, t-1)+Opt(t+1, j-1)))$
 - j in a base pair in optimal solution
 - Adds 1 pair
 - Look at remaining letters

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RNA Algorithm

- What order to solve the sub-problems?
 - Do shortest intervals first

```

Initialize M[i, j] = 0 for i >= j-4
RNA(b1, ..., bn):
  for k = 5, 6, ..., n-1 (distances)
    for i = 1, 2, ..., n-k (start)
      j = i + k (end)
      M[i, j] = max(M[i, j-1],
                    max_t(1+M[i, t-1]+M[t+1, j-1]))
  return M[1, n]
  
```

Costs?

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RNA Algorithm

- What order to solve the sub-problems?
 - Do shortest intervals first

```

Initialize M[i, j] = 0 for i >= j-4
RNA(b1, ..., bn):
  for k = 5, 6, ..., n-1 (distances)
    for i = 1, 2, ..., n-k (start)
      j = i + k (end)
      M[i, j] = max(M[i, j-1],
                    max_t(1+M[i, t-1]+M[t+1, j-1]))
  return M[1, n]
  
```

- Running time: $O(n^3)$

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Dynamic Programming Summary

- Recipe
 - Characterize structure of problem
 - Recursively define *value* of optimal solution
 - Compute value of optimal solution
 - Construct *optimal solution* from computed information
- Dynamic programming techniques
 - Binary choice: weighted interval scheduling
 - Multi-way choice: segmented least squares
 - Adding a new variable: knapsack
 - Dynamic programming over intervals: RNA secondary structure
- Top-down vs. bottom-up: different people have different intuitions

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This Week

- Wed: Wiki
 - Chapter 5.5; 6, up to and including 6.4
 - Jan Cuny's visit
 - 3 p.m. – reception to meet Jan
 - 4 p.m. – Broadening Participation in Computing
- Friday: Problem Set 7 due
 - Looks short but lots of parts
 - Exam 2 will be handed out

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