

Illustration (1/2)

- The (**inefficient**) recursive procedure that determines $m[i, j]$:

RECURSIVE-MATRIX-CHAIN(p, i, j)

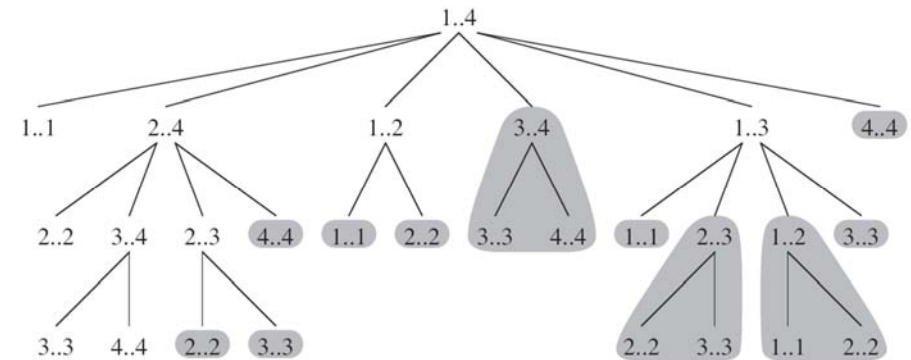
```

1  if  $i == j$ 
2      return 0
3   $m[i, j] = \infty$ 
4  for  $k = i$  to  $j - 1$ 
5       $q = \text{RECURSIVE-MATRIX-CHAIN}(p, i, k)$ 
        +  $\text{RECURSIVE-MATRIX-CHAIN}(p, k + 1, j)$ 
        +  $p_{i-1}p_kp_j$ 
6  if  $q < m[i, j]$ 
7       $m[i, j] = q$ 
8  return  $m[i, j]$ 
```

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Illustration (2/2)

- The recursion tree for the computation of RECURSIVE-MATRIX-CHAIN($p, 1, 4$):



The computations performed in a shaded subtree are replaced by a single table lookup in MEMOIZED-MATRIX-CHAIN.

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Reconstructing an Optimal Solution

- We often store which choice we made in each subproblem in a table so that we do not have to reconstruct this information from the costs that we stored.

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Memoization (1/5)

- There is an alternative approach to dynamic programming that often offers the efficiency of the bottom-up dynamic-programming approach while **maintaining a top-down strategy**.
- A memoized recursive algorithm maintains an entry in a table for the solution to each subproblem.
 - Each table entry initially contains a special value to indicate that the entry has yet to be filled in.
 - When the subproblem is first encountered as the recursive algorithm unfolds, its solution is computed and then stored in the table.

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Memoization (2/5)

- Each subsequent time that we encounter this subproblem, we simply look up the value stored in the table and return it.

- Memoized Version of RECURSIVE-MATRIX-CHAIN:

MEMOIZED-MATRIX-CHAIN(p)

```
1   $n = p.length - 1$ 
2  let  $m[1..n, 1..n]$  be a new table
3  for  $i = 1$  to  $n$ 
4      for  $j = i$  to  $n$ 
5           $m[i, j] = \infty$ 
6  return LOOKUP-CHAIN( $m, p, 1, n$ )
```

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Memoization (3/5)

LOOKUP-CHAIN(m, p, i, j)

```
1  if  $m[i, j] < \infty$ 
2      return  $m[i, j]$ 
3  if  $i == j$ 
4       $m[i, j] = 0$ 
5  else for  $k = i$  to  $j - 1$ 
6       $q = \text{LOOKUP-CHAIN}(m, p, i, k)$ 
            $+ \text{LOOKUP-CHAIN}(m, p, k + 1, j) + p_{i-1}p_kp_j$ 
7      if  $q < m[i, j]$ 
8           $m[i, j] = q$ 
9  return  $m[i, j]$ 
```

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Memoization (4/5)

- In summary, we can solve the matrix-chain multiplication problem by either a **top-down, memoized** dynamic-programming algorithm or a **bottom-up** dynamic-programming algorithm in $O(n^3)$ time.
- Without memoization, the natural recursive algorithm runs in **exponential time**, since solved subproblems are repeatedly solved.

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Memoization (5/5)

- In general practice, **if all subproblems must be solved at least once**, a bottom-up dynamic-programming algorithm usually outperforms the corresponding top-down memoized algorithm by a constant factor, because the bottom-up algorithm has no overhead for recursion and less overhead for maintaining the table.
- **If some subproblems in the subproblem space need not be solved at all**, the memoized solution has the advantage of solving only those subproblems that are definitely required.

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Outline

- Rod Cutting
- Matrix-Chain Multiplication
- Elements of Dynamic Programming
- **Longest Common Subsequence**
- Optimal Binary Search Trees

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Introduction (1/3)

- Biological applications often need to compare the DNA of two (or more) different organisms.
 - One reason to compare two strands of DNA is to determine how “similar” the two strands are, as some measure of how closely related the two organisms are.
- we can express a strand of DNA as a string over the finite set $\{A, C, G, T\}$.
 - For example, the DNA of one organism may be $S_1 = \text{ACCGGTCGAGTGC GCGGAAGCCGGCCGAA}$, and the DNA of another organism may be $S_2 = \text{GTCGTTCGGAATGCCGTTGCTCTGTAAA}$.

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Introduction (2/3)

- We can define **similarity** in many different ways:
 - We can say that two DNA strands are similar if one is a substring of the other. (Chapter 32)
 - We could say that two strands are similar if the number of changes needed to turn one into the other is small. (Problem 15-5)
 - Yet another way to measure the similarity of strands S_1 and S_2 is by finding a third strand S_3 in which the bases in S_3 appear in each of S_1 and S_2 ; these bases must appear in the same order, but not necessarily consecutively. The longer the strand S_3 we can find, the more similar S_1 and S_2 are.

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Introduction (3/3)

$S_1 = \text{ACCGGTCGAGTGC GCGGAAGCCGGCCGAA}$

$S_2 = \text{GTCGTTCGGAATGCCGTTGCTCTGTAAA}$

What should S_3 be?

➡ $S_3 = \text{GTCGTCGGAAGCCGGCCGAA}$

- We formalize this last notion of similarity as the **longest-common-subsequence problem**.
 - A **subsequence** of a given sequence is just the given sequence with zero or more elements left out.

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