Lecture 13: Dynamic Programming over Intervals

Longest Palindromic Substring

Def: A palindrome is a string that reads the same backward or forward.

Ex:

- **radar, level, racecar, madam**
- "A man, a plan, a canal – Panama!" (ignoring space, punctuation, etc.)

Problem: Given a string $X = x_1 x_2 \dots x_n$, find the longest palindromic substring.

Ex:

- $X =$ **ACCABA**
- Palindromic substrings: **ACCA, ABA**
- Longest palindromic substring: **ACCA**

Note:

- Brute-force algorithm takes $O(n^3)$ time.
- A substring must be contiguous
- A subsequence does not have to be contiguous

Dynamic Programming Solution

Def: Let $p[i,j]$ be $true$ iff $X[i..j]$ is a palindrome.

The recurrence:

- $p[i,i] = true$, for all i
- $p[i,i+1] = true$ if $x_i = x_{i+1}$
- $p[i,j] = true$ if $x_i = x_j$ and $p[i+1,j-1] = true$

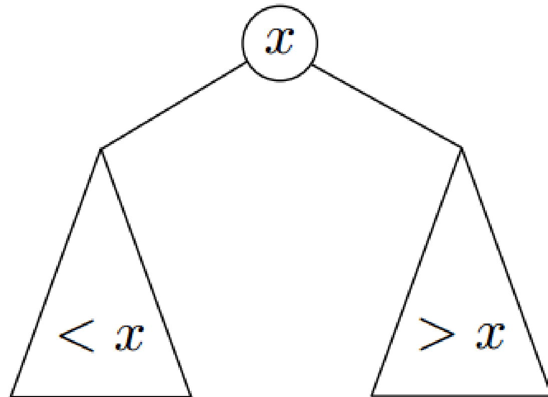
The Algorithm

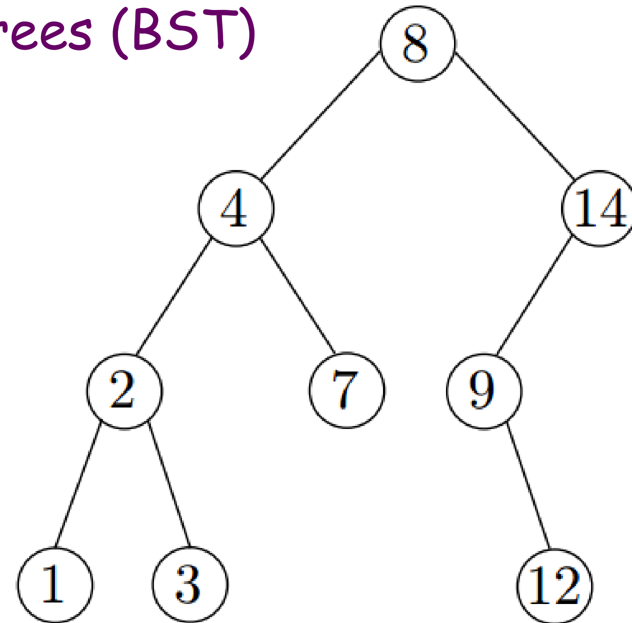
```
max ← 1
for i ← 1 to n − 1 do
    p[i, i] ← true
    if x_i = x_{i+1} then
        p[i, i + 1] ← true,  max ← 2
    else p[i, i + 1] ← false
for l ← 3 to n do
    for i ← 1 to n − l + 1 do
        j ← i + l − 1
        if p[i + 1, j − 1] = true and x_i = x_j then
            p[i, j] ← true,  max ← l
        else p[i, j] ← false
return max
```

Running time: $O(n^2)$

Space: $O(n^2)$ but can be improved to $O(n)$

Binary search trees (BST)






```
Tree-Search(T,k):
x ← T.root
while x ≠ nil and k ≠ x.key do
    if k < x.key then x ← x.left
    else x ← x.right
return x
```

The (worst-case) search time in a balanced BST is $\Theta(\log n)$

Q: If we know the probability of each key being searched for, can we design a (possibly unbalanced) BST to optimize the expected search time?

The Optimal Binary Search Tree Problem

Problem Definition (simpler than the version in textbook):

Given n keys $a_1 < a_2 < \cdots < a_n$, with weights $f(a_1), \ldots, f(a_n)$, find a binary search tree T on these n keys such that

$$B(T) = \sum_{i=1}^{n} f(a_i)(d(a_i) + 1)$$

is minimized, where $d(a_i)$ is the depth of a_i.

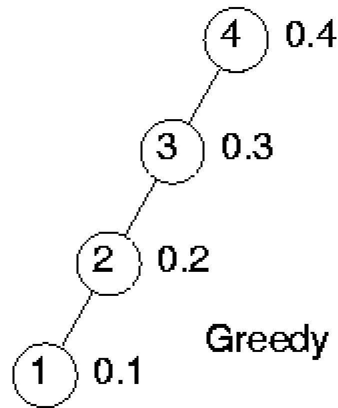
Note: This is similar to the Huffman coding problem but with 2 key differences:

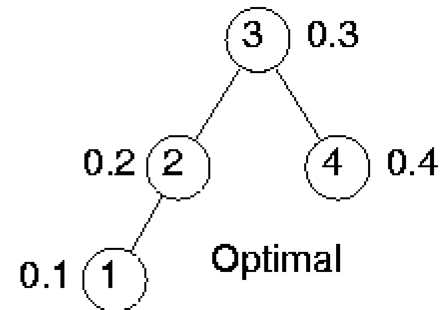
- The tree has to be a BST, i.e., the keys are stored in sorted order. In a Huffman tree, there is no ordering among the leaves.
- Keys appear as both internal and leaf nodes. In a Huffman tree, keys (characters) appear only at the leaf nodes.

Motivation: If the weights are the probabilities of the elements being searched for, then such a BST will minimize the expected search cost.

Greedy Won't Work

Greedy strategy: Always pick the heaviest key as root, then recursively build the tree top-down.





$B(T) = 0.4 \cdot 2 + 0.3 \cdot 1 + 0.2 \cdot 2 + 0.1 \cdot 3 = 1.8$

$B(T) = 0.4 \cdot 1 + 0.3 \cdot 2 + 0.2 \cdot 3 + 0.1 \cdot 4 = 2$

Dynamic Programming: The Recurrence

Def: $e[i,j]$ = the minimum cost of any BST on $a_i, \ldots, a_j$

Idea: The root of the BST can be any of $a_i, \ldots, a_j$. We try each of them.

Recurrence:

Let $w[i,j] = f(a_i) + \cdots + f(a_j)$

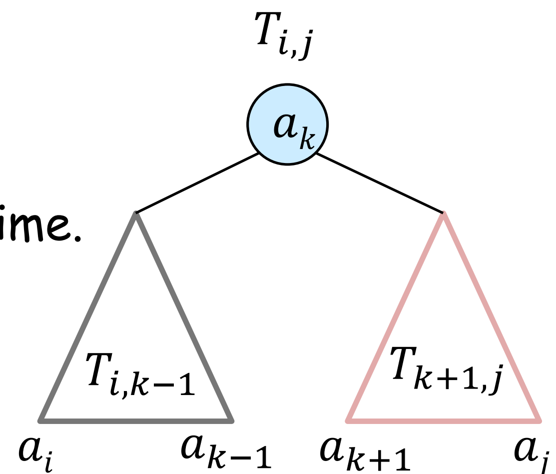
depth of each node in $T_{i,j}$ = its depth in $T_{i,k-1} + 1$

$$e[i,j] = \min_{i \le k \le j} \{e[i,k-1] + w[i,k-1] + e[k+1,j] + w[k+1,j] + f(a_k)\}$$

$$= \min_{i \le k \le j} \{e[i,k-1] + e[k+1,j] + w[i,j]\}$$

$e[i,j] = 0$ for $i \ge j$.

Note: All $w[i,j]$'s can be pre-computed in $O(n^2)$ time.



The Algorithm

Idea: We will do the bottom-up computation by the increasing order of the problem size.

```
let e[1..n, 1..n], w[1..n, 1..n], root[1..n, 1..n] be new arrays of all 0
for i = 1 to n
    w[i, i] ← f(a_i)
    for j = i + 1 to n
        w[i, j] ← w[i, j − 1] + f(a_j)
for l ← 1 to n
    for i ← 1 to n − l + 1
        j ← i + l − 1
        e[i, j] ← ∞
        for k ← i to j
            t ← e[i, k − 1] + e[k + 1, j] + w[i, j]
            if t < e[i, j] then
                e[i, j] ← t
                root[i, j] ← k
return Construct-BST(root, 1, n)
```

Running time: $O(n^3)$

Space: $O(n^2)$

Construct the Optimal BST

```
Construct-BST(root, i, j):
if i > j then return nil
create a node z
z.key ← a[root[i, j]]
z.left ← Construct-BST(root, i, root[i, j] − 1)
z.right ← Construct-BST(root, root[i, j] + 1, j)
return z
```

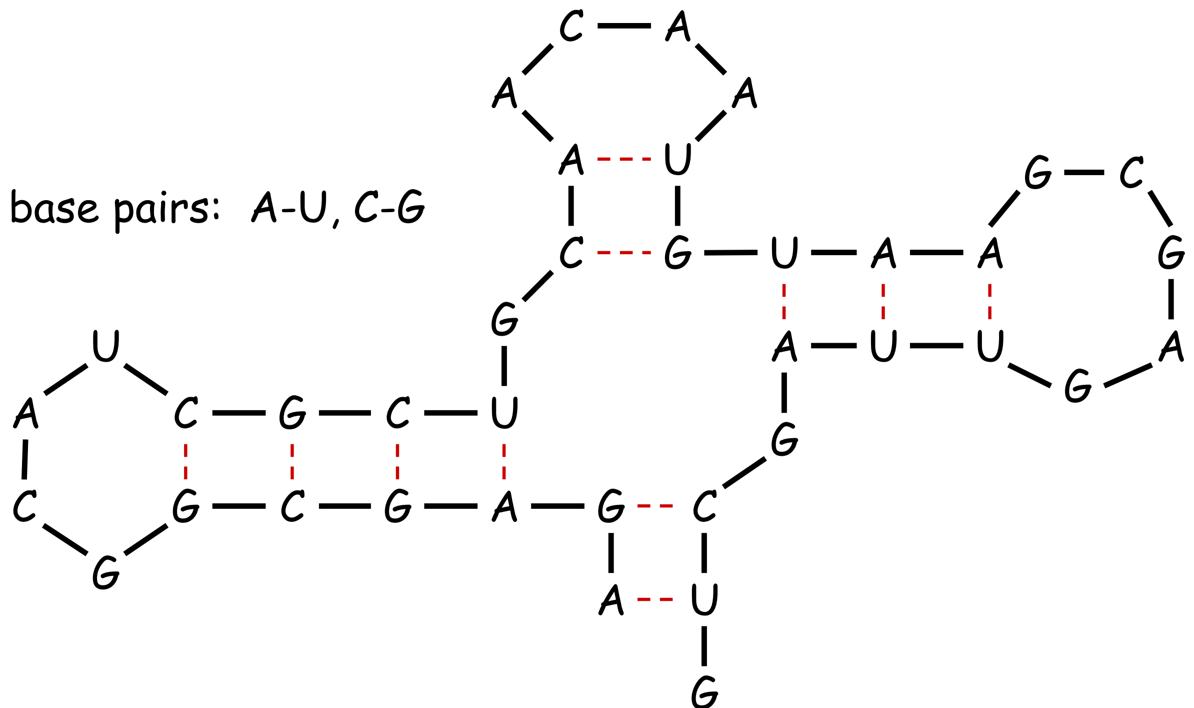
Running time of this part: $O(n)$

RNA Secondary Structure

RNA. String $B = b_1 b_2 \ldots b_n$ 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 the behavior of molecules.

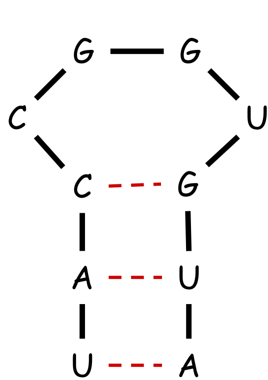
Ex: **GUCGAUUGAGCGAAUGUAACAACGUGGCUACGGCGAGA**

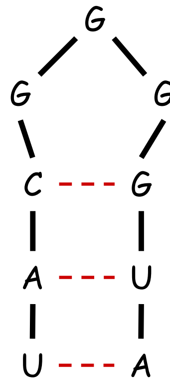


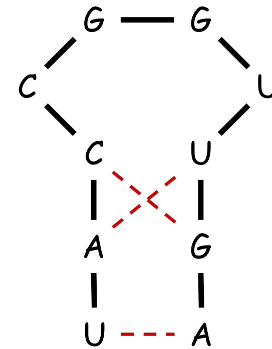
RNA Secondary Structure

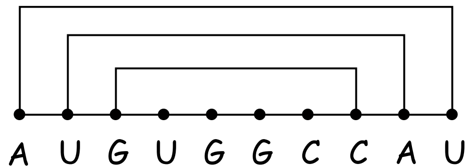
Secondary structure. A set of pairs $S = \{(b_i, b_j)\}$ that satisfy:

- [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 $i < k < j < l$.

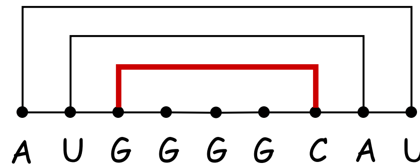




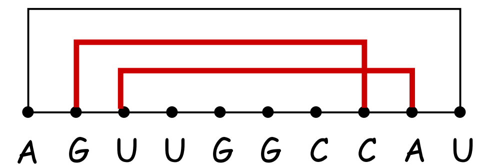




ok



sharp turn



crossing

The Problem

Free energy. Usual hypothesis is that an RNA molecule will form the secondary structure with the optimum total free energy, which is proportional to the number of base pairs.

Goal. Given an RNA molecule $B = b_1 b_2 \ldots b_n$, find a secondary structure S that maximizes the number of base pairs.

The Recurrence

Def. $M[i, j]$ = maximum number of base pairs in a secondary structure of the substring $b_i b_{i+1} \ldots b_j$.

Recurrence.

- Case 1. If $i \geq j - 4$.
  - $M[i, j] = 0$ by no-sharp turns condition.
- Case 2. Base b_j is not matched in OPT.
  - $M[i, j] = M[i, j-1]$
- Case 3. Base b_j pairs with b_k for some $i \leq k \leq j - 5$.
  - non-crossing constraint decouples problem into sub-problems
  - $M[i, j] = 1 + \max_k \{M[i, k-1] + M[k+1, j-1]\}$

take max over k such that $i \leq k \leq j - 5$ and b_k and b_j are Watson-Crick complements

The Algorithm

```
let M[1..n, 1..n], s[1..n, 1..n] be new arrays of all 0
for l ← 1 to n
    for i ← 1 to n − l + 1
        j ← i + l − 1
        M[i, j] ← M[i, j − 1]
        for k ← i to j − 5
            if b_k and b_j are not complements then continue
            t ← 1 + M[i, k − 1] + M[k + 1, j − 1]
            if t > M[i, j] then
                M[i, j] ← t
                s[i, j] ← k
Construct-RNA(s, 1, n)
```

Running time: $O(n^3)$

Space: $O(n^2)$

```
Construct-RNA(s, i, j):
if i ≥ j − 4 then return
if s[i, j] = 0 then Construct-RNA(s, i, j − 1)
print s[i, j], "-", j
Construct-RNA(s, i, s[i, j] − 1)
Construct-RNA(s, s[i, j] + 1, j)
```