

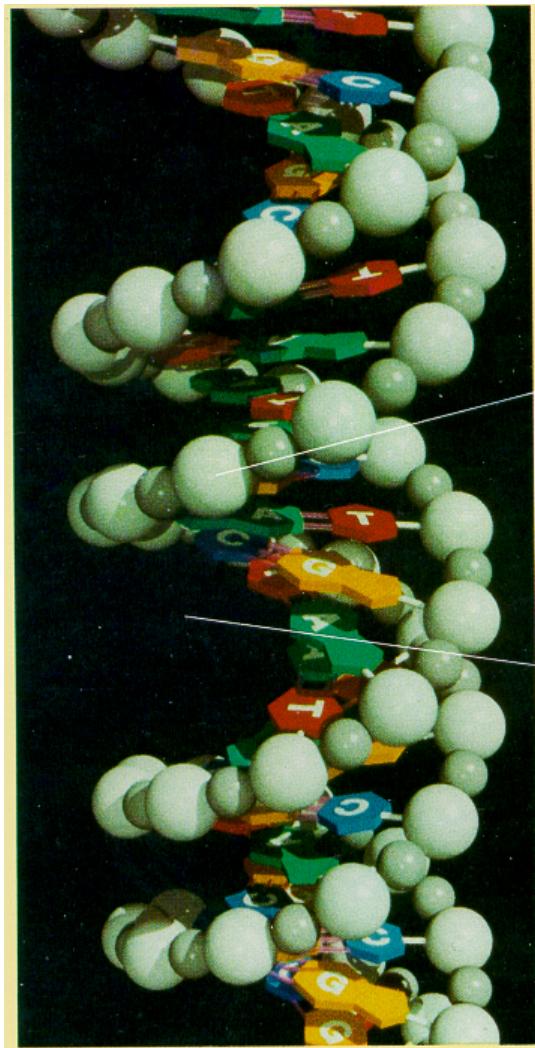
CSE 417: Algorithms and Computational Complexity

Winter 2007

W. L. Ruzzo

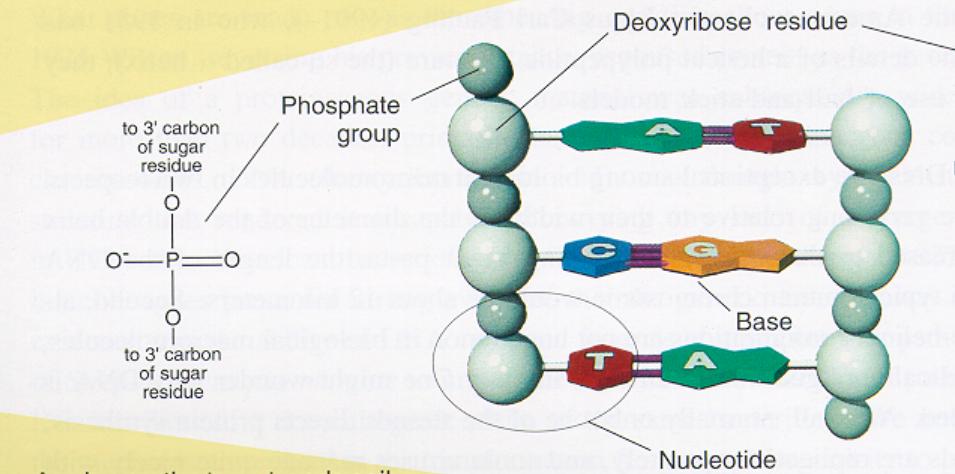
Dynamic Programming, II
RNA Folding

The Double Helix



(a) Computer-generated Image of DNA
(by Mel Prueitt)

(b) Uncoiled DNA Fragment



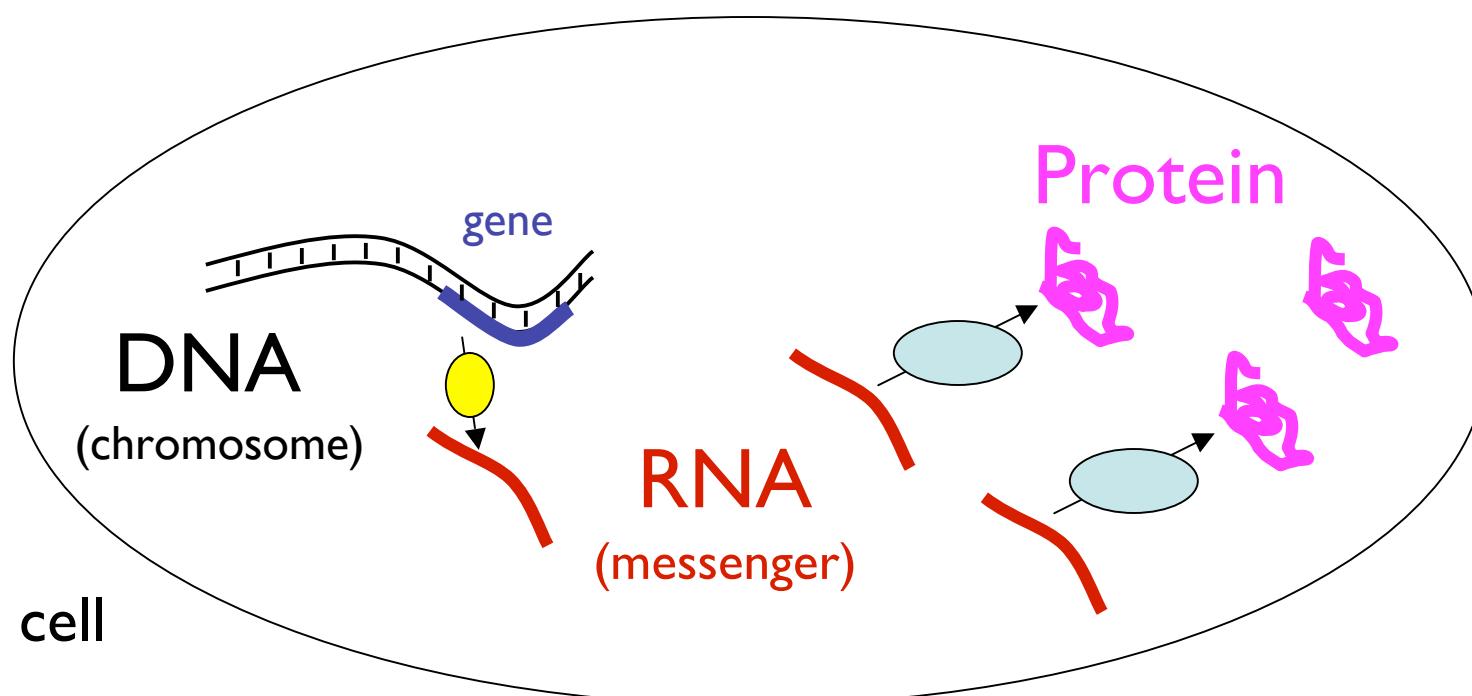
As shown, the two strands coil about each other in a fashion such that all the bases project inward toward the helix axis. The two strands are held together by hydrogen bonds (pink rods) linking each base projecting from one backbone to its so-called complementary base projecting from the other backbone. The base A always bonds to T (A and T are comple-

Shown in (b) is an uncoiled fragment of (a three complementary base pair. In a chemist's viewpoint, each strand is a polymer made up of four repeating units called deoxyribonucleotides.

Los Alamos Science

The “Central Dogma” of Molecular Biology

DNA → RNA → Protein

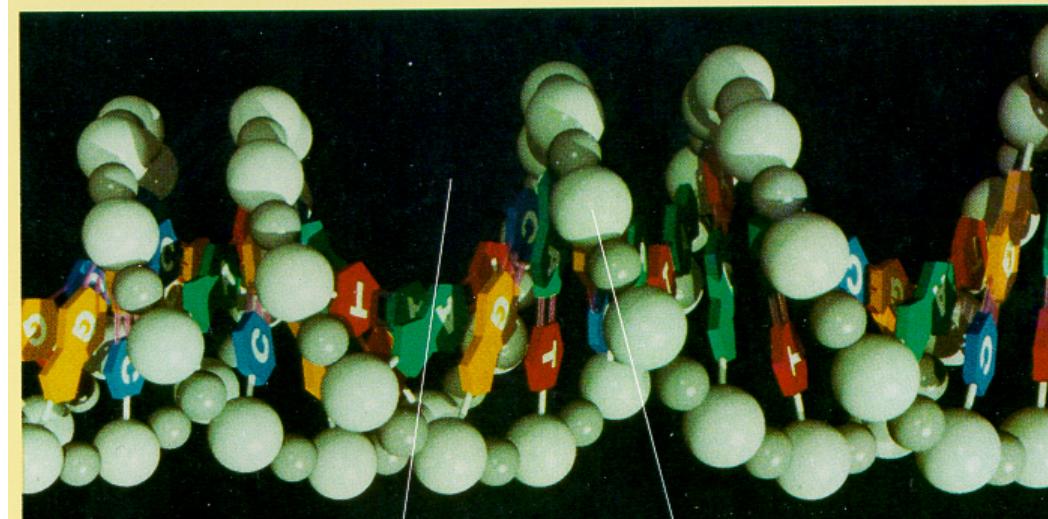


Non-coding RNA

- Messenger RNA - codes for proteins
- Non-coding RNA - all the rest
 - Before, say, mid 1990's, 1-2 dozen known (critically important, but narrow roles: e.g. ribosomal and transfer RNA, splicing, SRP)
- Since mid 90's dramatic discoveries
 - Regulation, transport, stability/degradation
 - E.g. "microRNA": hundreds in humans
 - E.g. "riboswitches": thousands in bacteria

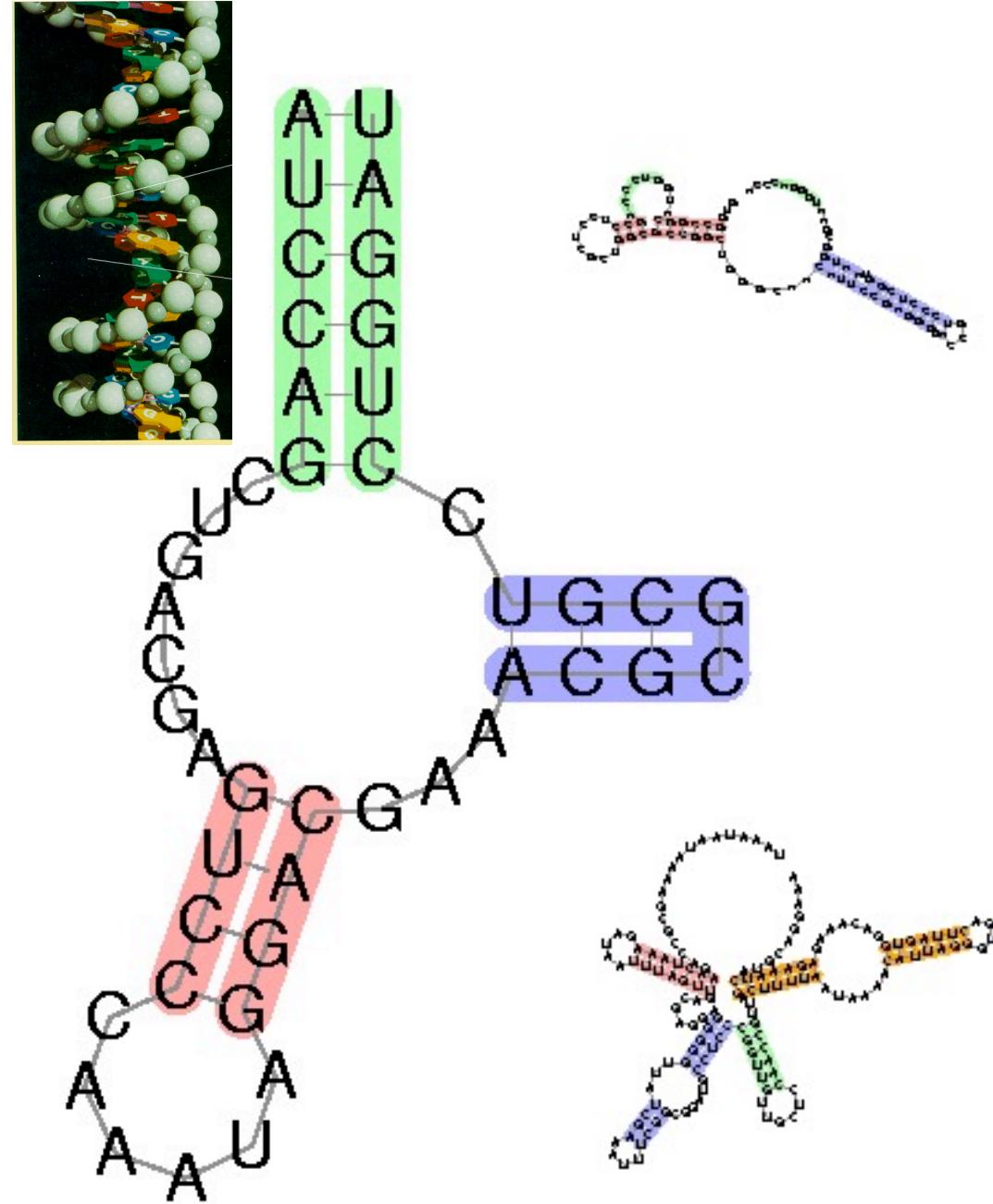
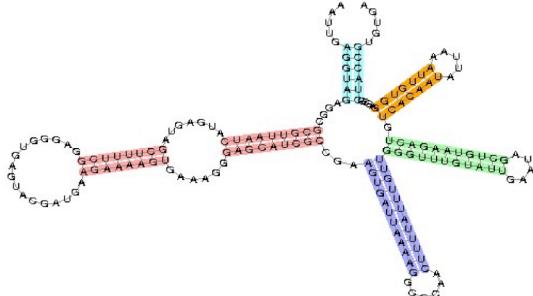
DNA structure: dull

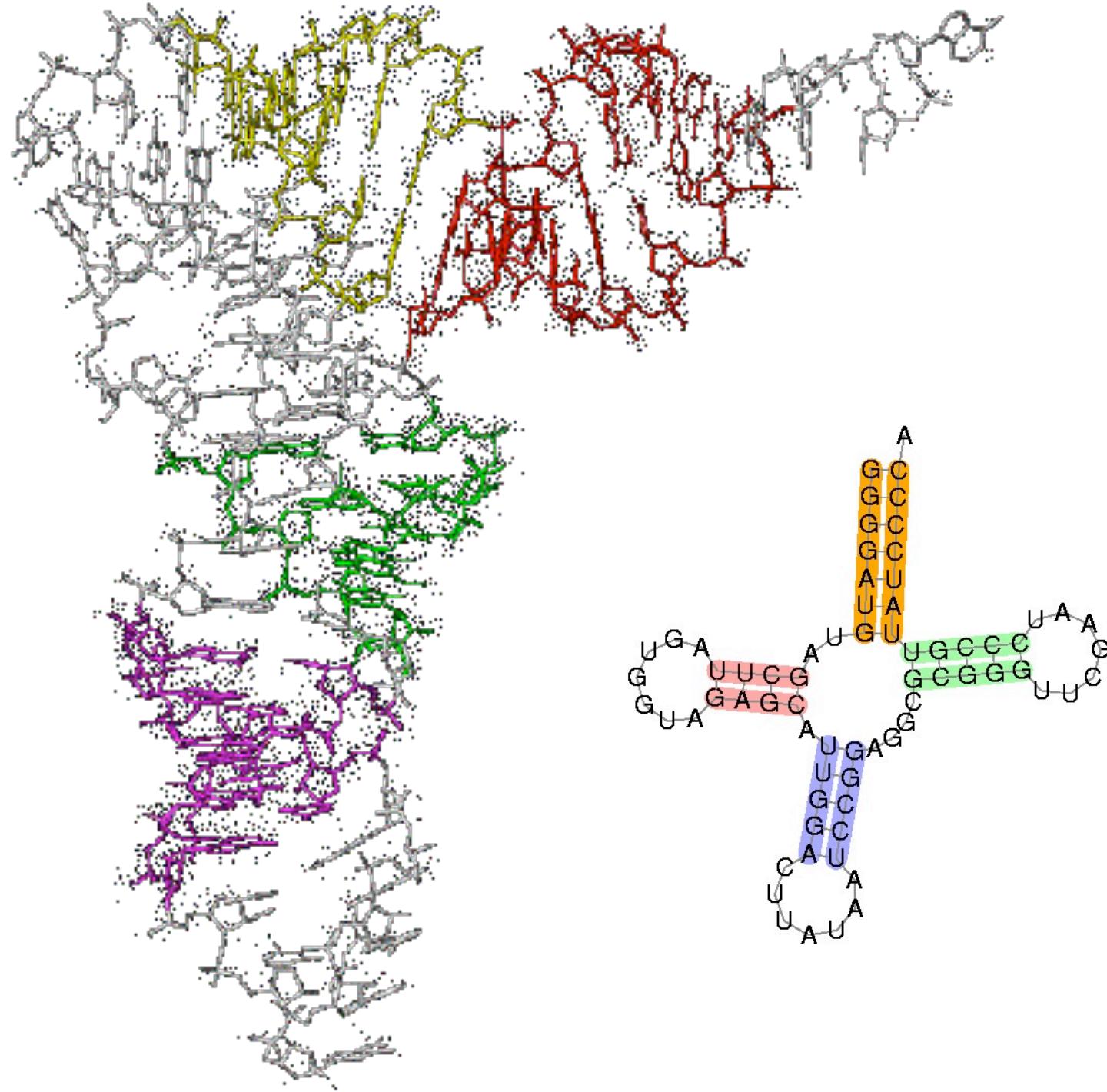
...ACCGCTAGATG...
||| | | | | | | | |
...TGGCGATCTAC...



RNA Structure: Rich

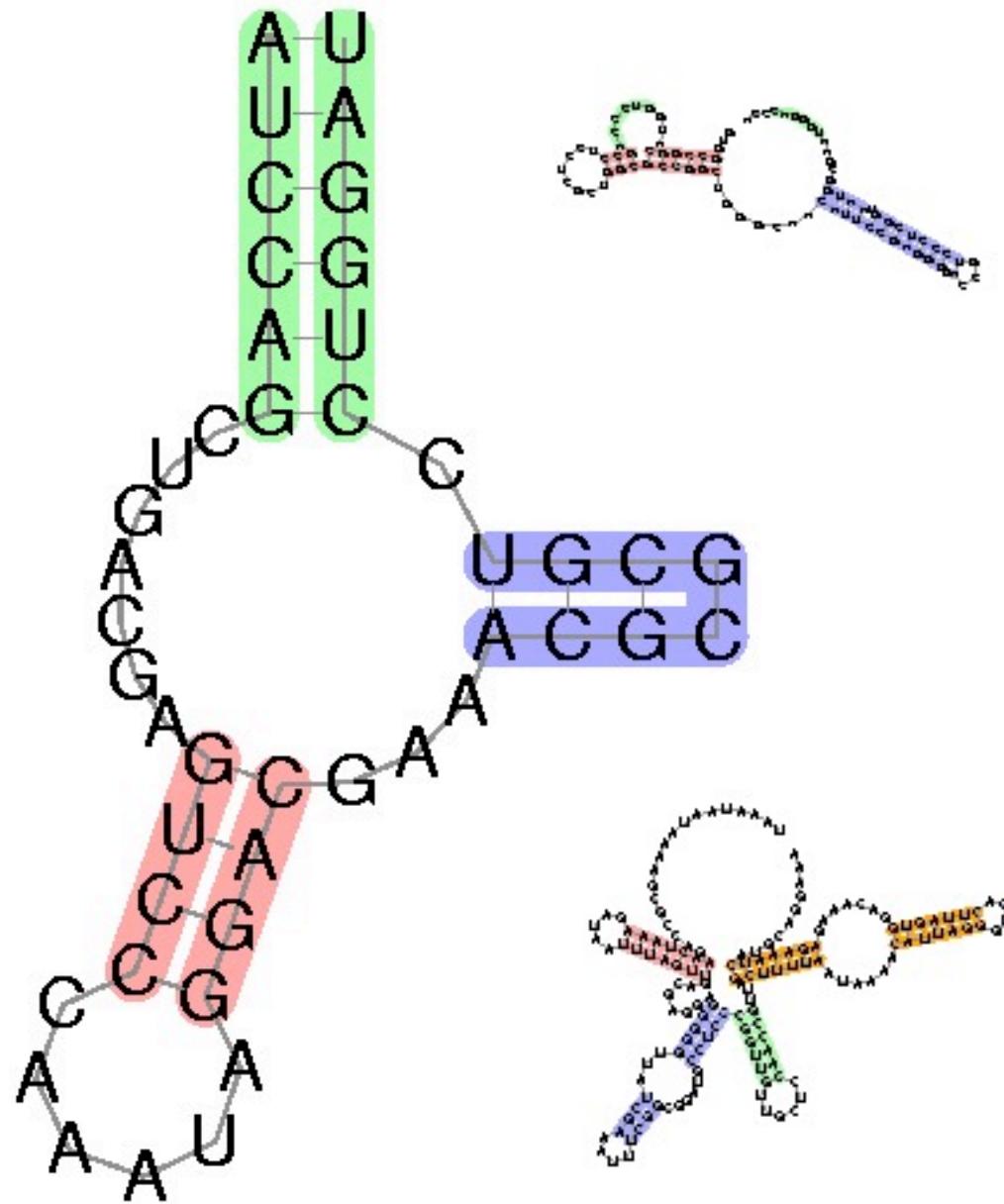
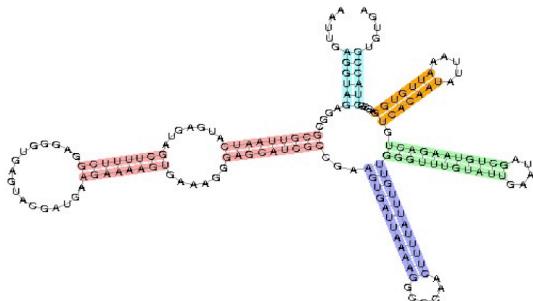
- RNA's fold, and function
- Nature uses what works





RNA Secondary Structure:

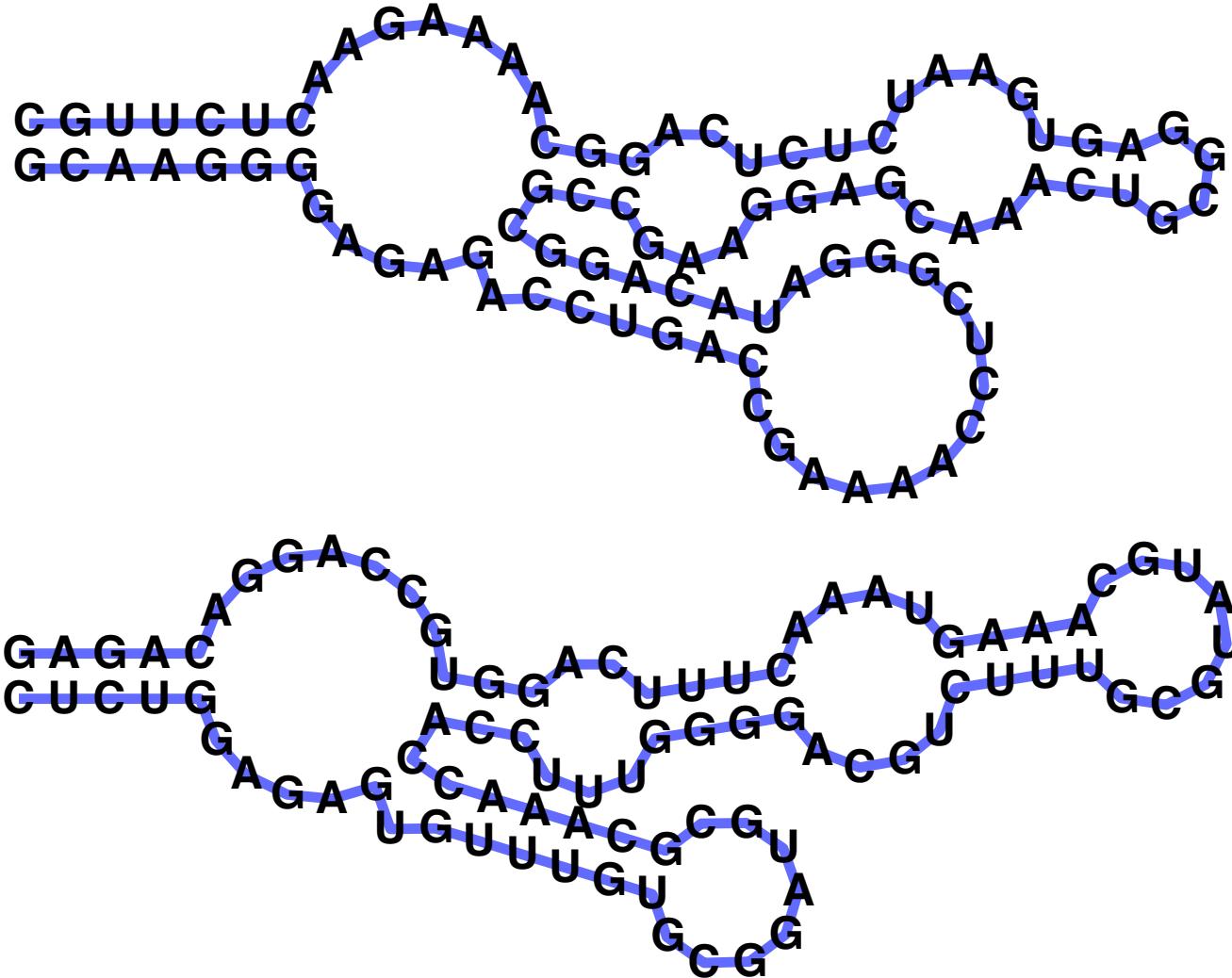
Not everything,
but important,
easier than 3d



Why is structure important?

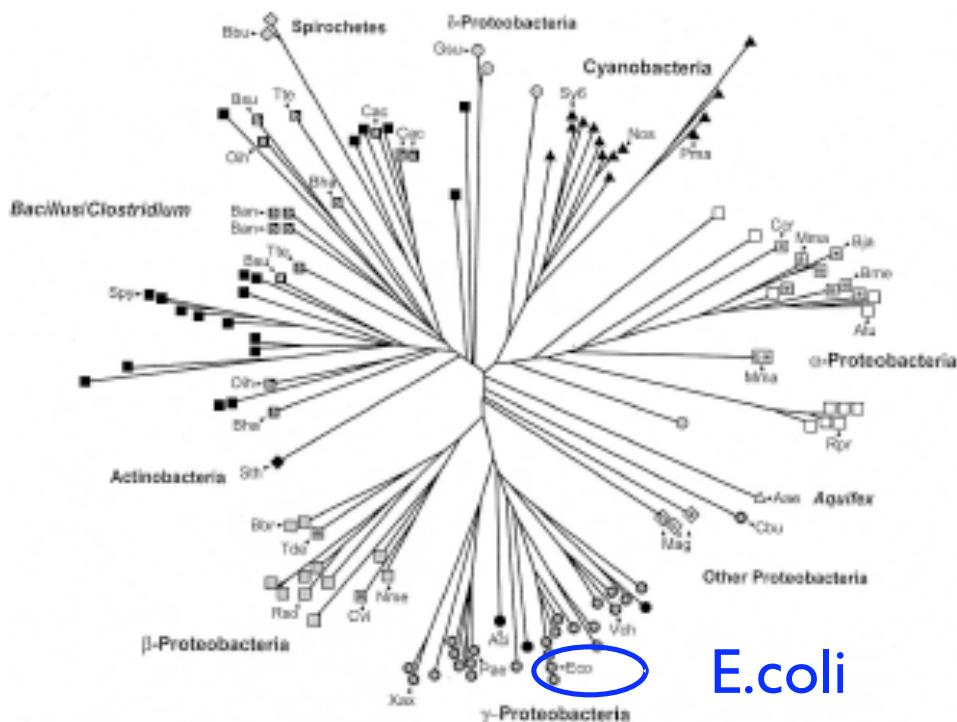
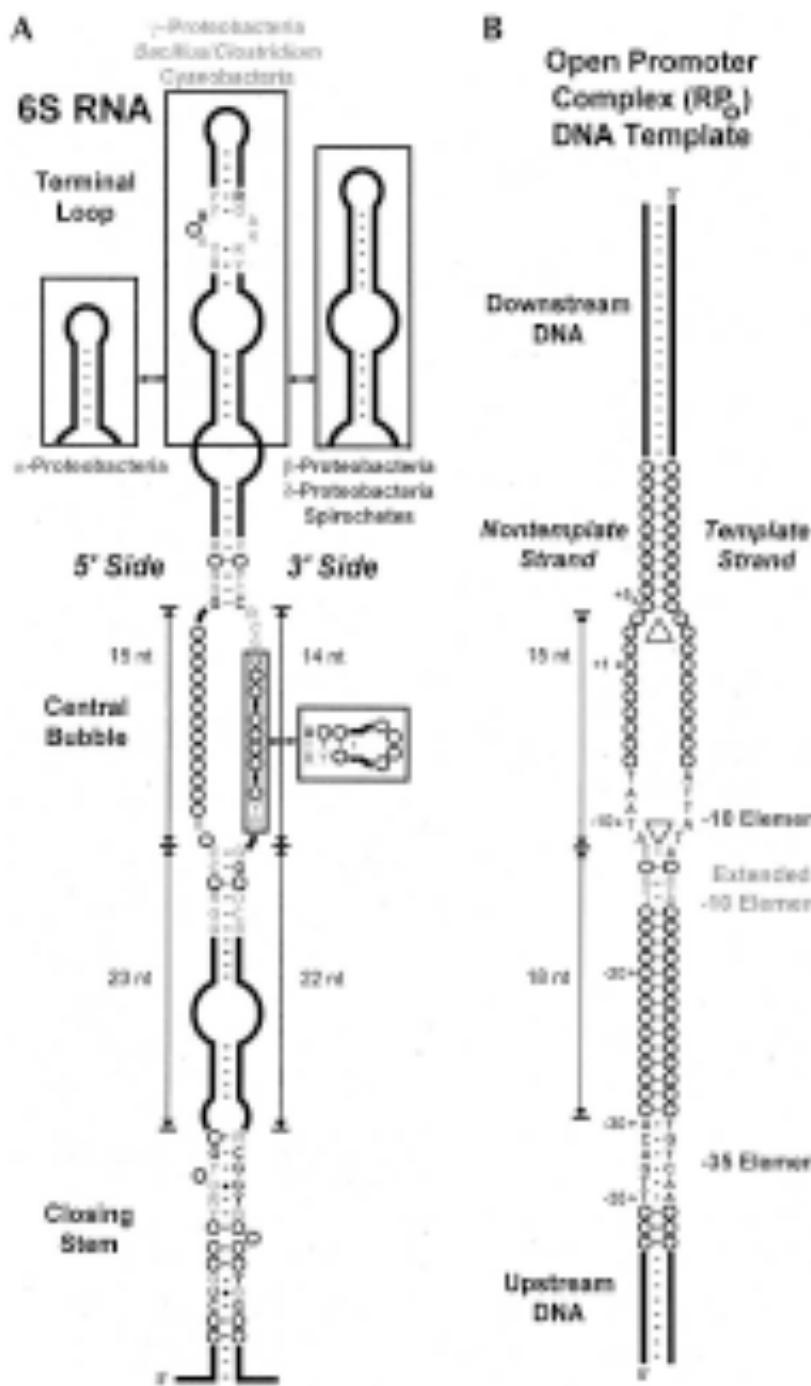
- For protein-coding, similarity in sequence is a powerful tool for finding related sequences
 - e.g. “hemoglobin” is easily recognized in all vertebrates
- For non-coding RNA, many different sequences have the same structure, and structure is most important for function.
 - So, using structure plus sequence, can find related sequences at much greater evolutionary distances

Q: What's so hard?



A: Structure often more important than sequence

6S mimics an open promoter



Barrick et al. *RNA* 2005
Trotocaud et al. *NSMB* 2005
Willkomm et al. *NAR* 2005

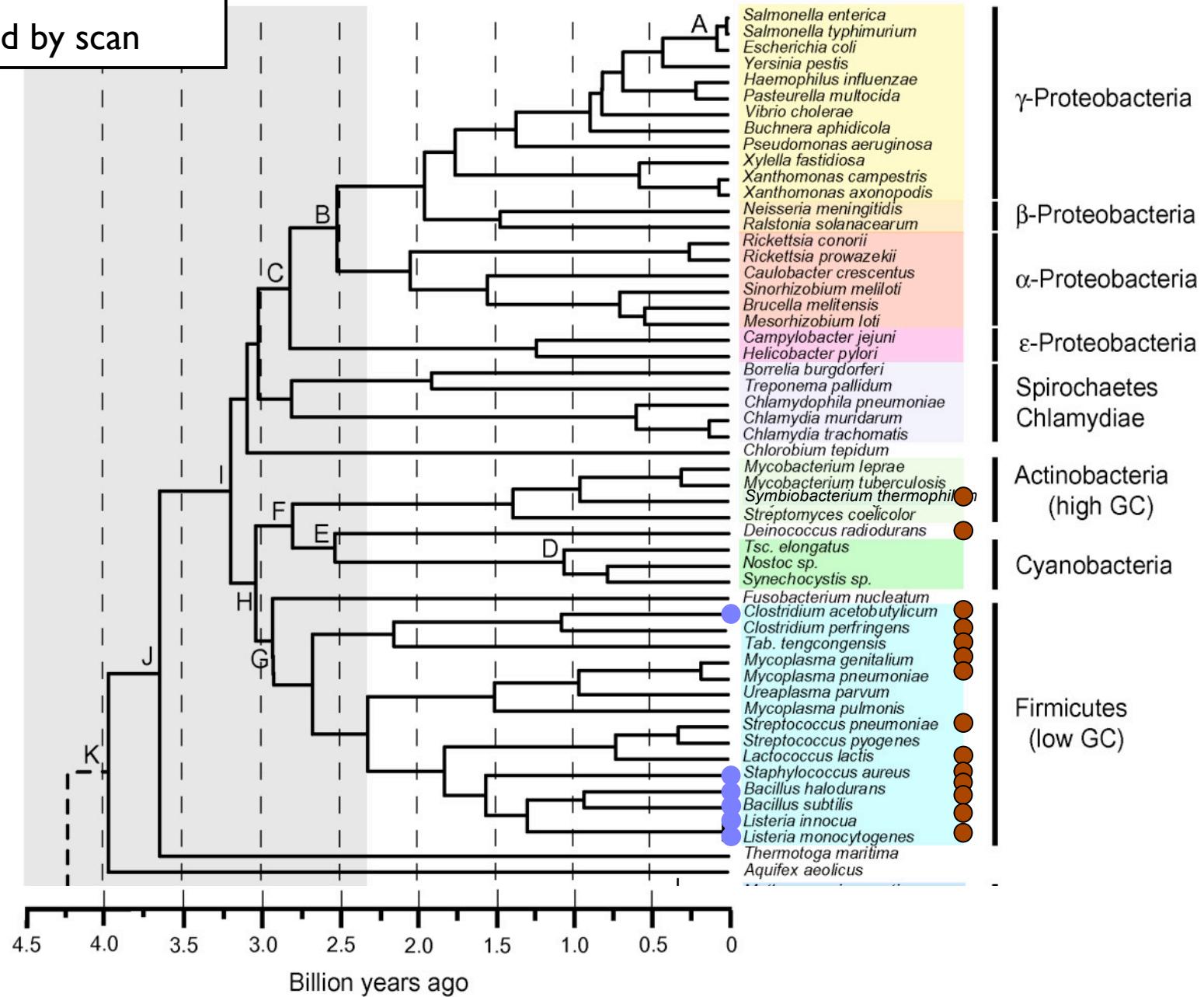
- Used by CMfinder
- Found by scan

Chloroflexus aurantiacus

● Chloroflexi

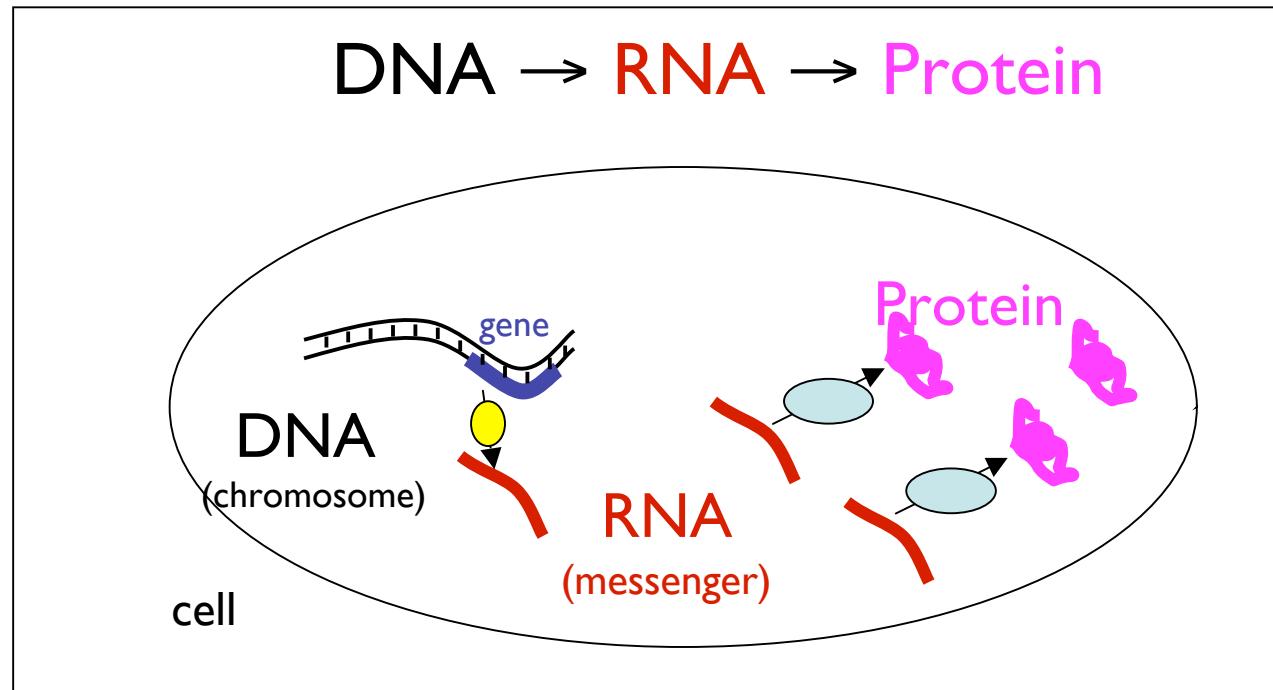
Geobacter metallireducens
Geobacter sulphurreducens

● δ -Proteobacteria



“Central Dogma” =

“Central Chicken & Egg”?



Was there once an “RNA World”?

6.5 RNA Secondary Structure

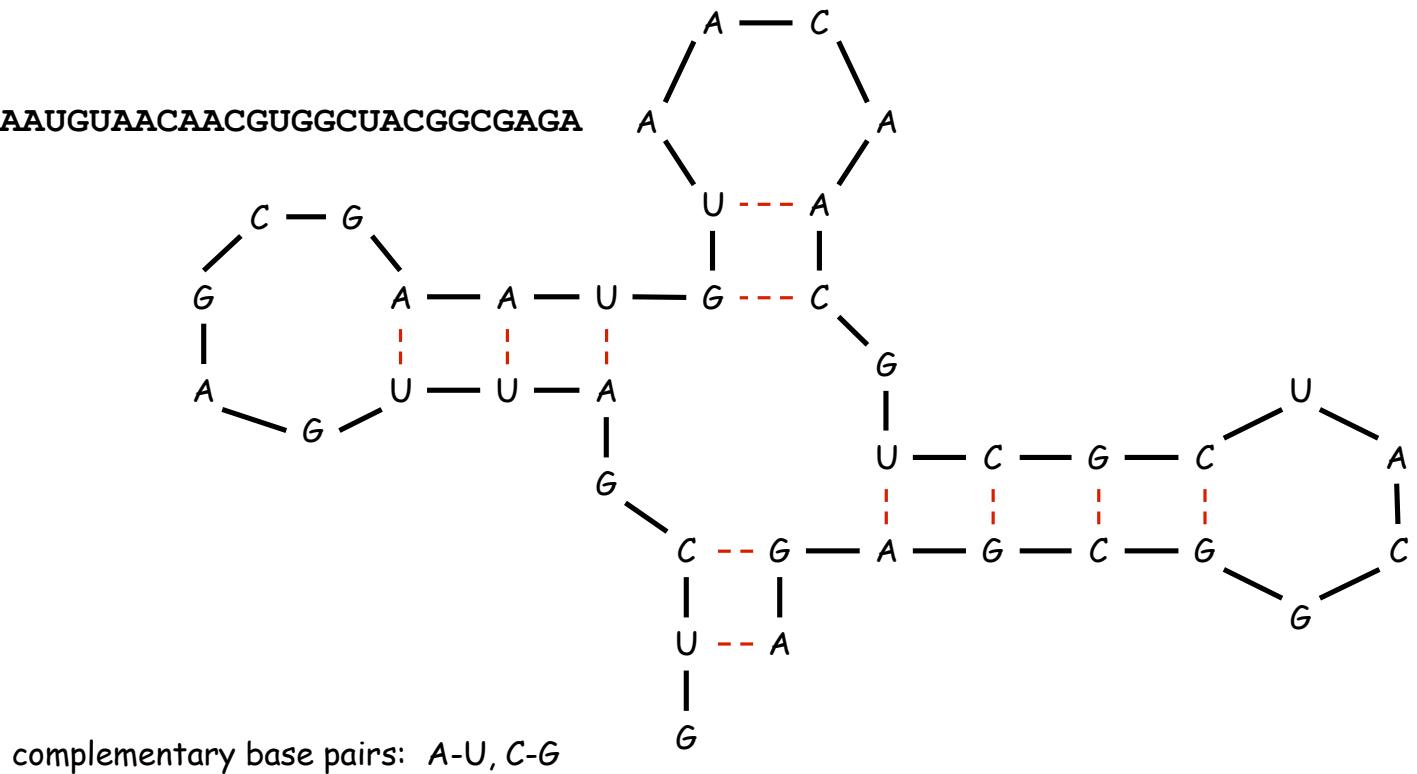
Nussinov's Algorithm

RNA Secondary Structure

RNA. String $B = b_1b_2\dots b_n$ over alphabet { A, C, G, U }.

Secondary structure. RNA is usually single-stranded, and tends to loop back and form base pairs with itself. This structure is essential for understanding behavior of molecule.

Ex: GUCAUUGAGCGAAUGUAACAAACGUGGUACGGCGAGA



RNA Secondary Structure (somewhat oversimplified)

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

- [Watson-Crick.]
 - S is a *matching*, i.e. each base pairs with at most one other, and
 - each pair in S is a Watson-Crick pair: 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 $i < k < j < l$. (Violation of this is called a *pseudoknot*.)

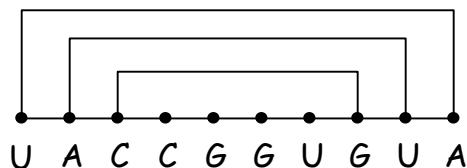
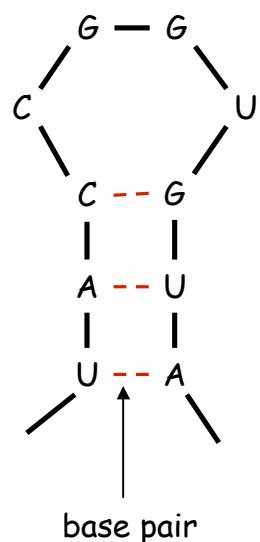
Free energy. Usual hypothesis is that an RNA molecule will form the secondary structure with the optimum total free energy.

approximate by number of base pairs

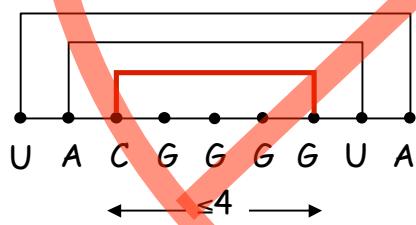
Goal. Given an RNA molecule $B = b_1 b_2 \dots b_n$, find a secondary structure S that maximizes the number of base pairs.

RNA Secondary Structure: Examples

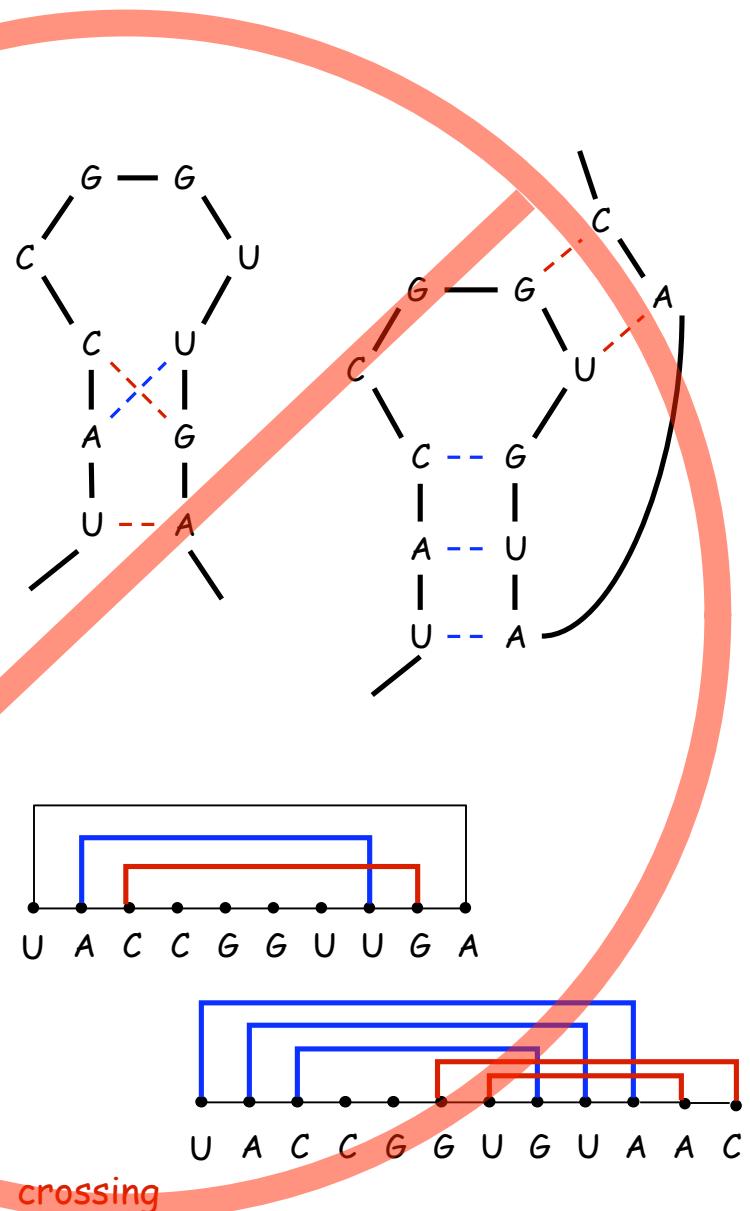
Examples.



ok

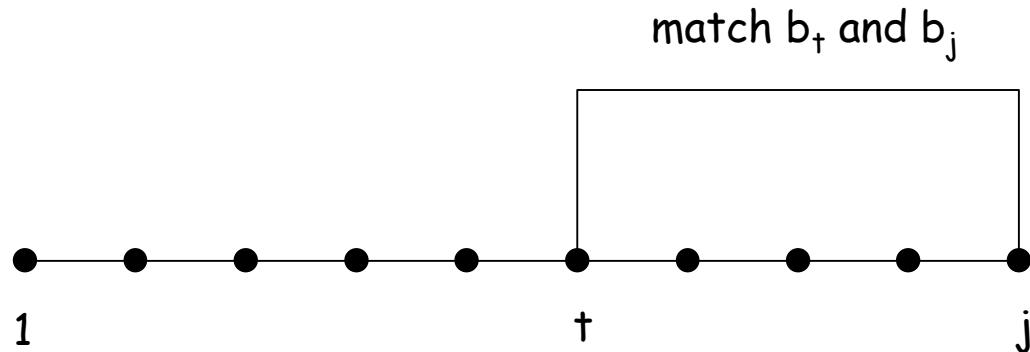


sharp turn



RNA Secondary Structure: Subproblems

First attempt. $\text{OPT}[j] = \text{maximum number of base pairs in a secondary structure of the substring } b_1b_2\dots b_j.$



Difficulty. Results in two sub-problems.

- Finding secondary structure in: $b_1b_2\dots b_{t-1}.$ $\leftarrow \text{OPT}(t-1)$
- Finding secondary structure in: $b_{t+1}b_{t+2}\dots b_{j-1}.$ $\leftarrow \text{not OPT of anything; need more sub-problems}$

Dynamic Programming Over Intervals: (R. Nussinov's algorithm)

Notation. $OPT[i, j]$ = 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

Key point:
Either last base
is unpaired
(case 1,2) or
paired (case 3)

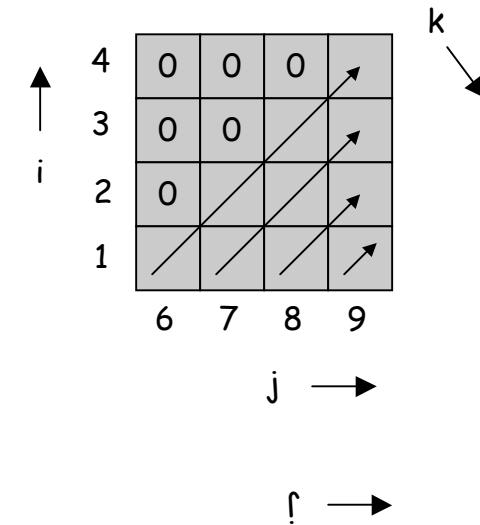
Remark. Same core idea in CKY algorithm to parse context-free grammars.

Bottom Up Dynamic Programming Over Intervals

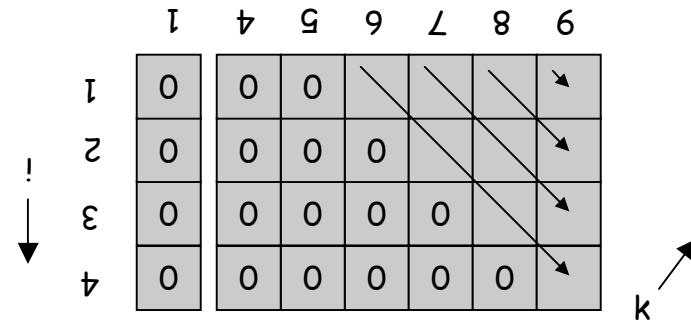
Q. What order to solve the sub-problems?

A. Do shortest intervals first.

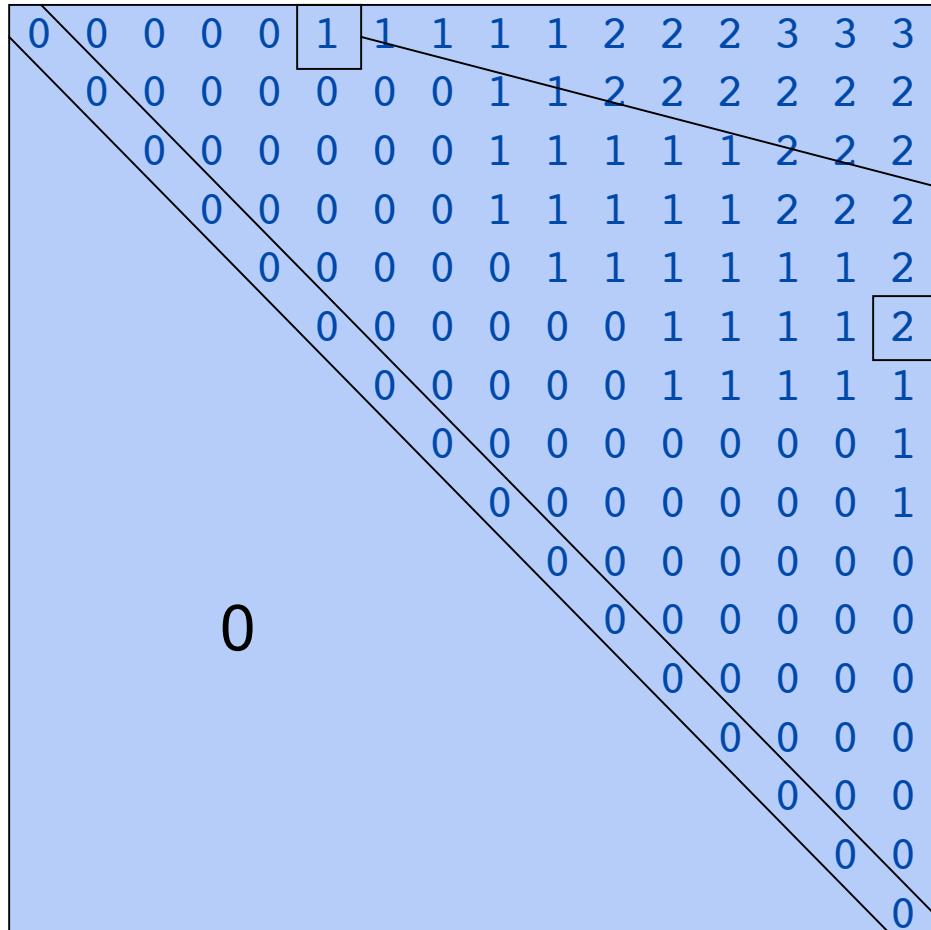
```
RNA(b1, ..., bn) {  
    for k = 5, 6, ..., n-1  
        for i = 1, 2, ..., n-k  
            j = i + k  
            Compute OPT[i, j]  
    return OPT[1, n] using recurrence  
}
```



Running time. $O(n^3)$.



C U C C G G U U G C A A U G U C
(` ` . (. . . .) .) . .) . .

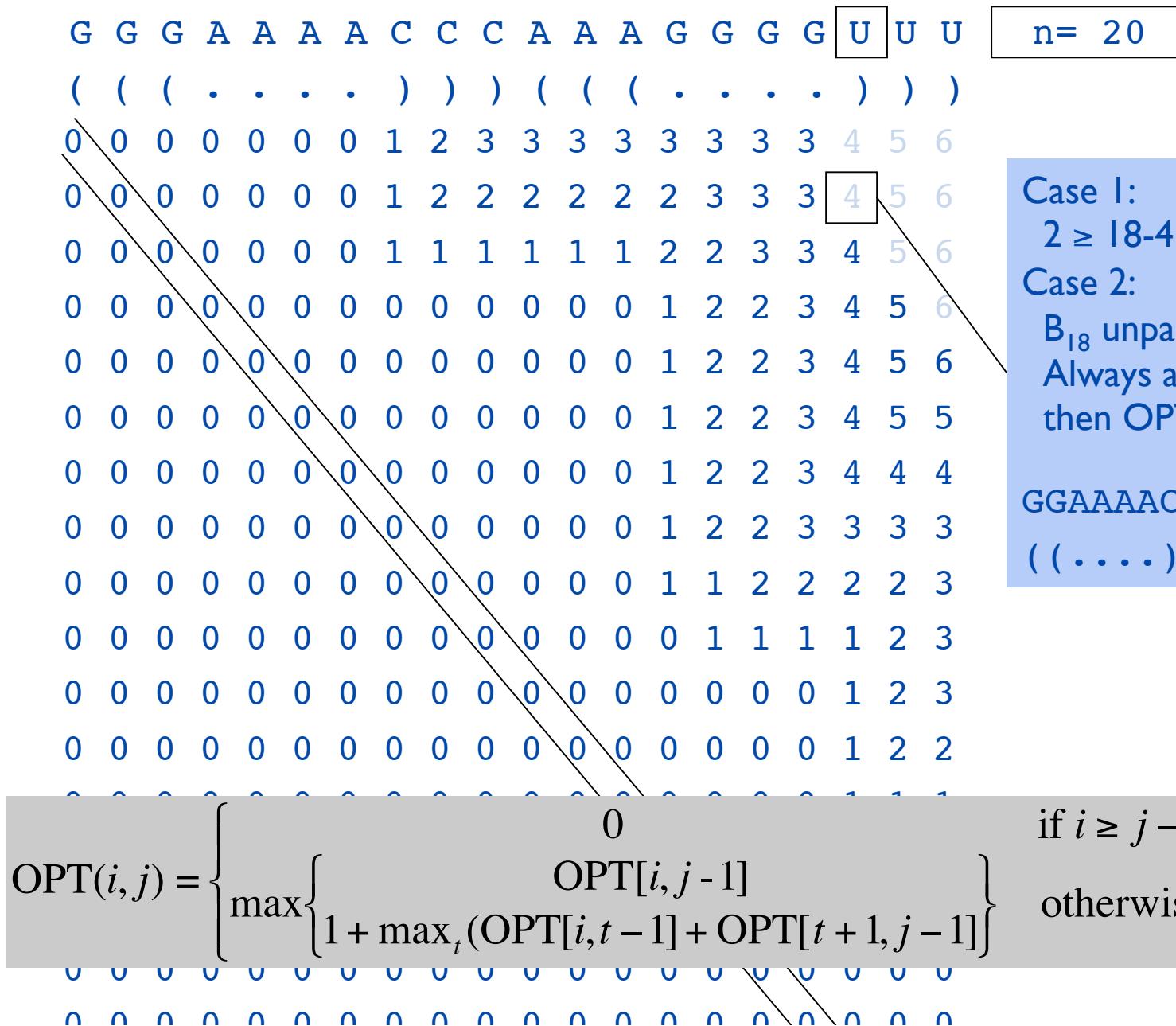


n = 16

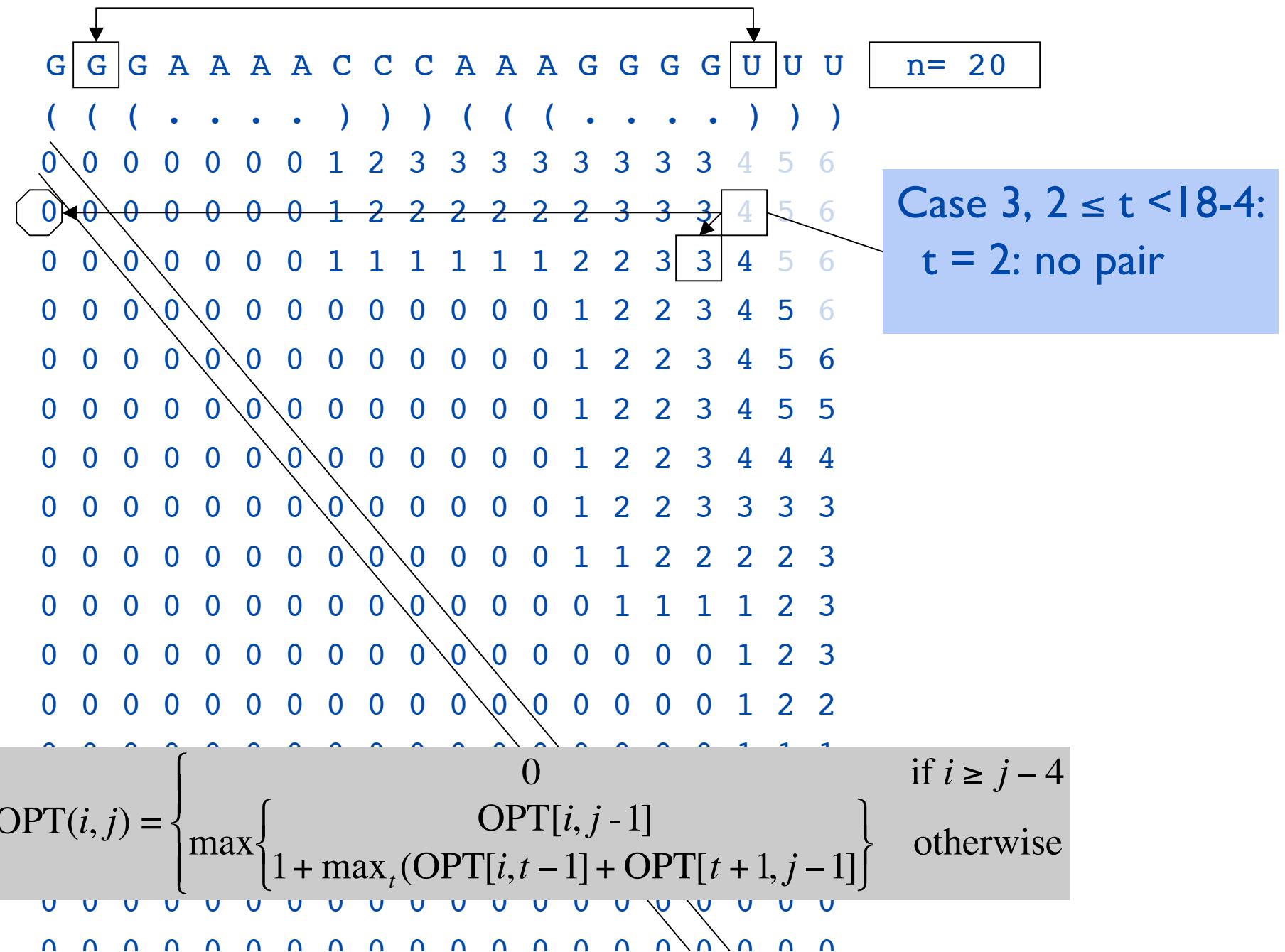
E.g.:
OPT[1,6] = 1:
CUCCGG
(....)

E.g.:
OPT[6,16] = 2:
GUUGCAAUAGUC
((....)....)

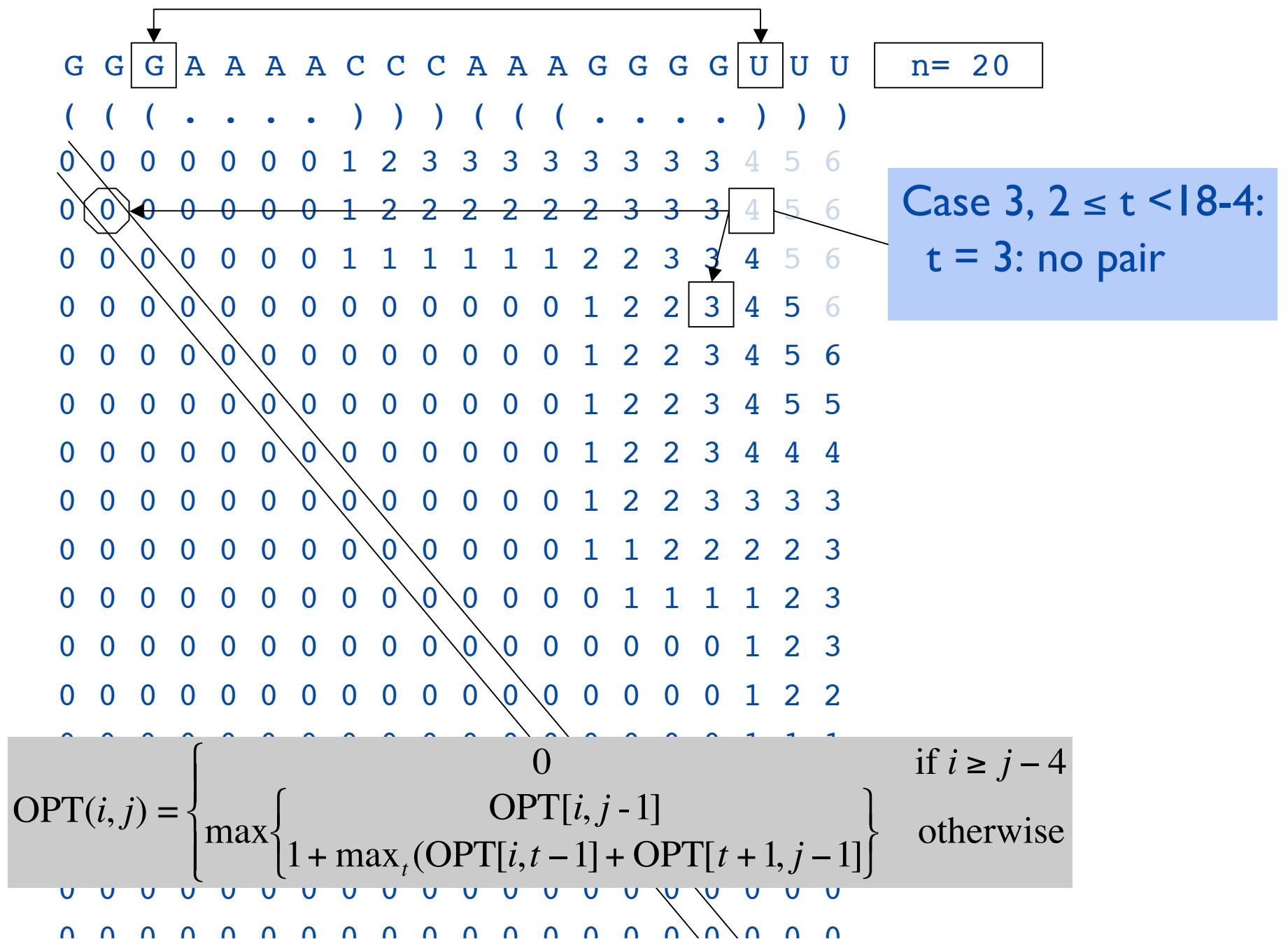
Computing one cell: $\text{OPT}[2,18] = ?$



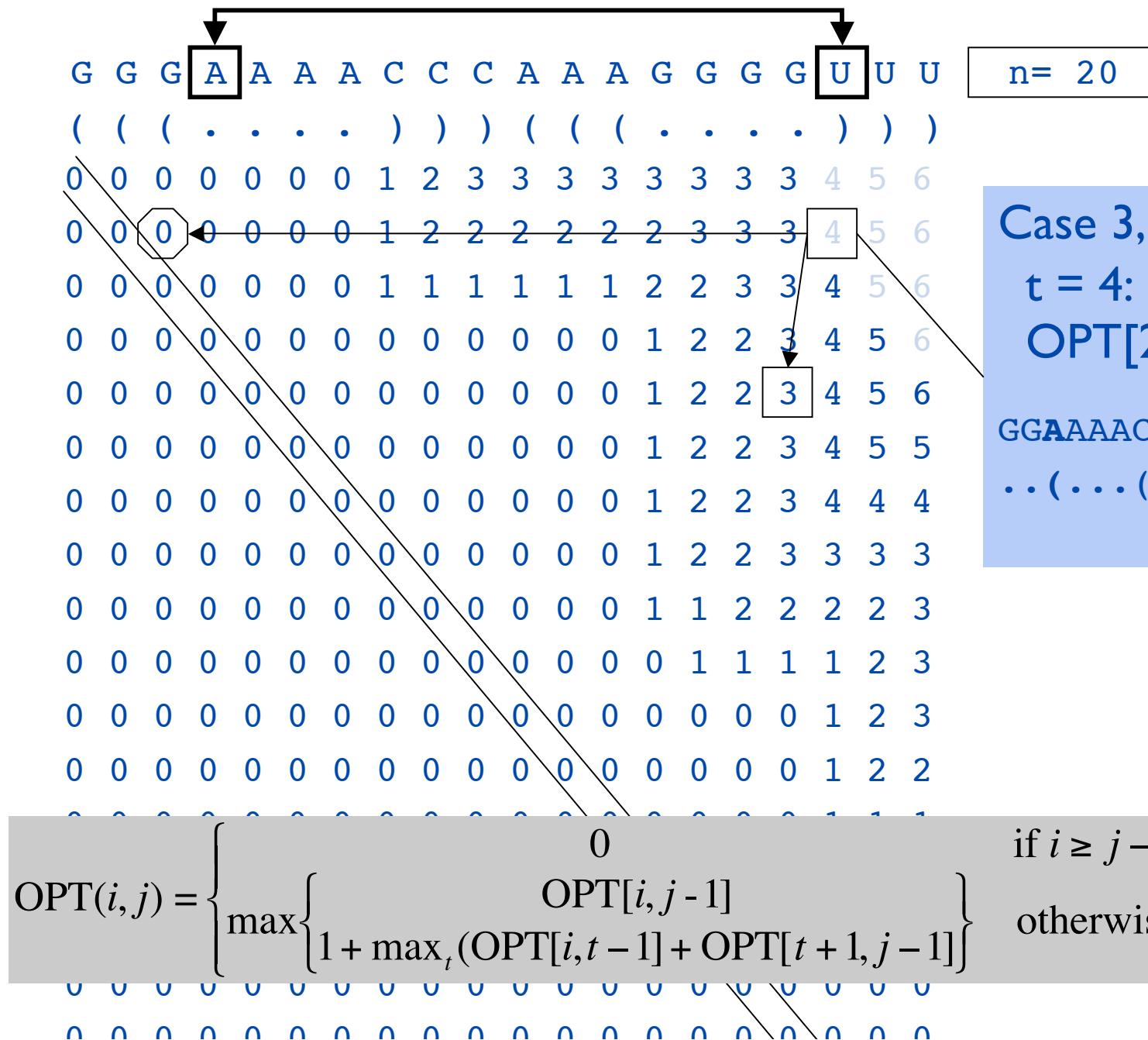
Computing one cell: $\text{OPT}[2,18] = ?$



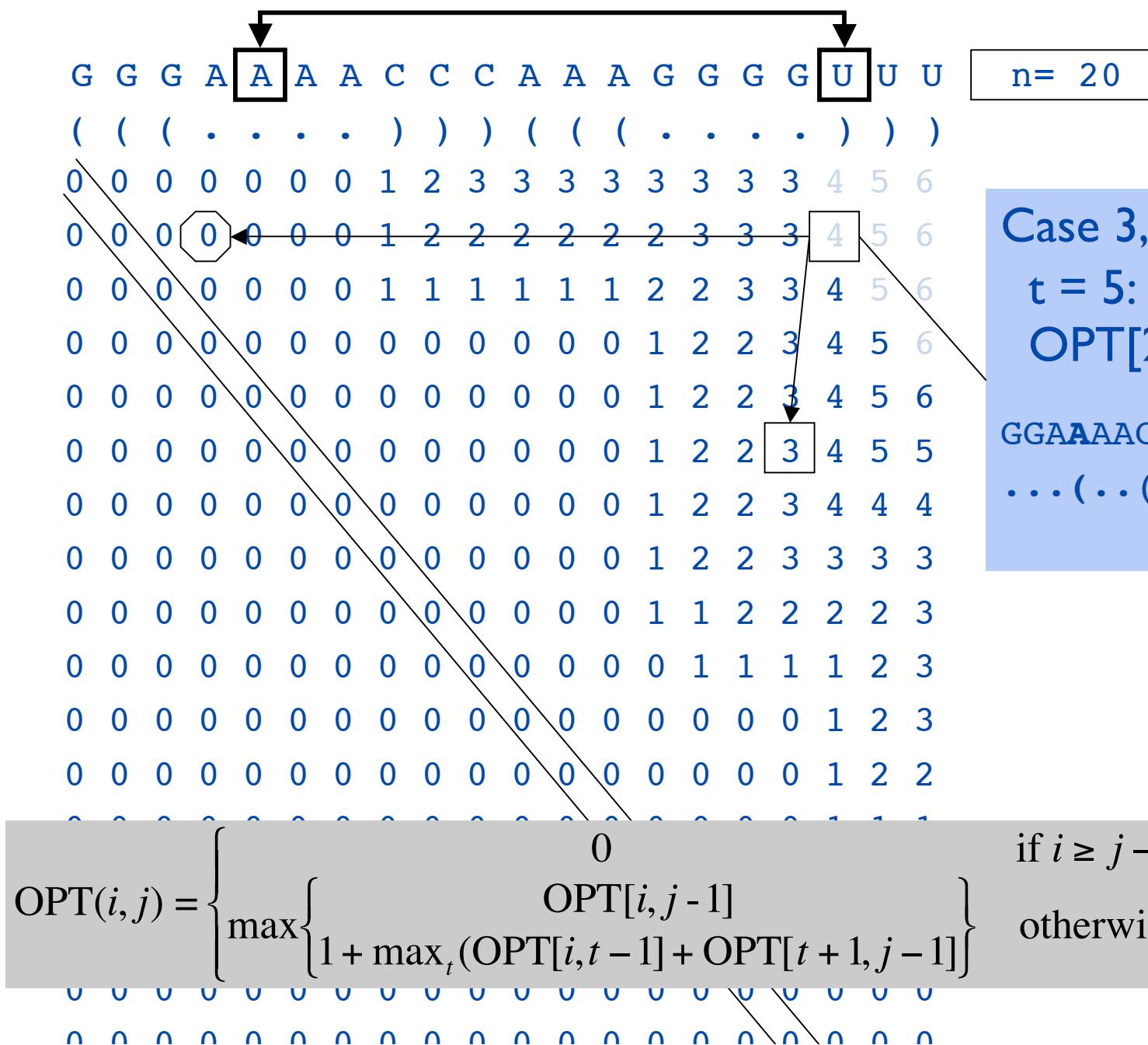
Computing one cell: $\text{OPT}[2,18] = ?$



Computing one cell: $\text{OPT}[2,18] = ?$



Computing one cell: $\text{OPT}[2,18] = ?$



Case 3, $2 \leq t < 18-4$:

$t = 5$: yes pair

$\text{OPT}[2,18] \geq 1 + 0 + 3$

GGAAAACCCAAAGGGGU

...((...))()

Computing one cell: $\text{OPT}[2,18] = ?$

G G G A A **A** A C C C A A A G G G G U U U $n = 20$

(((. . .))) (((. . .)))

0 0 0 0 0 0 0 1 2 3 3 3 3 3 3 3 4 5 6

0 0 0 0 0 0 0 1 2 2 2 2 2 2 3 3 4 5 6

0 0 0 0 0 0 0 1 1 1 1 1 1 2 2 3 3 4 5 6

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 4 5 6

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 4 5 6

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 4 5 5

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 4 5 4

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 4 4 4

0 1 2 2 3 3 3 3

0 1 2 2 2 2 2 3

0 1 1 2 2 2 2 3

0 1 1 1 1 2 3

0 1 2 3

0 1 2 2

0 1 2 2

0 1 2 2

0 1 2 2

0 1 2 2

0 1 2 2

0 1 2 2

0 1 2 2

Case 3, $2 \leq t < 18-4$:

$t = 6$: yes pair

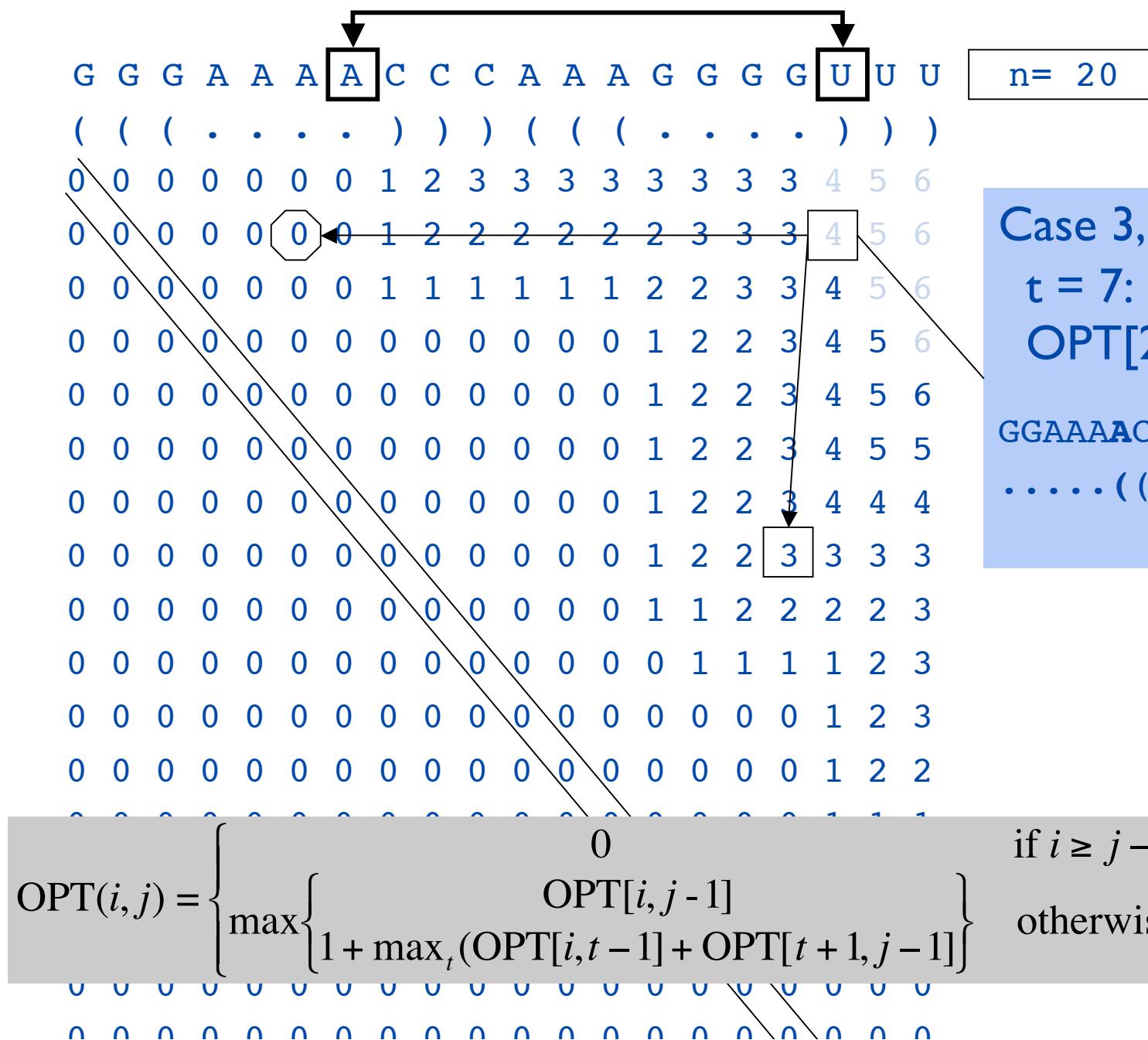
$\text{OPT}[2,18] \geq 1 + 0 + 3$

GGAAAACCCAAAGGGGU

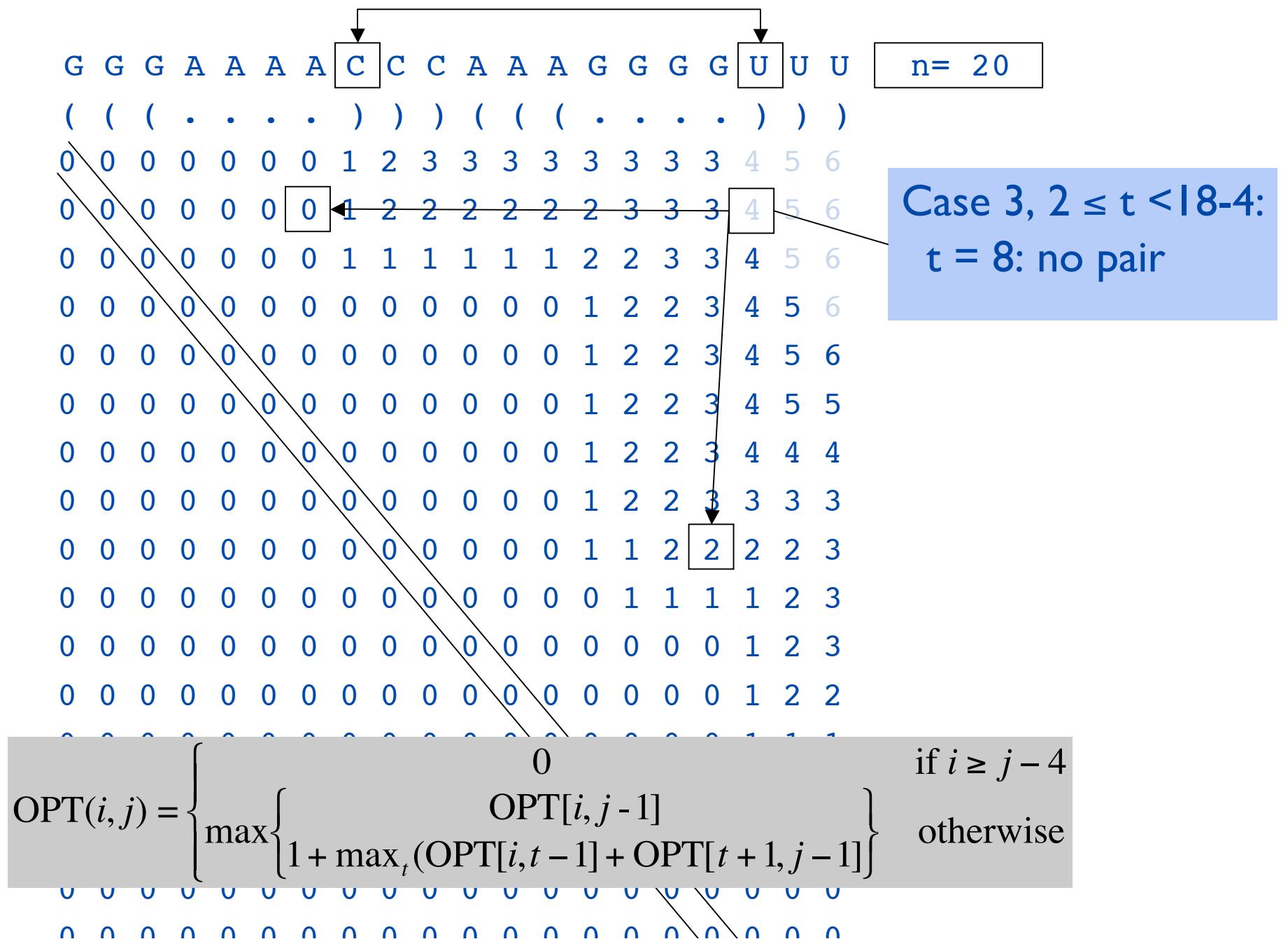
.....(((((.....))))

$$\text{OPT}(i, j) = \begin{cases} \max \left\{ \begin{array}{c} 0 \\ \text{OPT}[i, j - 1] \\ 1 + \max_t (\text{OPT}[i, t - 1] + \text{OPT}[t + 1, j - 1]) \end{array} \right\} & \text{if } i \geq j - 4 \\ \text{otherwise} \end{cases}$$

Computing one cell: $\text{OPT}[2,18] = ?$



Computing one cell: $\text{OPT}[2,18] = ?$



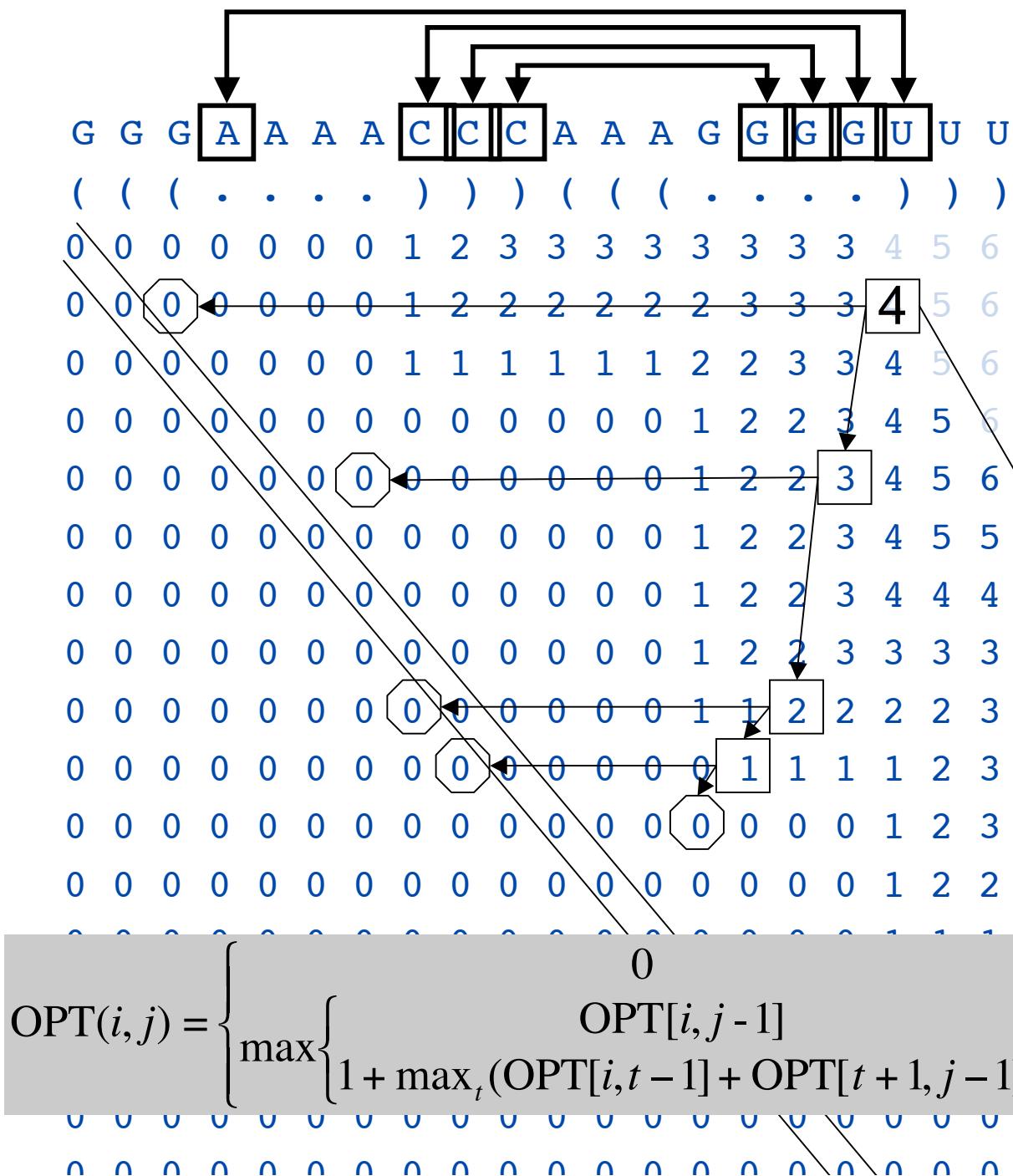
Computing one cell: OPT[2,18] = ?

Case 3,
t = 11;
OPT[2]

GGAAAAAC
((.....

(note
t=11)

$$\text{OPT}(i, j) = \begin{cases} 0 & \text{if } i \geq j - 4 \\ \max \left\{ \begin{array}{l} \text{OPT}[i, j - 1] \\ 1 + \max_t (\text{OPT}[i, t - 1] + \text{OPT}[t + 1, j - 1]) \end{array} \right\} & \text{otherwise} \end{cases}$$



Computing one cell: $\text{OPT}[2,18] = 4$

$n = 20$

Overall, Max = 4
several ways, e.g.:

GGAAAACCCAAAGGGGU
...((...(((.....))))

tree shows trace back:
square = case 3
octagon = case 1

Another Trace Back Example

