

CSEP 527

Computational Biology

RNA: Function, Secondary Structure
Prediction, Search, Discovery

The Message

Cells make lots of ~~RNA~~ *noncoding* RNA

Functionally important, functionally diverse

Structurally complex

New tools required

alignment, discovery, search, scoring, etc.

Rough Outline

Today

Noncoding RNA Examples

RNA structure prediction

RNA

DNA: DeoxyriboNucleic Acid

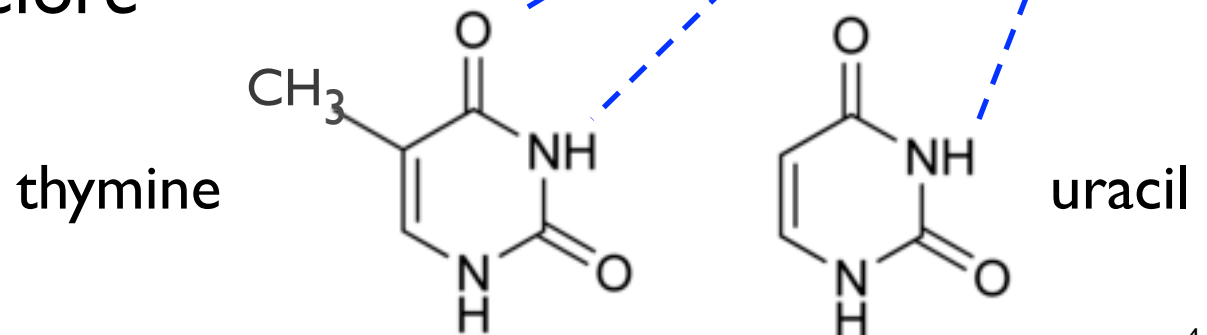
RNA: RiboNucleic Acid

Like DNA, except:

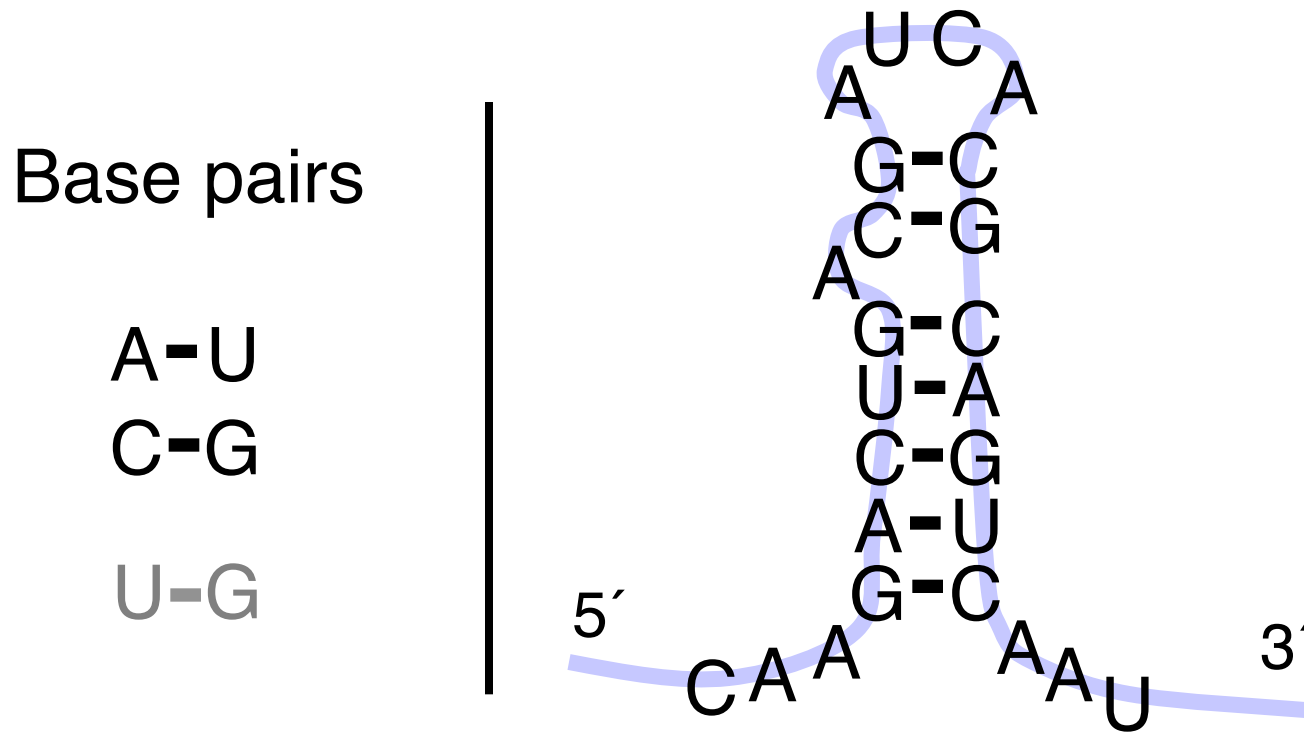
Adds an OH on ribose (backbone sugar)

Uracil (U) in place of thymine (T)

A, G, C as before



RNA Secondary Structure: RNA makes helices too



Usually *single* stranded

Central Dogma of Molecular Biology

by

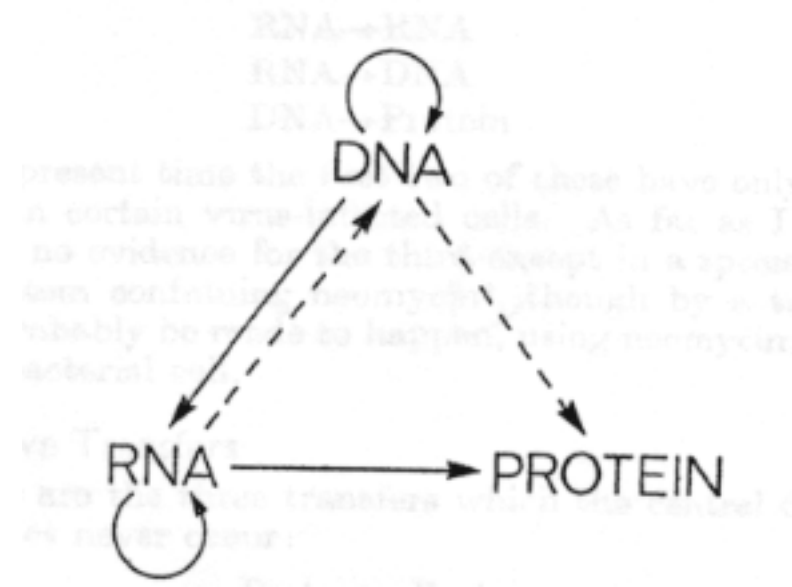
FRANCIS CRICK

MRC Laboratory
Hills Road,
Cambridge CB2 2QH

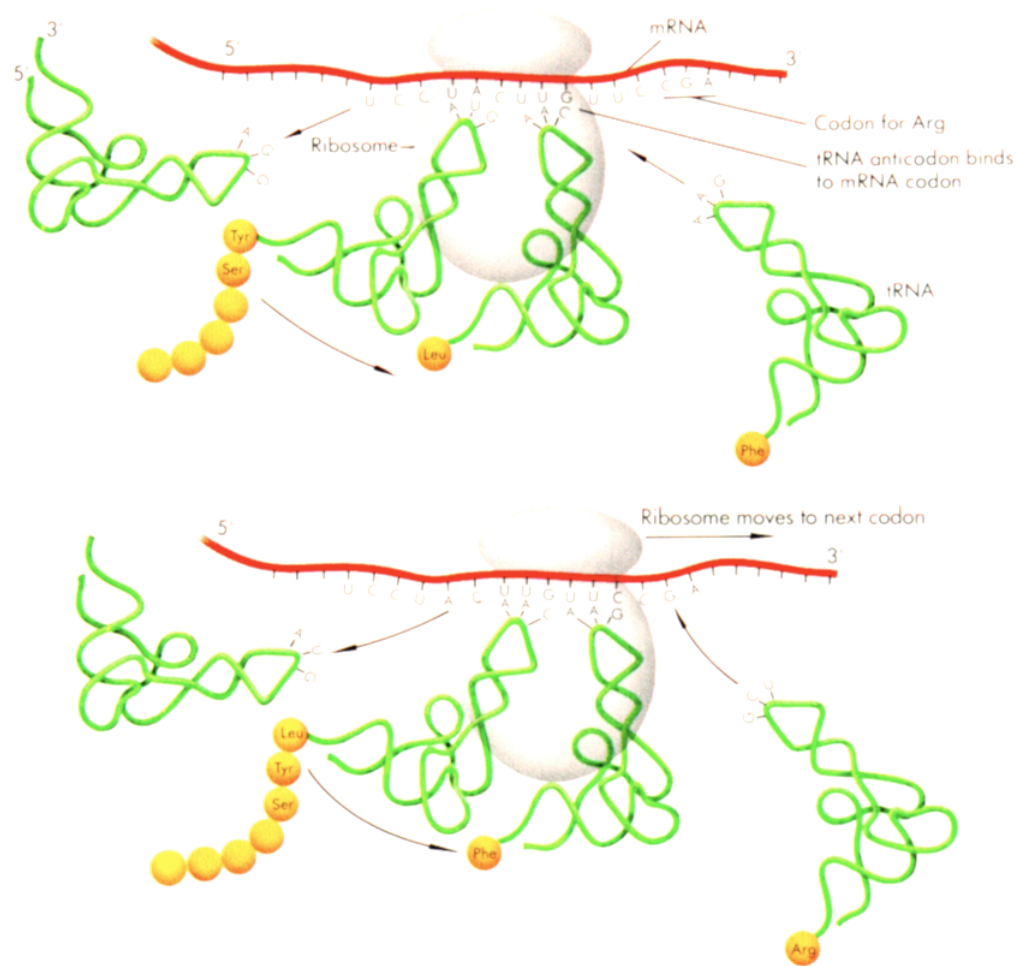
The central dogma of molecular biology deals with the detailed residue-by-residue transfer of sequential information. It states that such information cannot be transferred from protein to either protein or nucleic acid.

“The central dogma, enunciated by Crick in 1958 and the keystone of molecular biology ever since, is likely to prove a considerable over-simplification.”

Fig. 2. The arrows show the situation as it seemed in 1958. Solid arrows represent probable transfers, dotted arrows possible transfers. The absent arrows (compare Fig. 1) represent the impossible transfers postulated by the central dogma. They are the three possible arrows starting from protein.



Ribosomes



Ribosomes

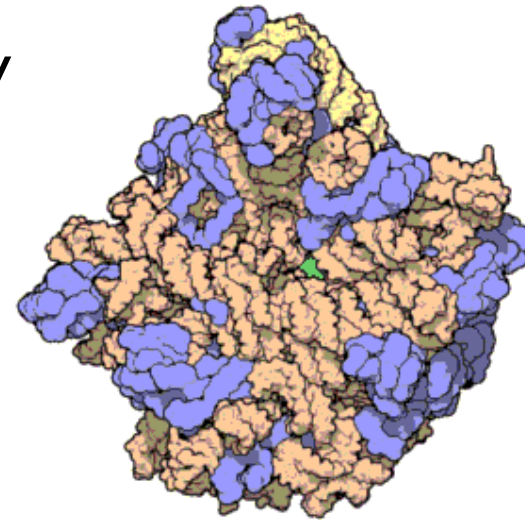
1974 Nobel prize to Romanian biologist George Palade (1912-2008) for discovery in mid 50's

50-80 proteins

3-4 RNAs (half the mass)

Catalytic core is RNA

Of course, mRNAs and tRNAs (messenger & transfer RNAs) are critical too



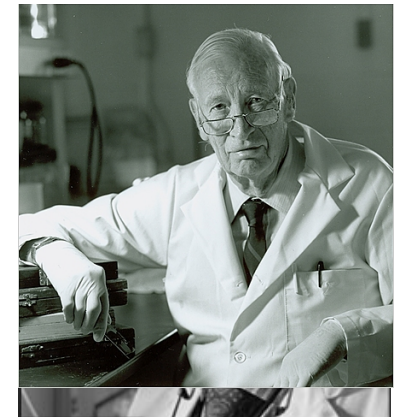
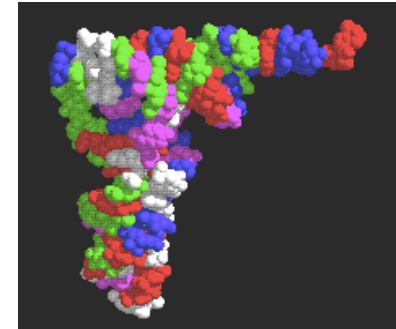
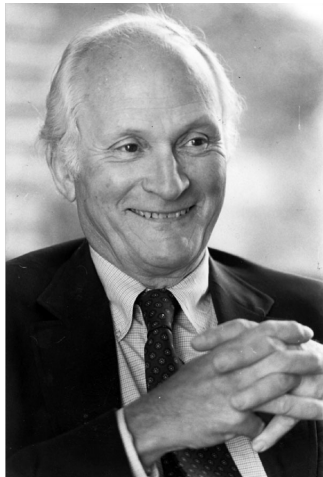
Atomic structure of the 50S Subunit from *Haloarcula marismortui*. Proteins are shown in blue and the two RNA strands in orange and yellow. The small patch of green in the center of the subunit is the active site.

- Wikipedia

Transfer RNA

The “adapter” coupling mRNA to protein synthesis.

Discovered in the mid-1950s by Mahlon Hoagland (1921-2009, left), Mary Stephenson, and Paul Zamecnik (1912-2009; Lasker award winner, right).



Bacteria

Triumph of proteins

80% of genome is coding DNA

Functionally diverse

receptors

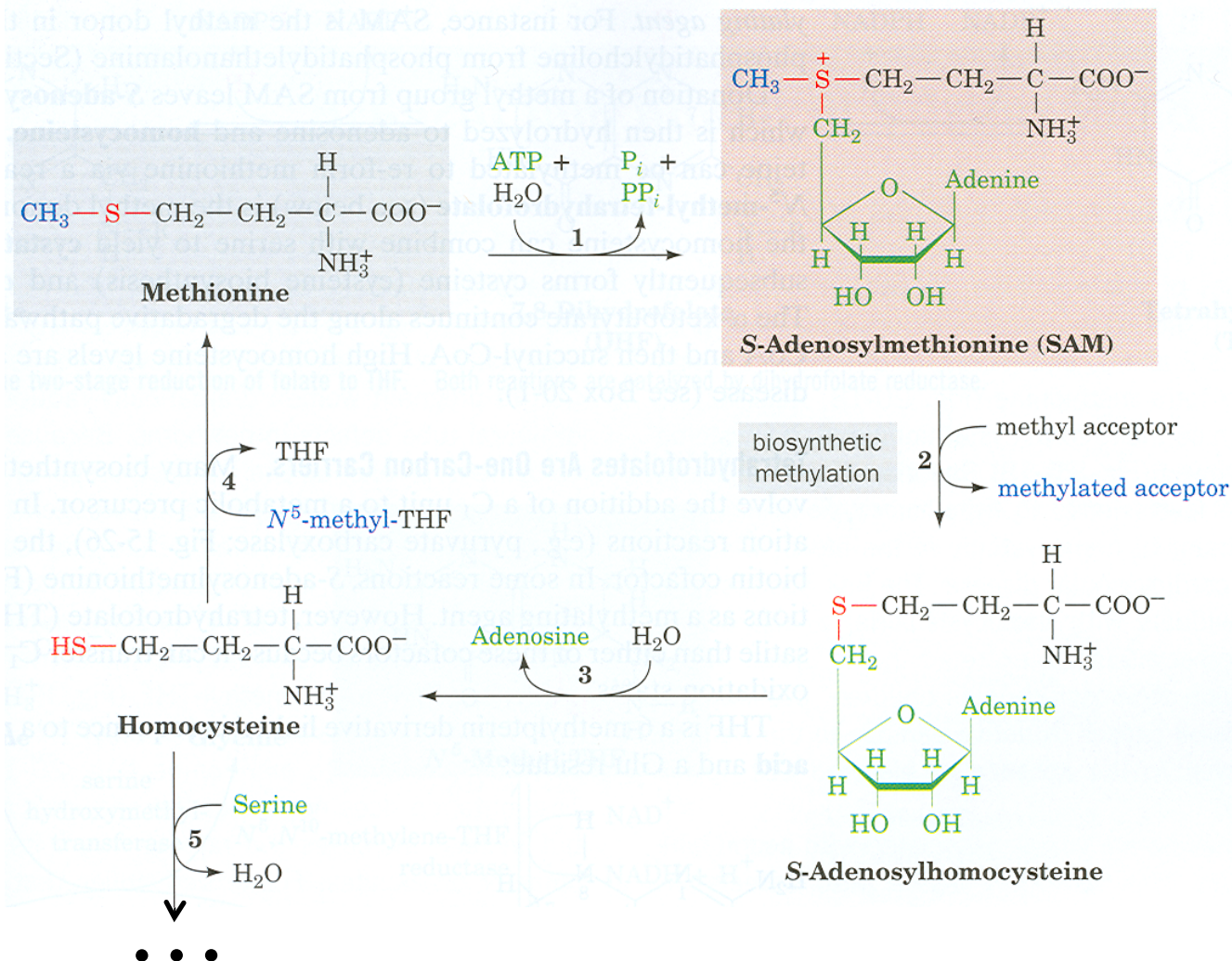
motors

catalysts

regulators (Monod & Jakob, Nobel prize 1965)

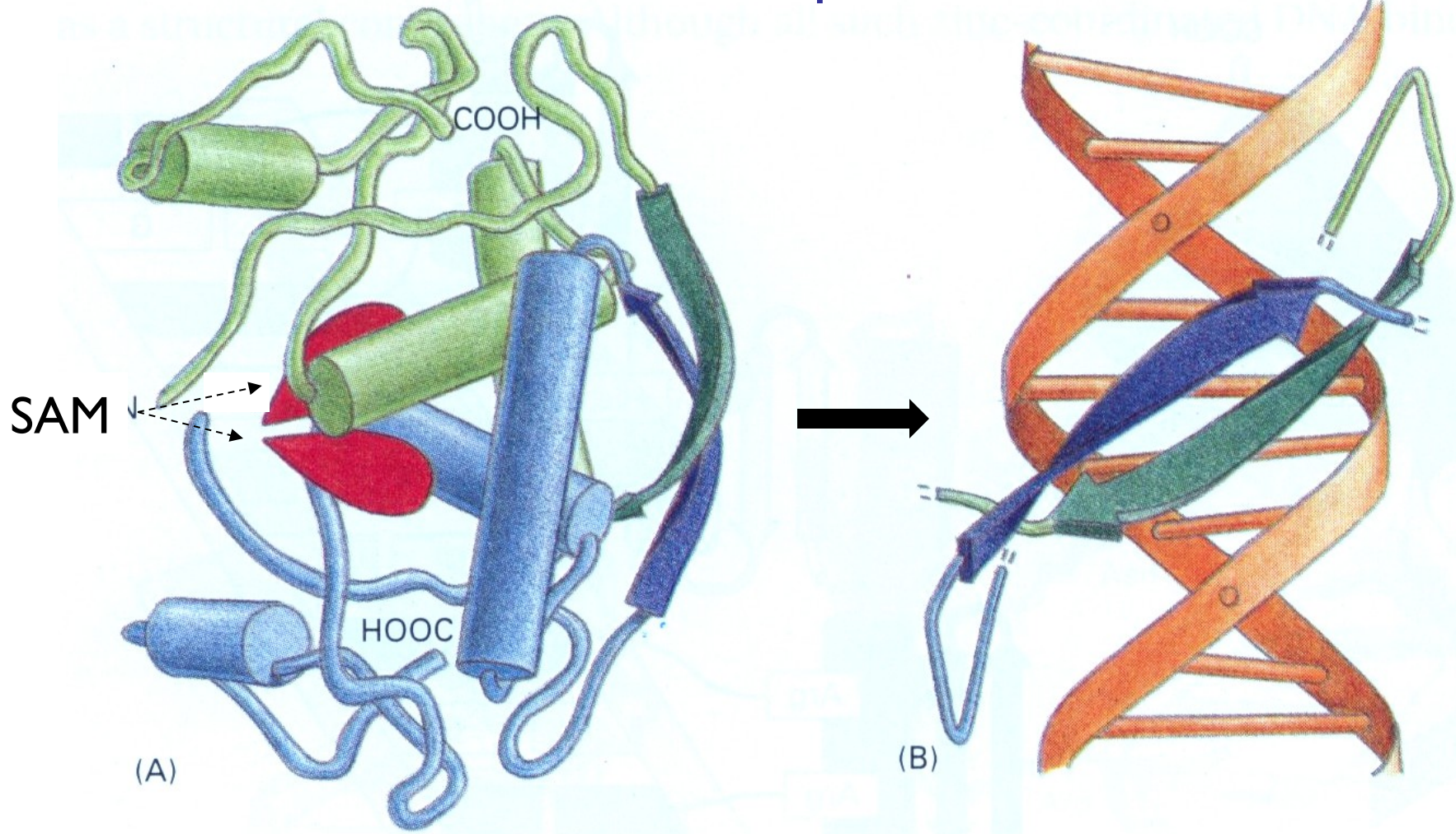
...

Proteins Catalyze Biochemistry: Met Pathways



Proteins Regulate Biochemistry:

The MET Repressor

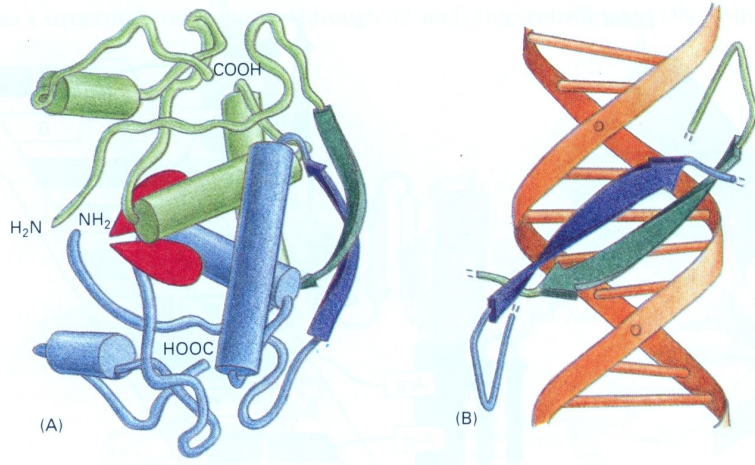


Protein

Alberts, et al, 3e.

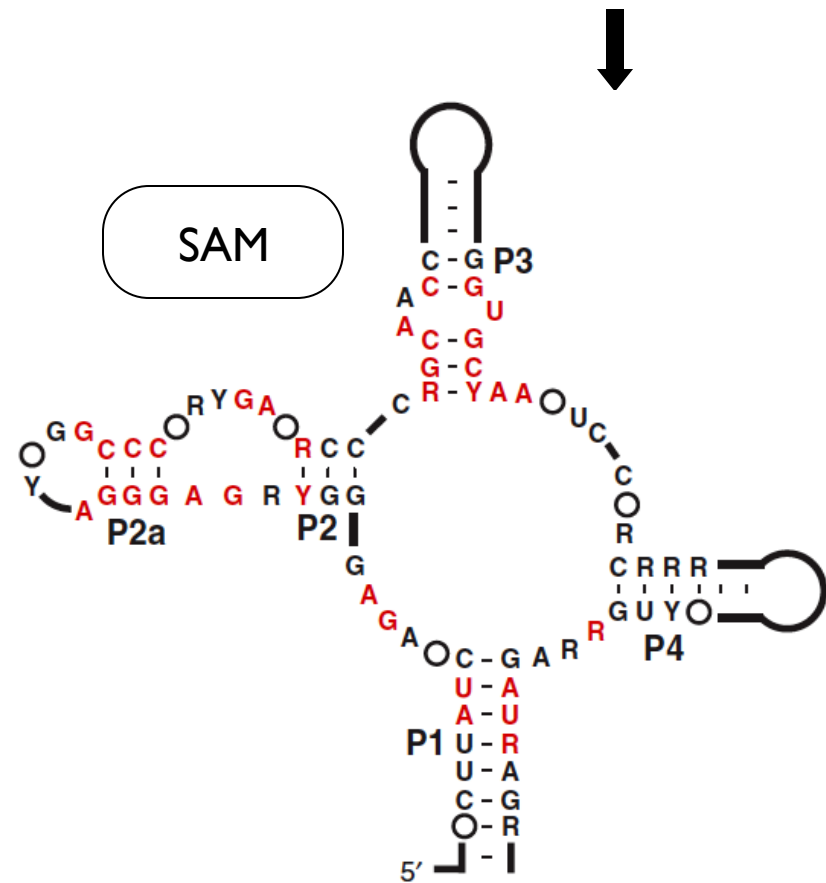
DNA

Alberts, et al, 3e.



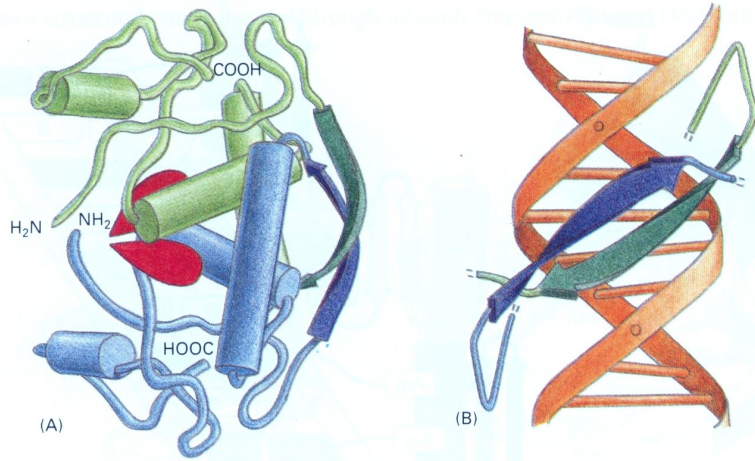
Not the only way!

← Protein way Riboswitch alternative



Grundy & Henkin, Mol. Microbiol 1998
Epshtein, et al., PNAS 2003
Winkler et al., Nat. Struct. Biol. 2003

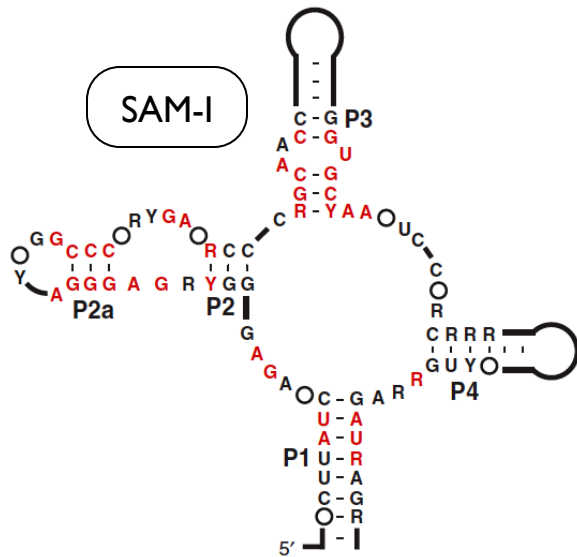
Alberts, et al, 3e.



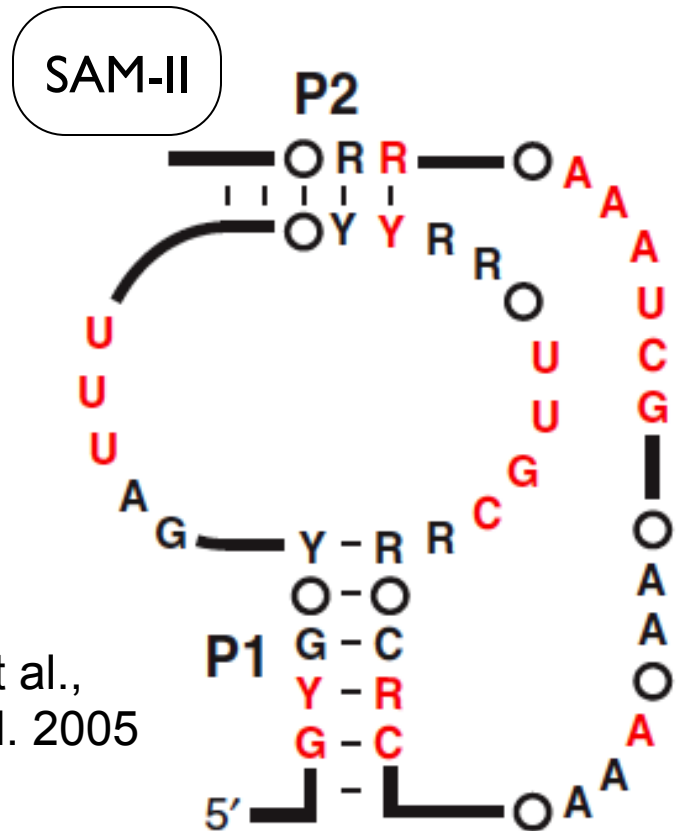
Not the only way!

Protein way

Riboswitch alternatives

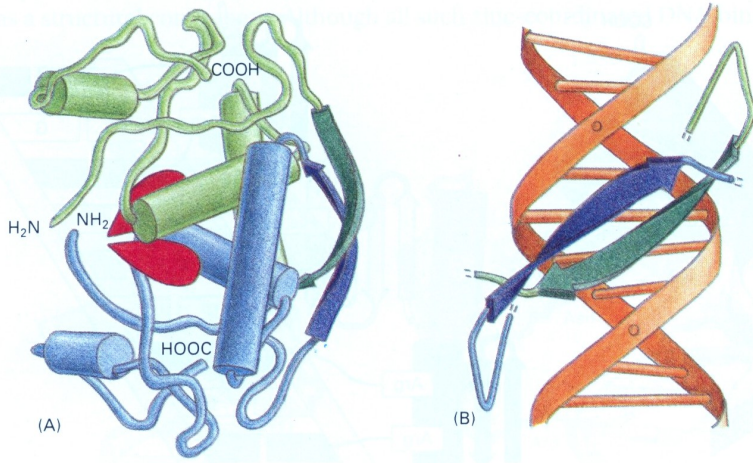


Grundy, Epshtein, Winkler et al., 1998, 2003



Corbino et al.,
Genome Biol. 2005

Alberts, et al, 3e.



Not the only way!

Protein way

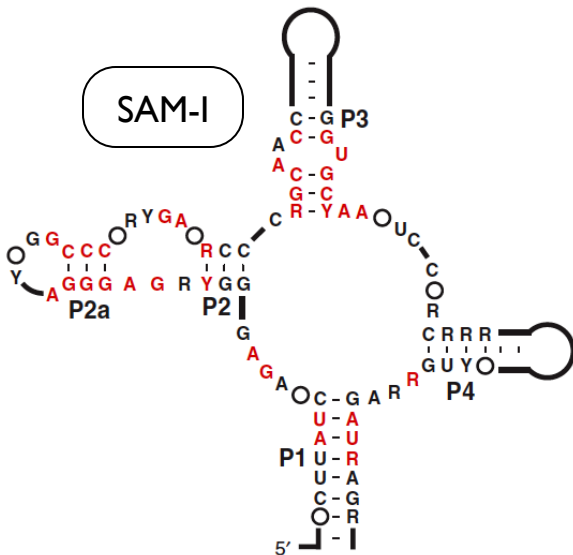
Riboswitch alternatives



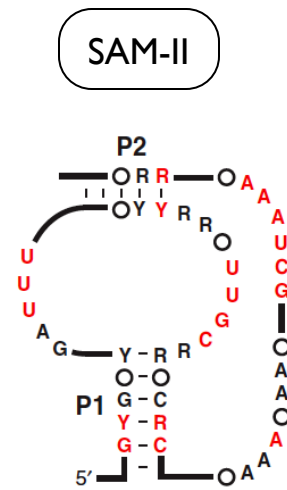
SAM-III



Fuchs et al.,
NSMB 2006

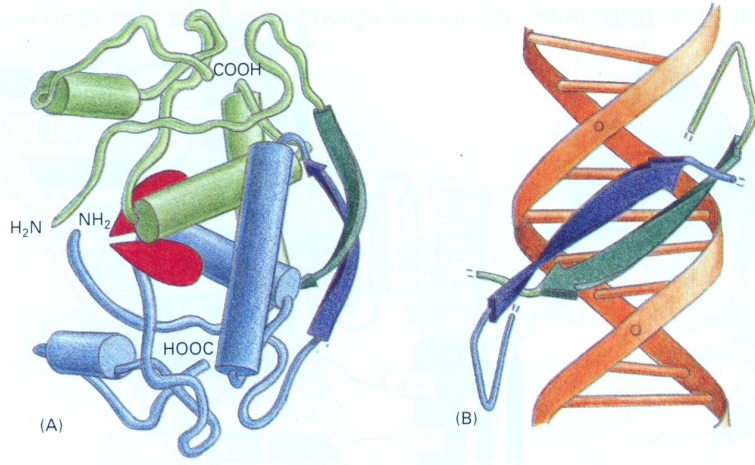


Grundy, Epshtein, Winkler et al., 1998, 2003



Corbino et al.,
Genome Biol. 2005

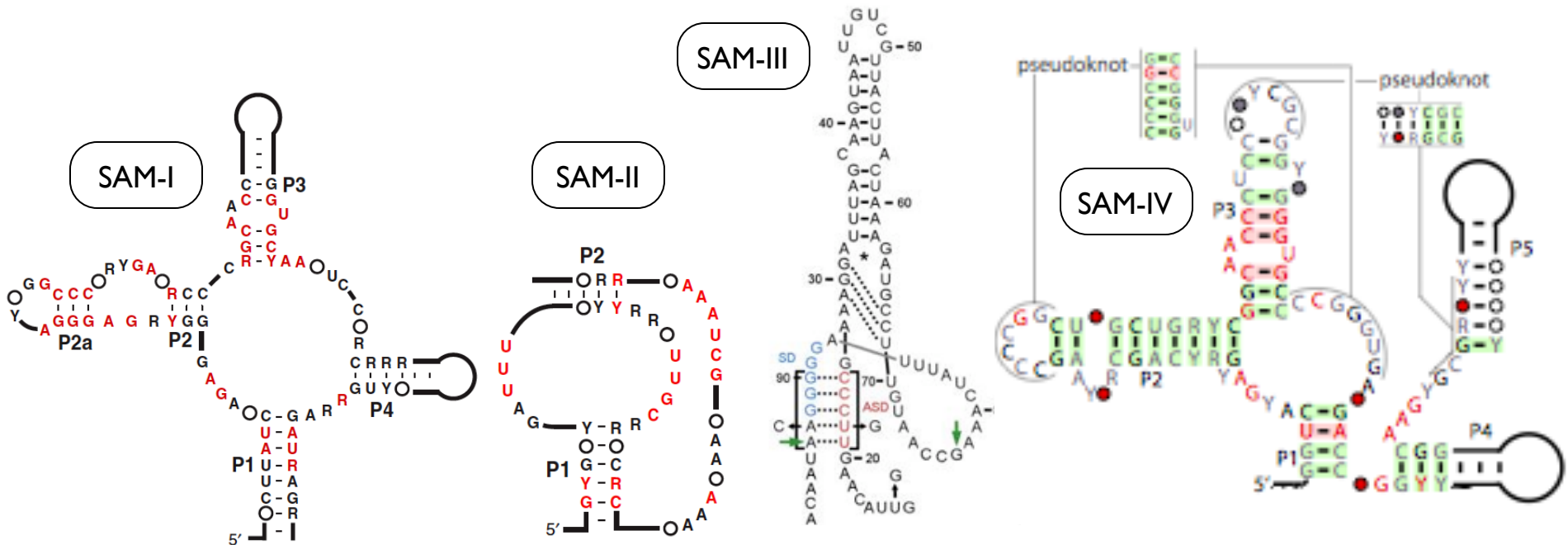
Alberts, et al, 3e.



Not the only way!

Protein way

Riboswitch alternatives



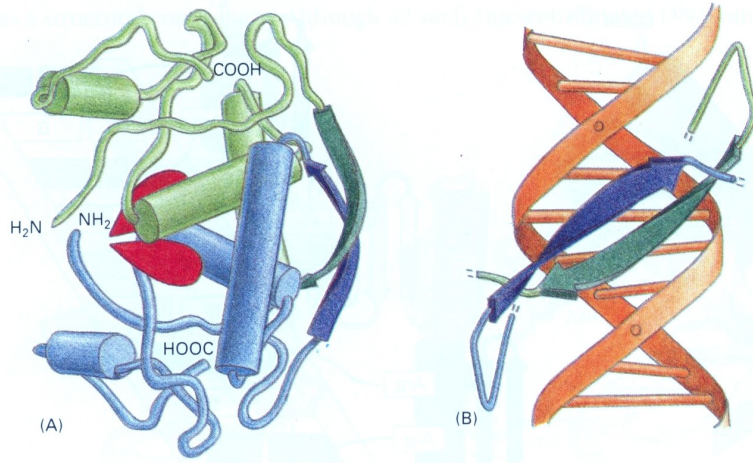
Grundy, Epshtein, Winkler et al., 1998, 2003

Corbino et al., Genome Biol. 2005

Fuchs et al., NSMB 2006

Weinberg et al., RNA 2008

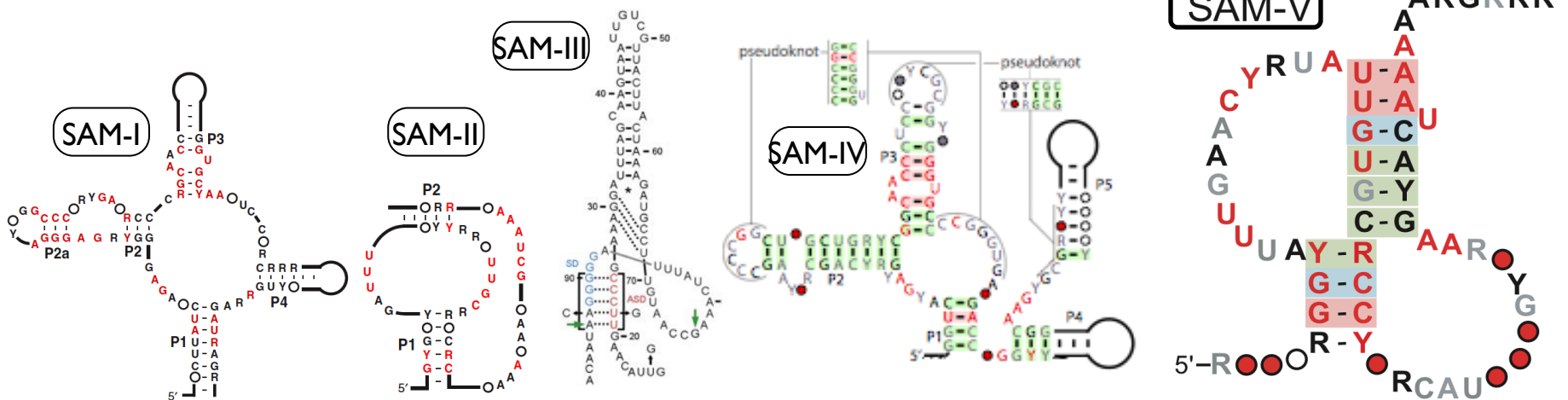
Alberts, et al, 3e.



Not the only way!

Protein way

Riboswitch alternatives



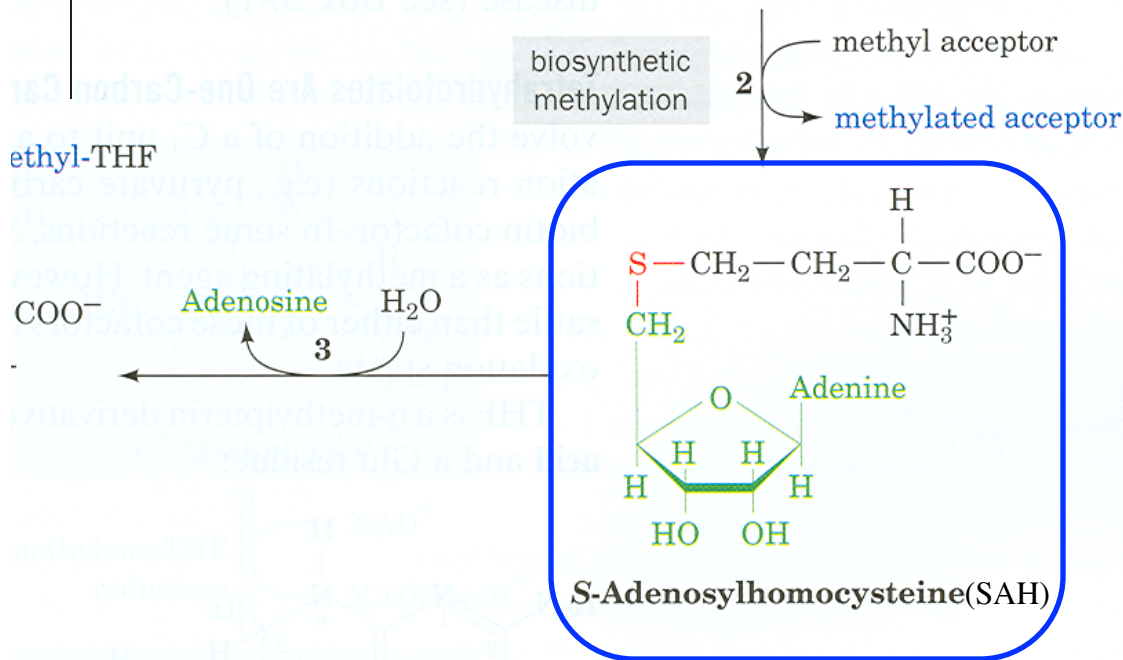
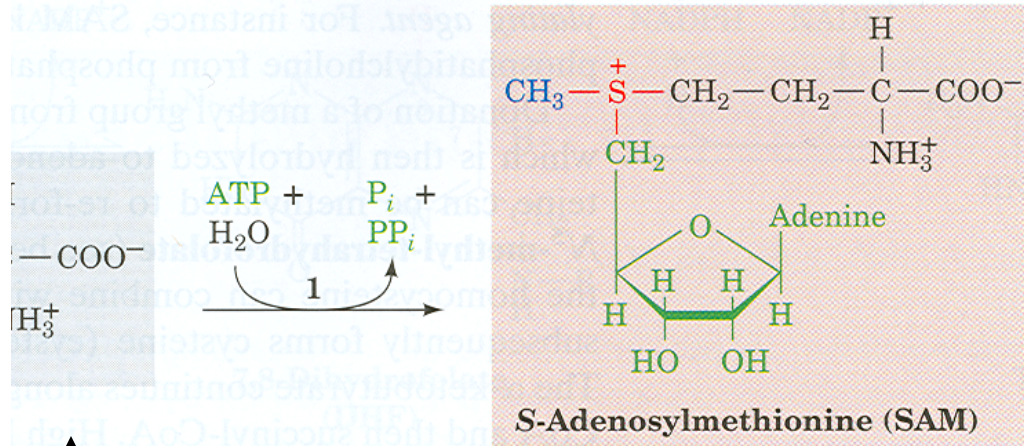
Grundy, Epshtein, Winkler et al., 1998, 2003

Corbino et al., Genome Biol. 2005

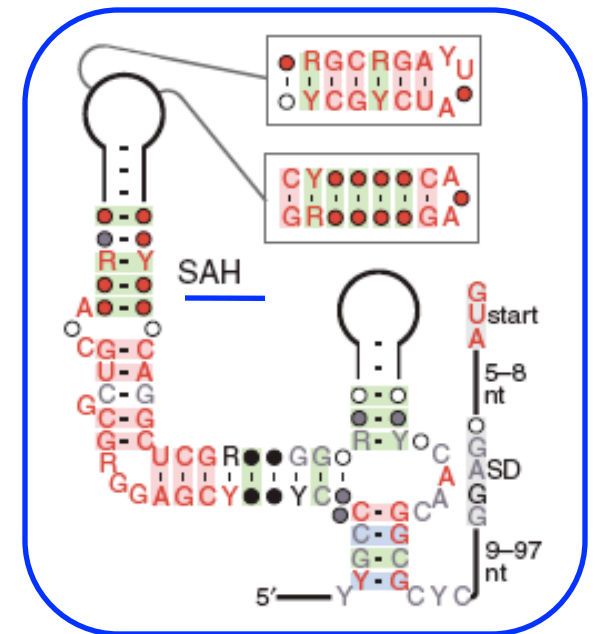
Fuchs et al., NSMB 2006

Weinberg et al., RNA 2008

Meyer, et al., BMC Genomics 2009



And in other bacteria, a riboswitch senses SAH



ncRNA Example: Riboswitches

UTR structure that directly senses/binds small molecules & regulates mRNA

widespread in prokaryotes

some in eukaryotes & archaea, one in a phage

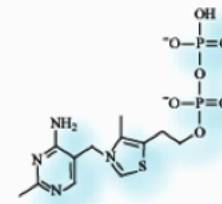
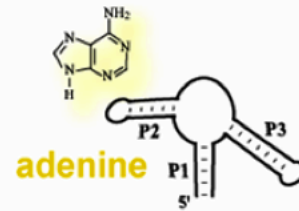
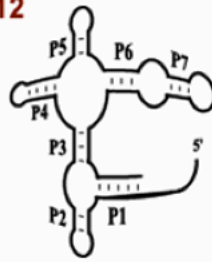
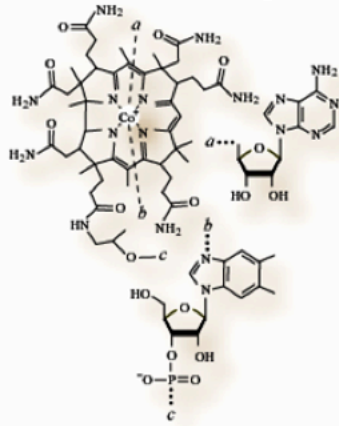
~ 20 ligands known; multiple nonhomologous solutions for some

dozens to hundreds of instances of each

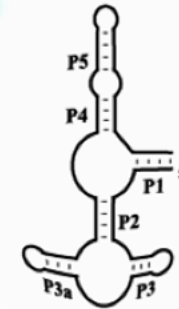
on/off; transcription/translation; splicing; combinatorial control

all found since ~2003; most via bioinformatics

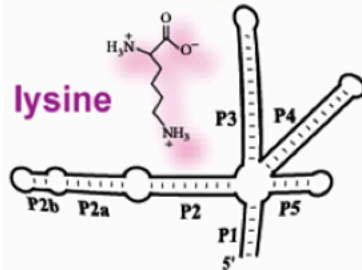
coenzyme B₁₂



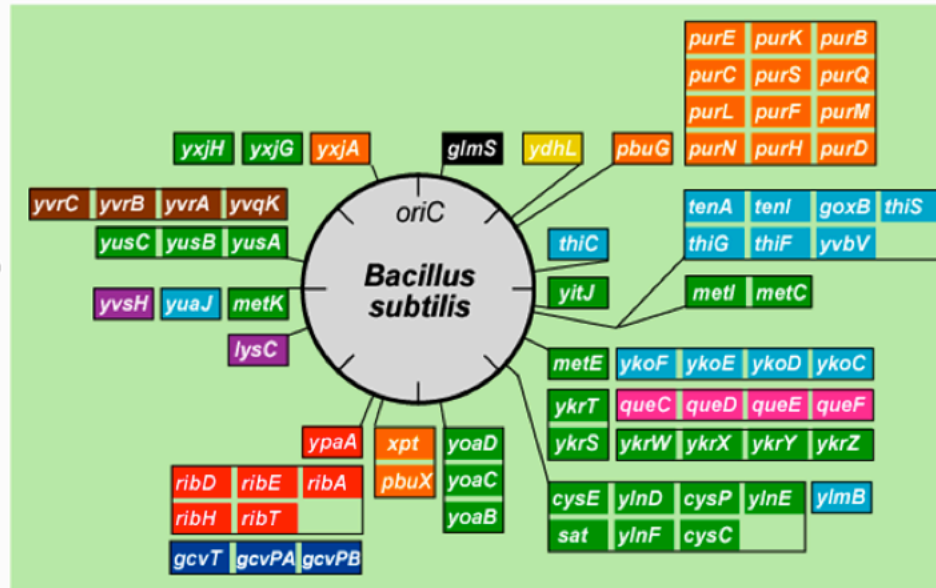
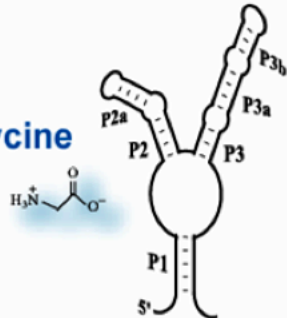
thiamine pyrophosphate



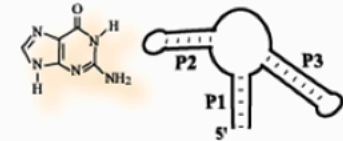
lysine



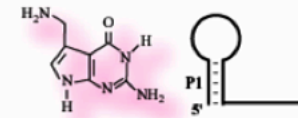
glycine



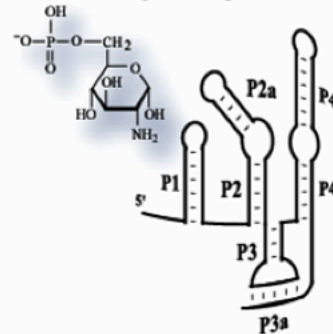
guanine



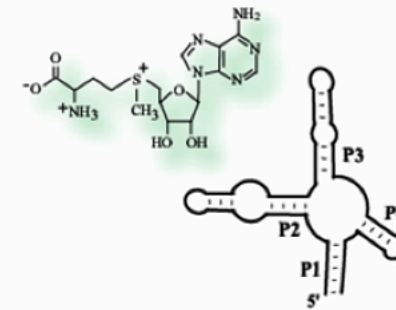
pre-queosine₁



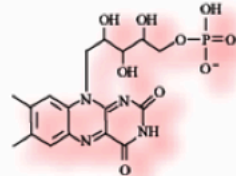
glucosamine-6-phosphate



S-adenosyl-methionine



flavin mononucleotide



New Antibiotic Targets?

Old drugs, new understanding:

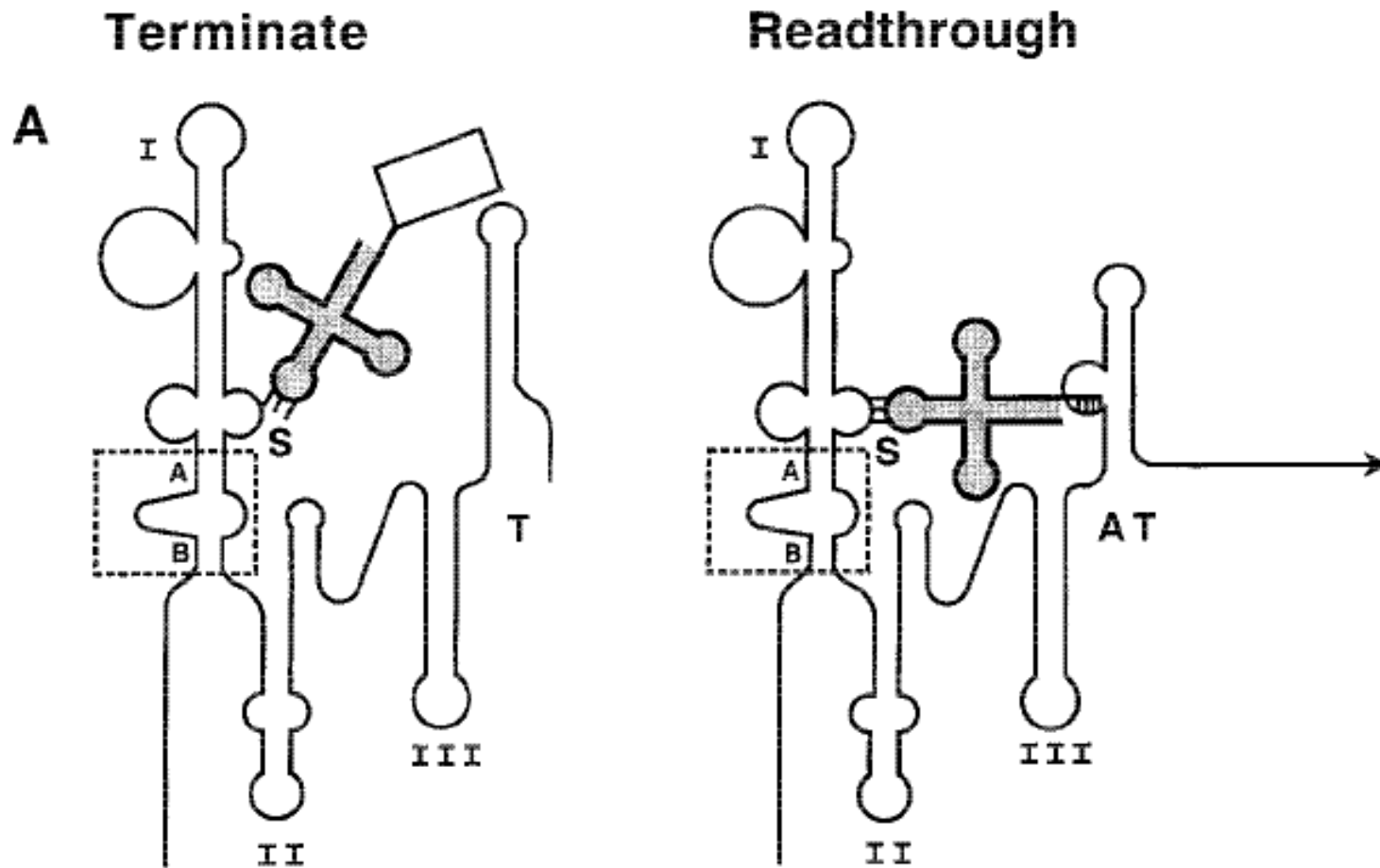
TPP riboswitch ~ pyriithiamine

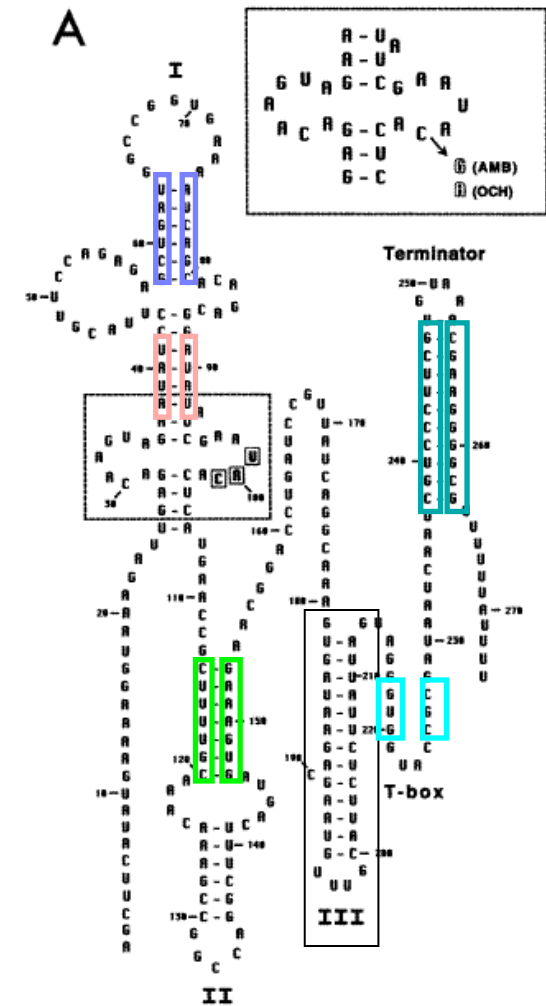
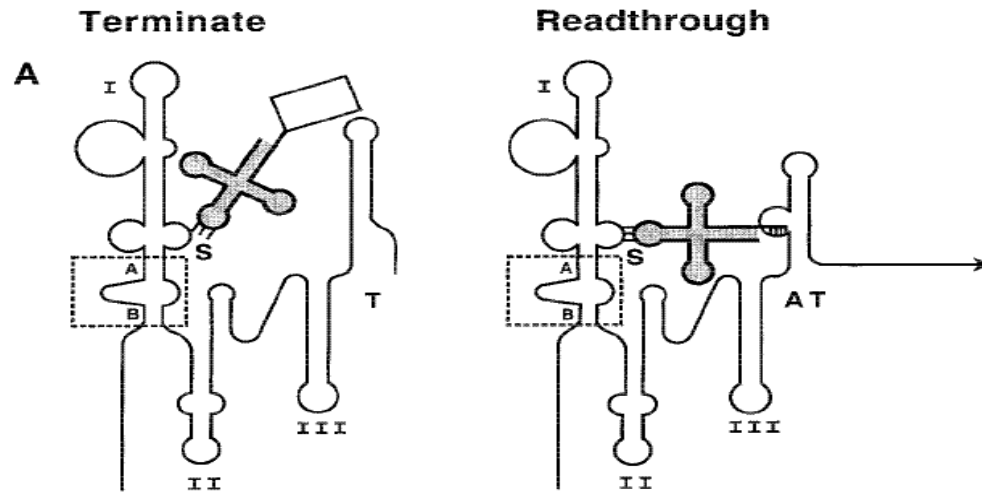
lysine riboswitch ~ L-aminoethylcysteine, DL-4-oxalysine

FMN riboswitch ~ roseoflavin

Potential advantages - no (known) human riboswitches, but often multiple copies in bacteria, so potentially efficacious with few side effects?

ncRNA Example: T-boxes





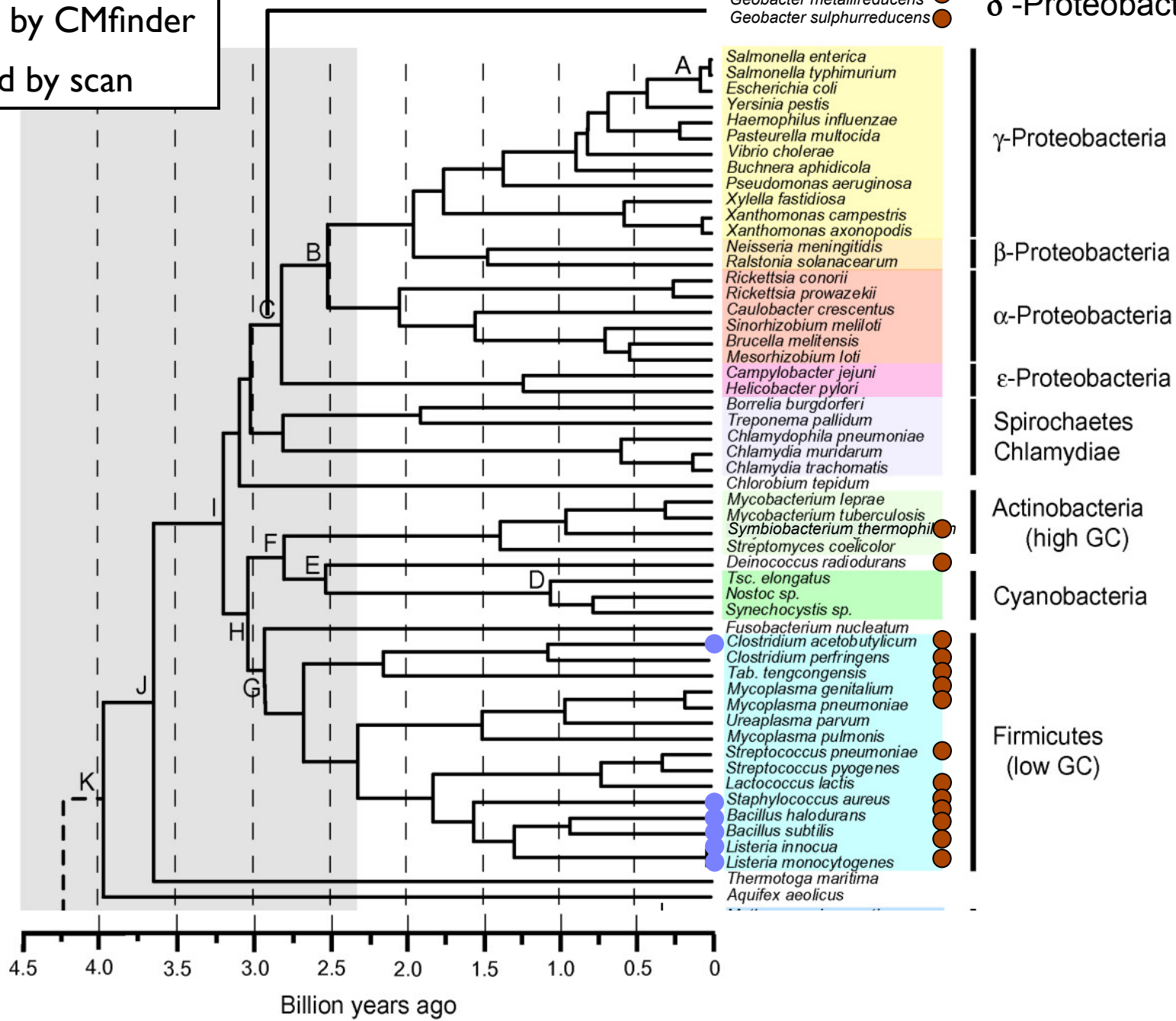
NC_000964.1 **AUAU**C.CUUACGU..UCCAGAGAG**CUGAU**GGCCGGUGAAA.**AUCAGC**ACAGACGGAU**AUAU**
 NC_004722.1 **CAAAU**.GUCGUUUcUUUAGAGAG**GUCGAU**GGUUGGUGGAA.**AUCGAU**AG..AAACA**GUUUG**
 NC_004193.1 **AAAAG**UAGAACCG.AUCUAGCGAA**AUUGAG**GAU.GGUGUGAG**CUCAGU**GC.GGAAAG**CUUUU**
 NC_003997.3 **CAAAU**.GUCGUUUcUUUAGAGAG**GUCGAU**GGUUGGUGGAA.**AUCGAU**AG..AAACA**GUUUG**

NC_000964.1 CGAA..UACACUCAUGAACCG**CUUUUGC**AAACAAAGccggccaggcuuucAGUA.**GUGAAAG**
 NC_004722.1 UGAA..UCCAUCCUGGAAU..**GGAAUGU**GGAAUAUCUuuuggauu....AGUA**GCAUUC**
 NC_004193.1 AGAAAUC.ACUCUUGAGUU.**UUCAUUAC**GAAA..CA.....AGUA**GUAUUGGA**
 NC_003997.3 UGAA..UCCAUCCUGGAAU..**GGAAUGU**GGAAUAUCUuuuugauu....AGUAA**ACAUUC**

NC_000964.1 acGGAC.CUGAUCCGUUAUCAGGCAAAG**GUG**GUAC**CGC**GAUAAUCA**AAU**CGUCCCUUC**G**UGUAAa**CGAAGGGGCGUUU**
 NC_004722.1 .CGGUG.AAGAGCCGUUAUU...UCu**AGUG**GCAA**CGCGG**..GUU**AACUCCCGUCCCU**UUUAUu**AGGGACGGGAGUU**
 NC_004193.1 .CGGUUcAUC.UCCGUUAUCGAUCUUAG**GUG**GUAC**CGCGA**.....**GUCUUCU**CGUCCCUUUU..**GGGAU**AGAAGGC
 NC_003997.3 .CGGUG.AAGAGCCGUUAUU...UCu**AGUG**GCAA**CGCGG**..GUU**AACUCCCGUCCCU**UUUAUu**AGGGACGGGAGUU**

● Used by CMfinder
● Found by scan

Chloroflexus aurantiacus ● Chloroflexi
Geobacter metallireducens ● δ -Proteobacteria
Geobacter sulphurreducens ●



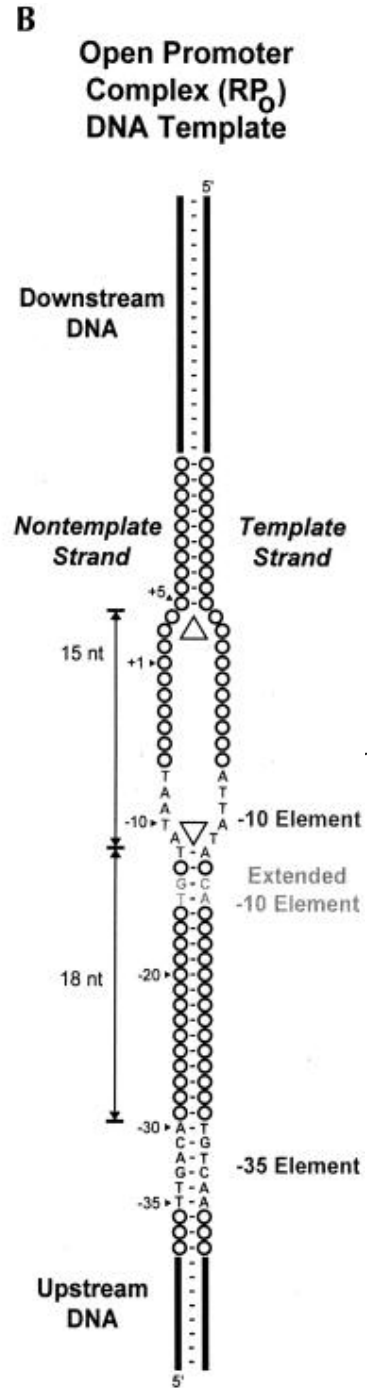
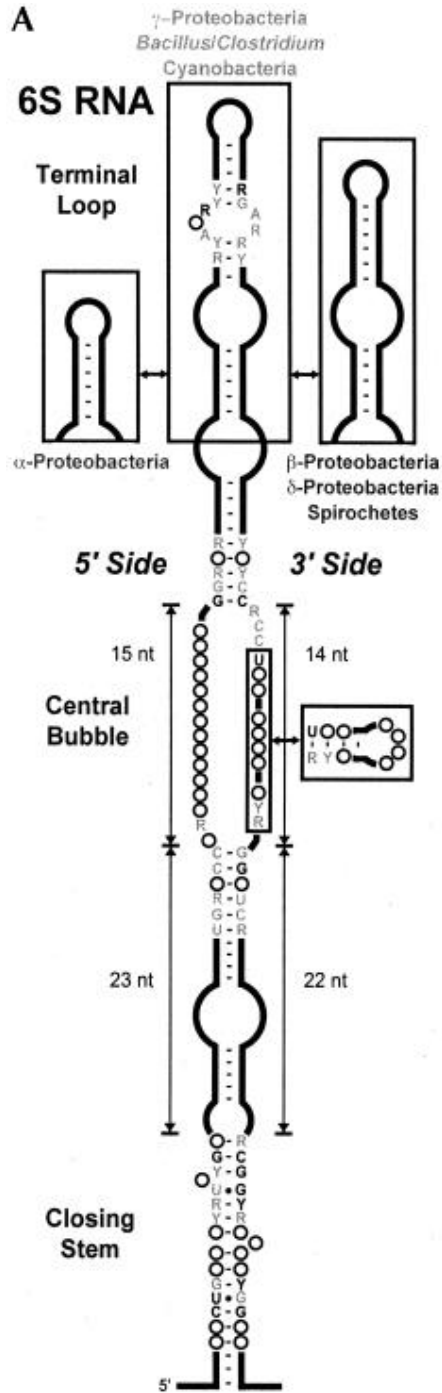
ncRNA Example: 6S

medium size (175nt)

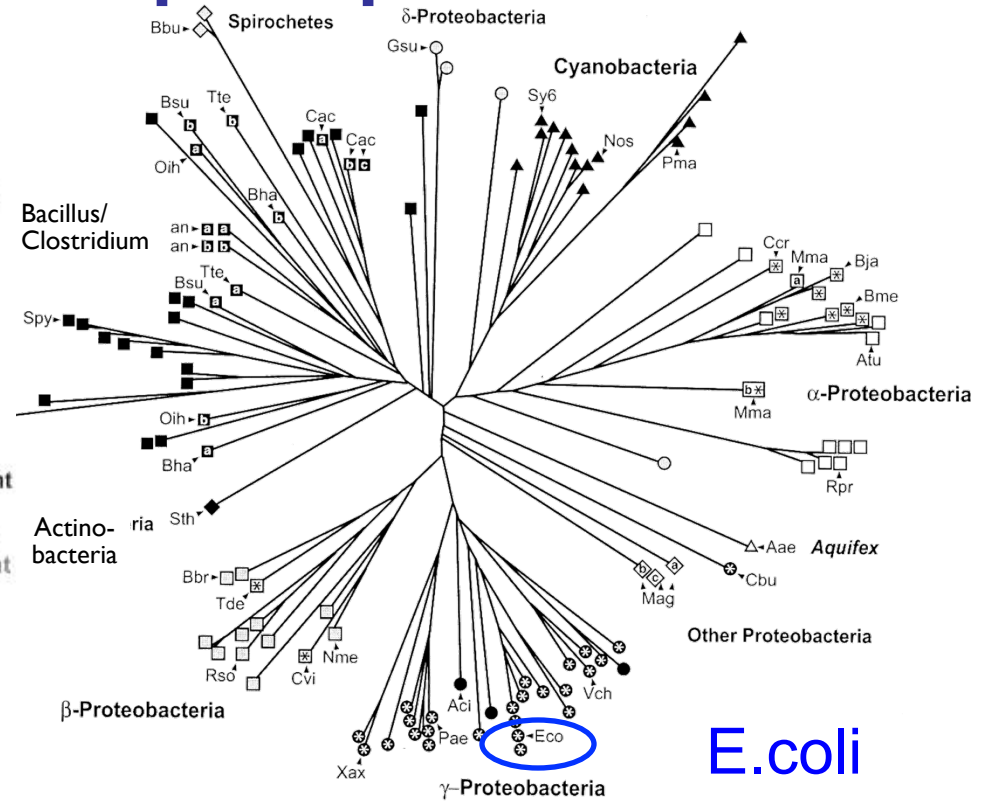
structured

highly expressed in *E. coli* in certain growth conditions

sequenced in 1971; function unknown for 30 years



6S mimics an open promoter



E.coli

Barrick et al. *RNA* 2005

Trotochaud et al. *NSMB* 2005

Willkomm et al. *NAR* 2005

Summary: RNA in Bacteria

Widespread, deeply conserved, structurally sophisticated, functionally diverse, biologically important uses for ncRNA throughout prokaryotic world.

Regulation of MANY genes involves RNA

In some species, we know identities of more riboregulators than protein regulators

Dozens of classes & thousands of new examples in just the last 5-10 years

Vertebrate ncRNAs

mRNA, tRNA, rRNA, ... of course

PLUS:

snRNA, spliceosome, snoRNA, telomerase,
microRNA, RNAi, SECIS, IRE, piwi-RNA,
XIST (X-inactivation), ribozymes, ...

MicroRNA

1st discovered 1992 in *C. elegans*

2nd discovered 2000, also *C. elegans*

and human, fly, everything between – basically all
multi-celled plants & animals

21-23 nucleotides

literally fell off ends of gels

Hundreds now known in human

may regulate 1/3-1/2 of all genes

development, stem cells, cancer, infectious disease,

...

siRNA

2006 Nobel Prize
Fire & Mello

“Short Interfering RNA”

Also discovered in *C. elegans*

Possibly an antiviral defense, shares
machinery with miRNA pathways

Allows artificial repression of most genes in
most higher organisms

Huge tool for biology & biotech

ncRNA Example: Xist

large ($\approx 12\text{kb}$)

largely unstructured RNA

required for X-inactivation in mammals

(Remember calico cats?)

Human Predictions

Evofold

S Pedersen, G Bejerano, A Siepel, K Rosenbloom, K Lindblad-Toh, ES Lander, J Kent, W Miller, D Haussler, "Identification and classification of conserved RNA secondary structures in the human genome." [PLoS Comput. Biol., 2, #4 \(2006\) e33.](#)

48,479 candidates (~70% FDR?)

RNAz

S Washietl, IL Hofacker, M Lukasser, A Huttenhofer, F Stadler, "Mapping of conserved RNA secondary structures predicts thousands of functional noncoding RNAs in the human genome." [Nat. Biotechnol., 23, #11 \(2005\) 1383-90.](#)
30,000 structured RNA elements
1,000 conserved across all vertebrates.
~1/3 in introns of known genes, ~1/6 in UTRs
~1/2 located far from any known gene

FOLDALIGN

E Torarinsson, M Sawera, JH Havgaard, M Fredholm, J Gorodkin, "Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure." [Genome Research, 16, #7 \(2006\) 885-9.](#)

1800 candidates from 36970 (of 100,000) pairs

CMfinder

Torarinsson, Yao, Wiklund, Bramsen, Hansen, Kjems, Tommerup, Ruzzo and Gorodkin. Comparative genomics beyond sequence based alignments: RNA structures in the ENCODE regions.

[Genome Research, Feb 2008, 18\(2\):242-251](#) PMID: [18096747](#)

6500 candidates in ENCODE alone (better FDR, but still high)

Thousands of Predictions

Bottom line?

A significant number of “one-off” examples

Extremely wide-spread ncRNA expression

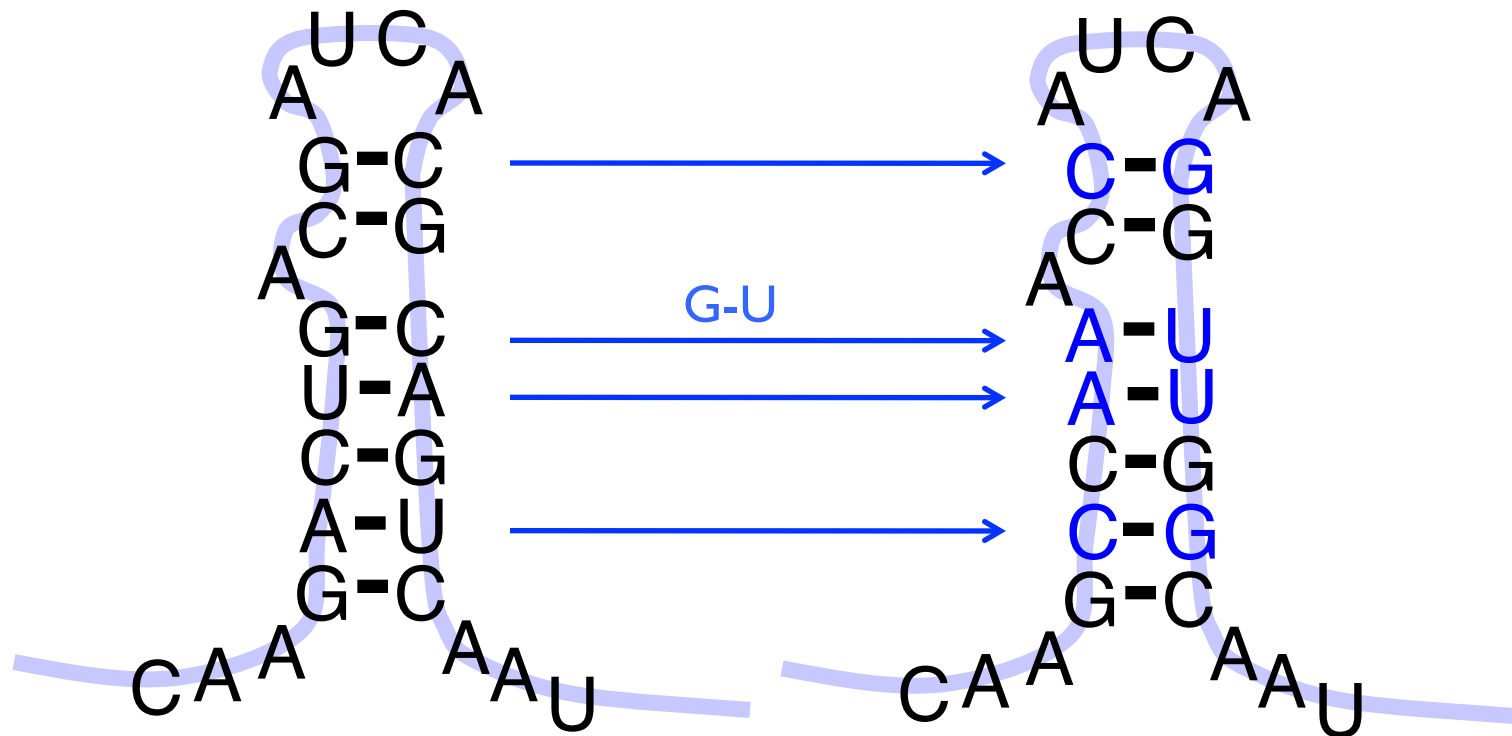
At a minimum, a vast evolutionary substrate

New technology (e.g., RNAseq) exposing
more

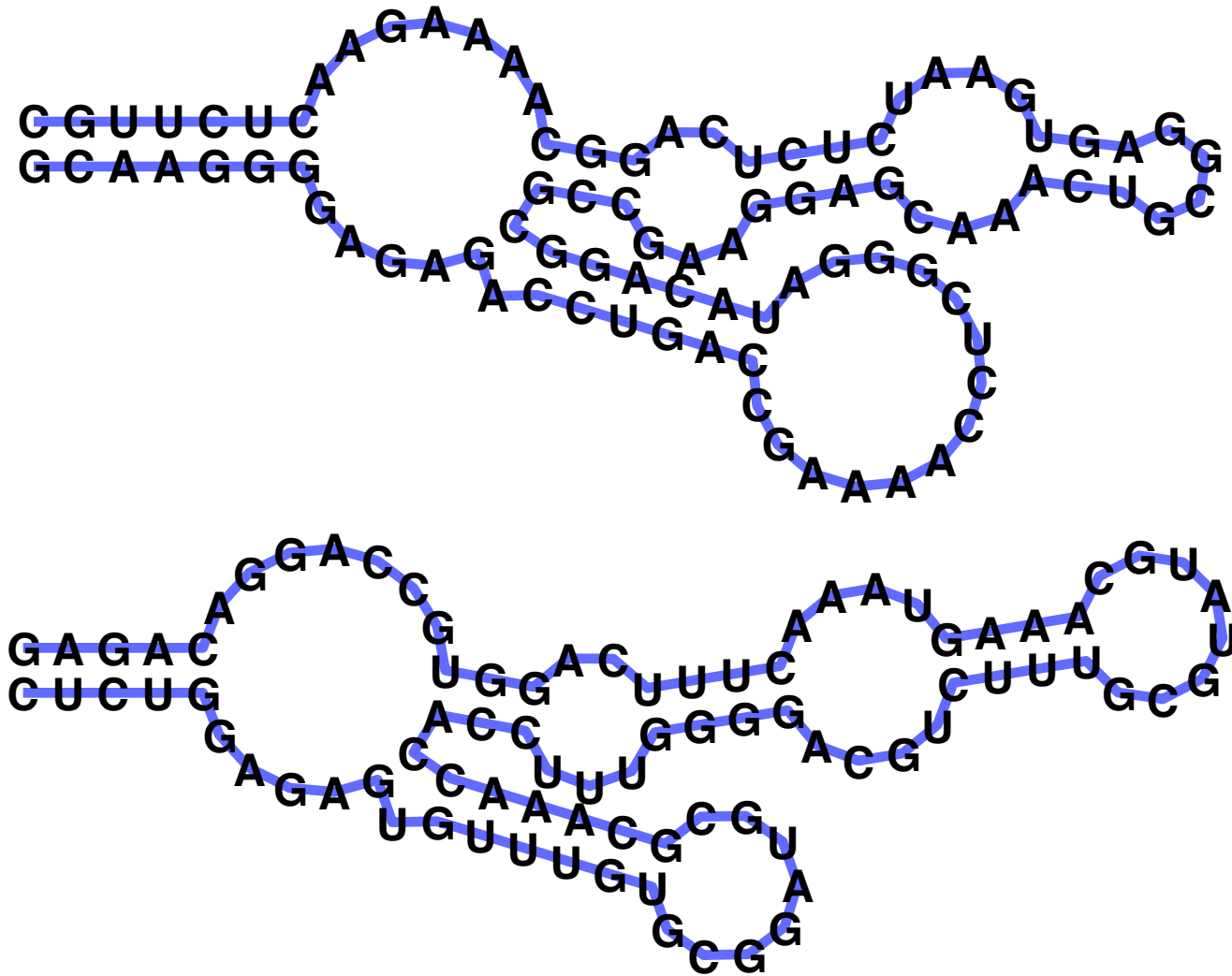
How do you recognize an interesting one?

A Clue: Conserved secondary structure

RNA Secondary Structure: can be fixed while sequence evolves



Why is RNA hard to deal with?



A: *Structure* often more important than *sequence*₃₅

Structure Prediction

RNA Structure

Primary Structure: Sequence

Secondary Structure: Pairing

Tertiary Structure: 3D shape

RNA Pairing

Watson-Crick Pairing

C - G

~ 3 kcal/mole

A - U

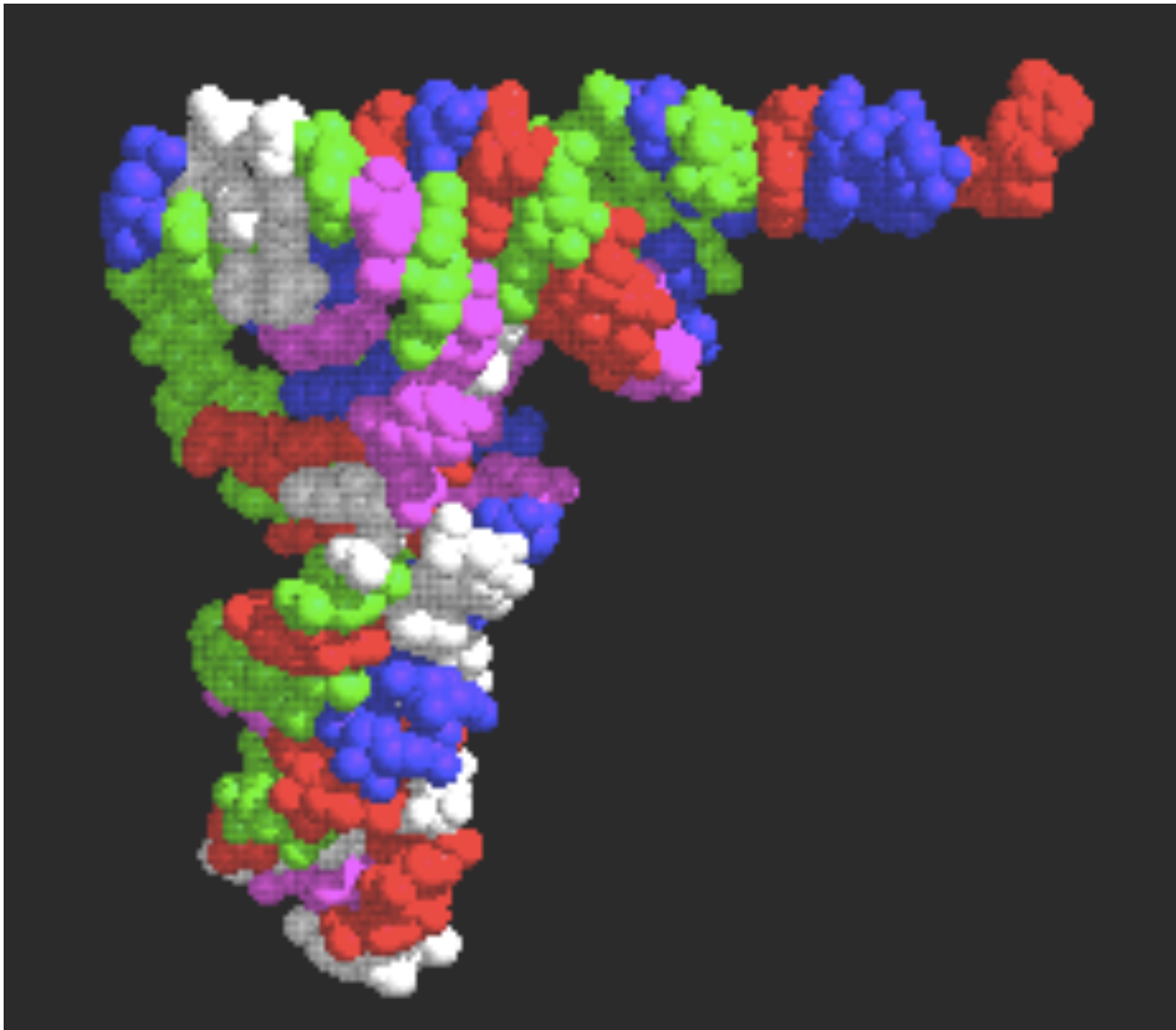
~ 2 kcal/mole

“Wobble Pair” G - U

~ 1 kcal/mole

Non-canonical Pairs (esp. if modified)

tRNA 3d Structure



tRNA - Alt. Representations

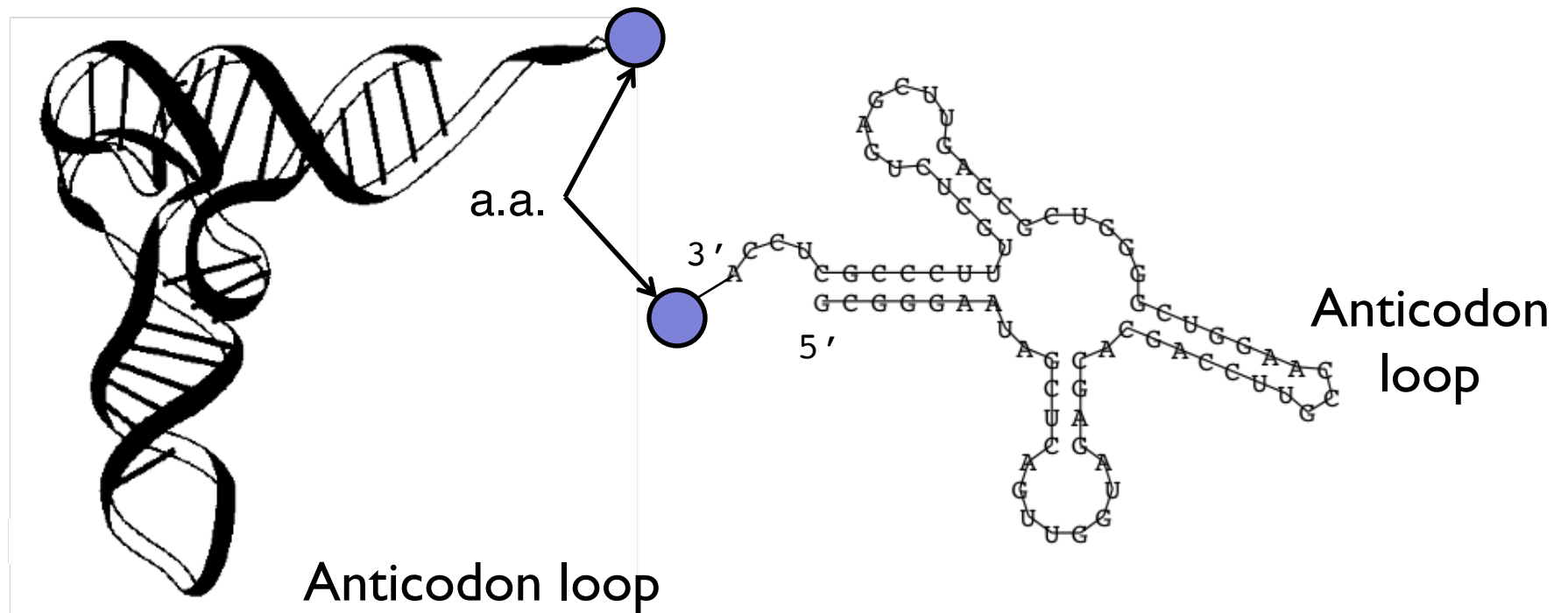
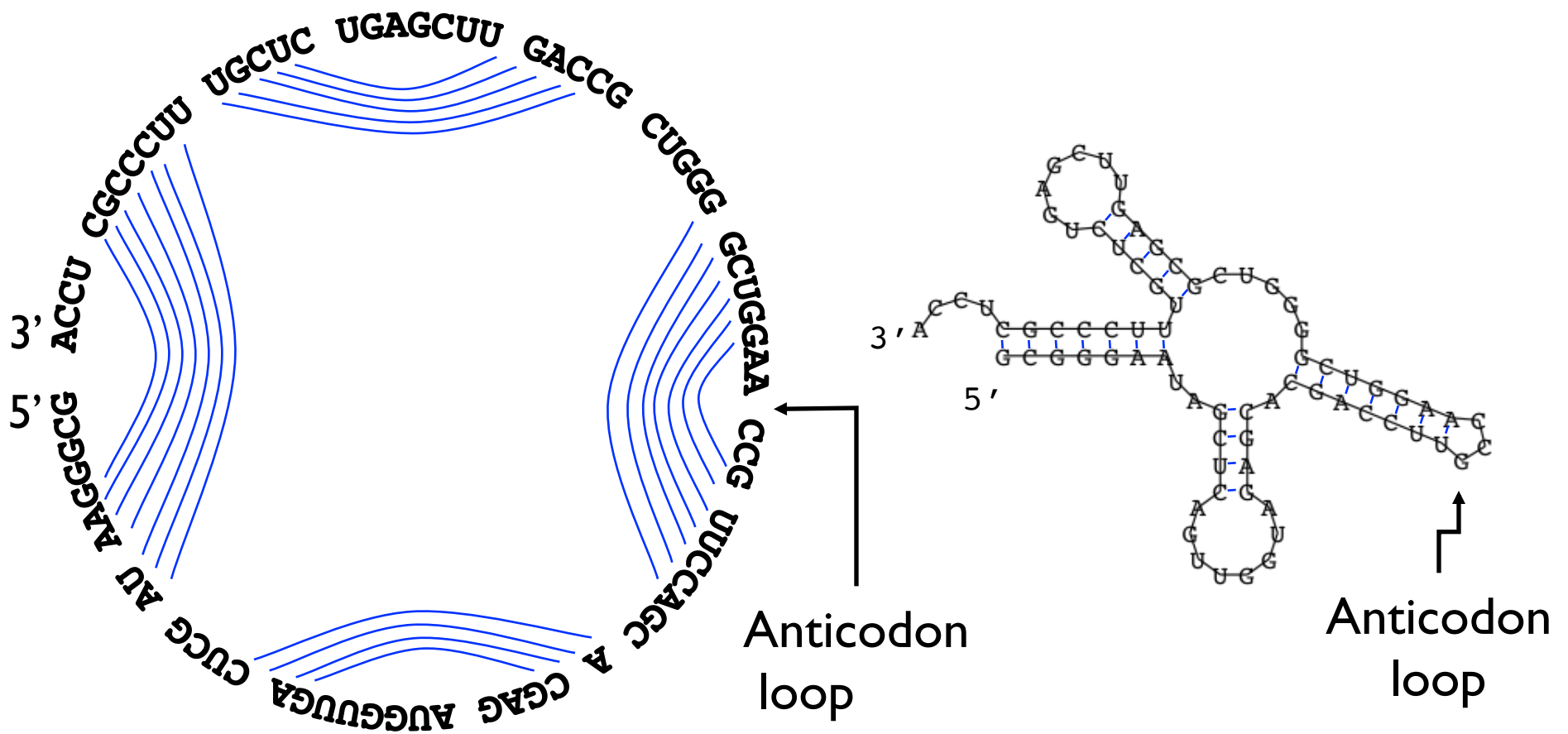


Figure 1: a) The spatial structure of the phenylalanine tRNA from yeast

b) The secondary structure extracts the most important information about the structure, namely the pattern of base pairings.

tRNA - Alt. Representations



Definitions

Sequence $5' r_1 r_2 r_3 \dots r_n 3'$ in $\{A, C, G, T/U\}$

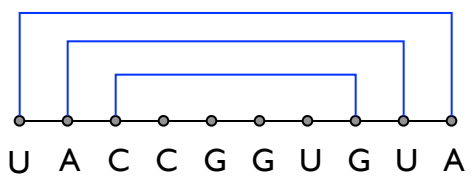
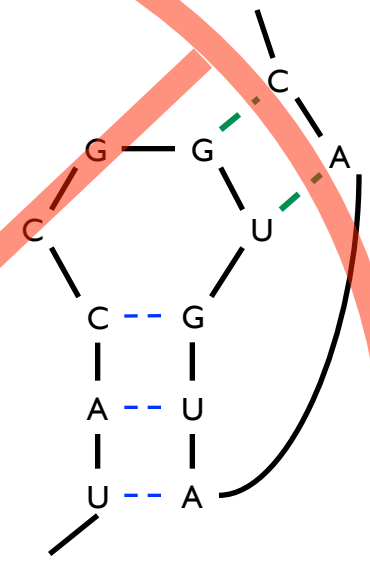
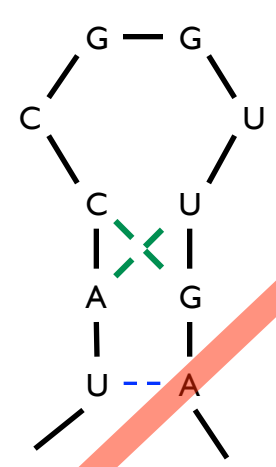
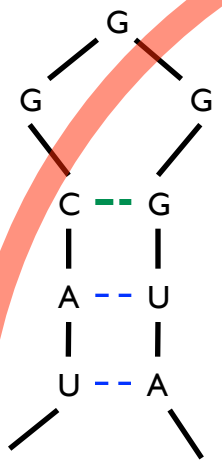
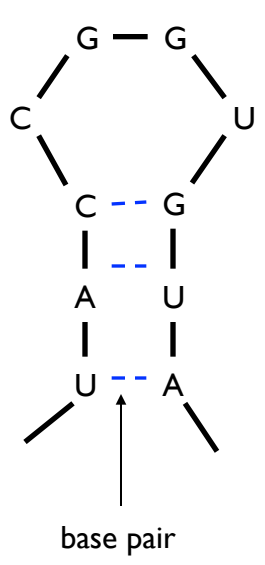
A **Secondary Structure** is a set of pairs $i \bullet j$ s.t.

$i < j-4$, and $\}$ no sharp turns

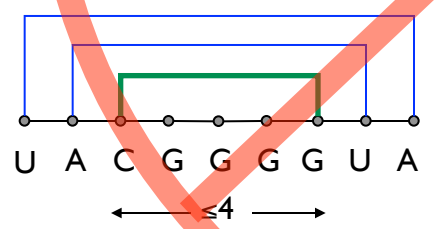
if $i \bullet j$ & $i' \bullet j'$ are two different pairs with $i \leq i'$, then

$j < i'$, or
 $i < i' < j' < j$ $\}$ 2nd pair follows 1st, or is nested within it;
no “pseudoknots.”

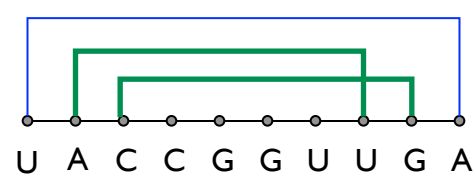
RNA Secondary Structure: Examples



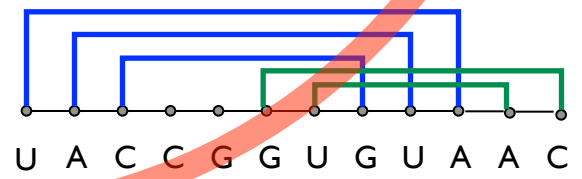
ok



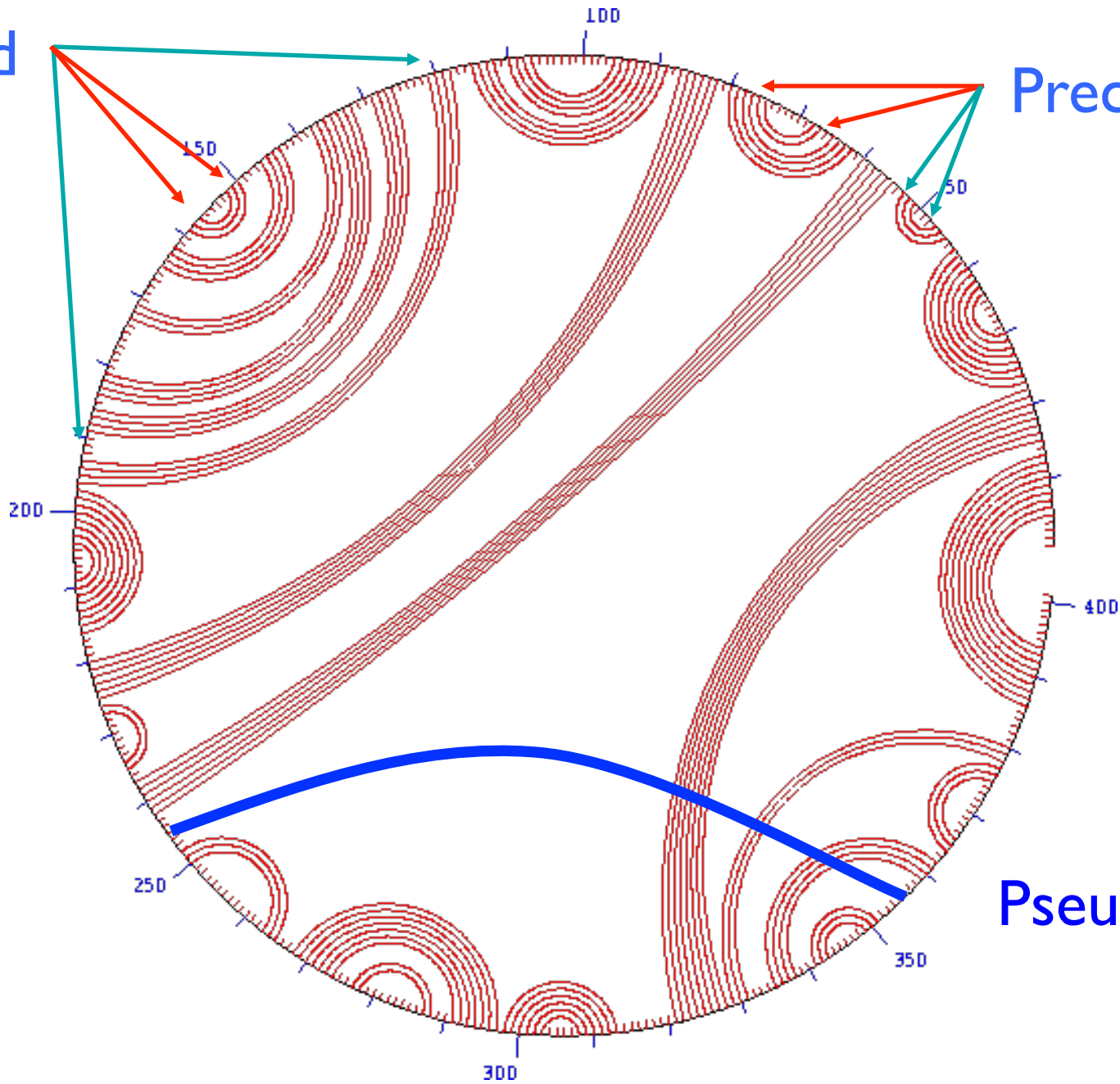
sharp turn



crossing



Nested



Precedes

Pseudoknot

Approaches to Structure Prediction

Maximum Pairing

- + works on single sequences
- + simple
- too inaccurate

Minimum Energy

- + works on single sequences
- ignores pseudoknots
- only finds “optimal” fold

Partition Function

- + finds all folds
- ignores pseudoknots

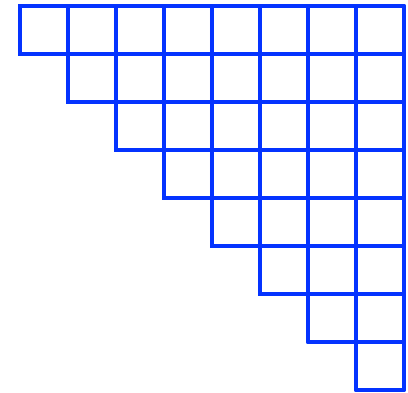
Nussinov: Max Pairing

$B(i,j)$ = # pairs in optimal pairing of $r_i \dots r_j$

$B(i,j) = 0$ for all i, j with $i \geq j-4$; otherwise

$B(i,j) = \max$ of:

$$\left\{ \begin{array}{l} B(i,j-1) \\ \max \{ B(i,k-1) + 1 + B(k+1,j-1) \mid \\ \quad i \leq k < j-4 \text{ and } r_k - r_j \text{ may pair} \} \end{array} \right.$$

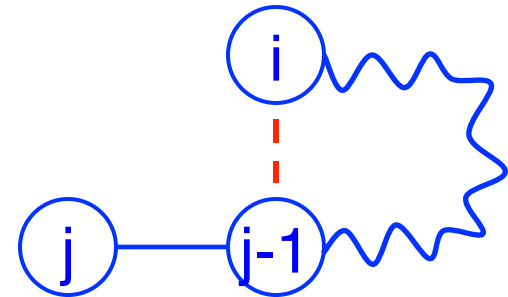


“Optimal pairing of $r_i \dots r_j$ ”

Two possibilities

j Unpaired:

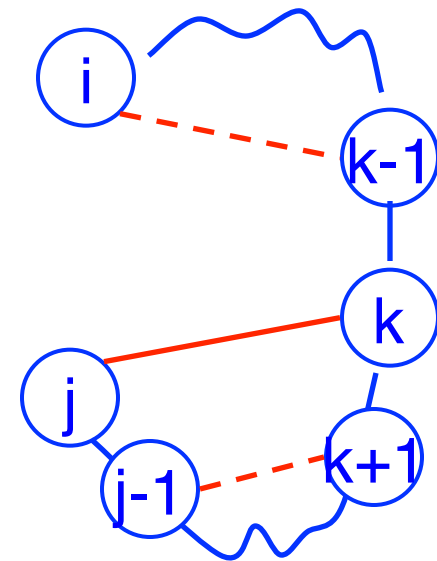
Find best pairing of $r_i \dots r_{j-1}$



j Paired (with some k):

Find best $r_i \dots r_{k-1}$ +

best $r_{k+1} \dots r_{j-1}$ **plus 1**



Why is it slow?

Why do pseudoknots matter?

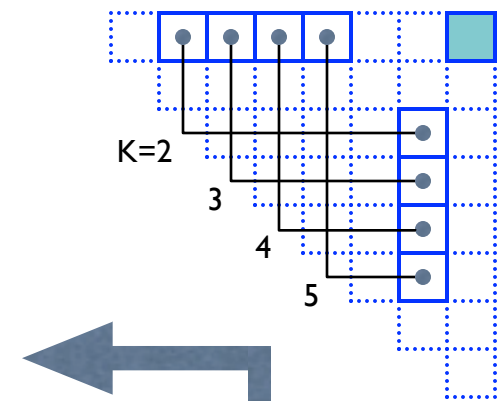
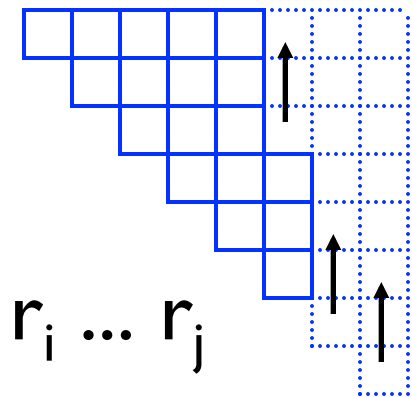
Nussinov: A Computation Order

$B(i,j) = \#$ pairs in optimal pairing of $r_i \dots r_j$

$B(i,j) = 0$ for all i, j with $i \geq j-4$; otherwise

$B(i,j) = \max$ of:

$$\left\{ \begin{array}{l} B(i,j-1) \\ \max \{ B(i,k-1) + 1 + B(k+1,j-1) \mid \\ \quad i \leq k < j-4 \text{ and } r_k - r_j \text{ may pair} \} \end{array} \right.$$



Time: $O(n^3)$

Which Pairs?

Usual dynamic programming “trace-back” tells you *which* base pairs are in the optimal solution, not just how many

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

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

Case 1:
 $2 \geq 18-4?$ no.

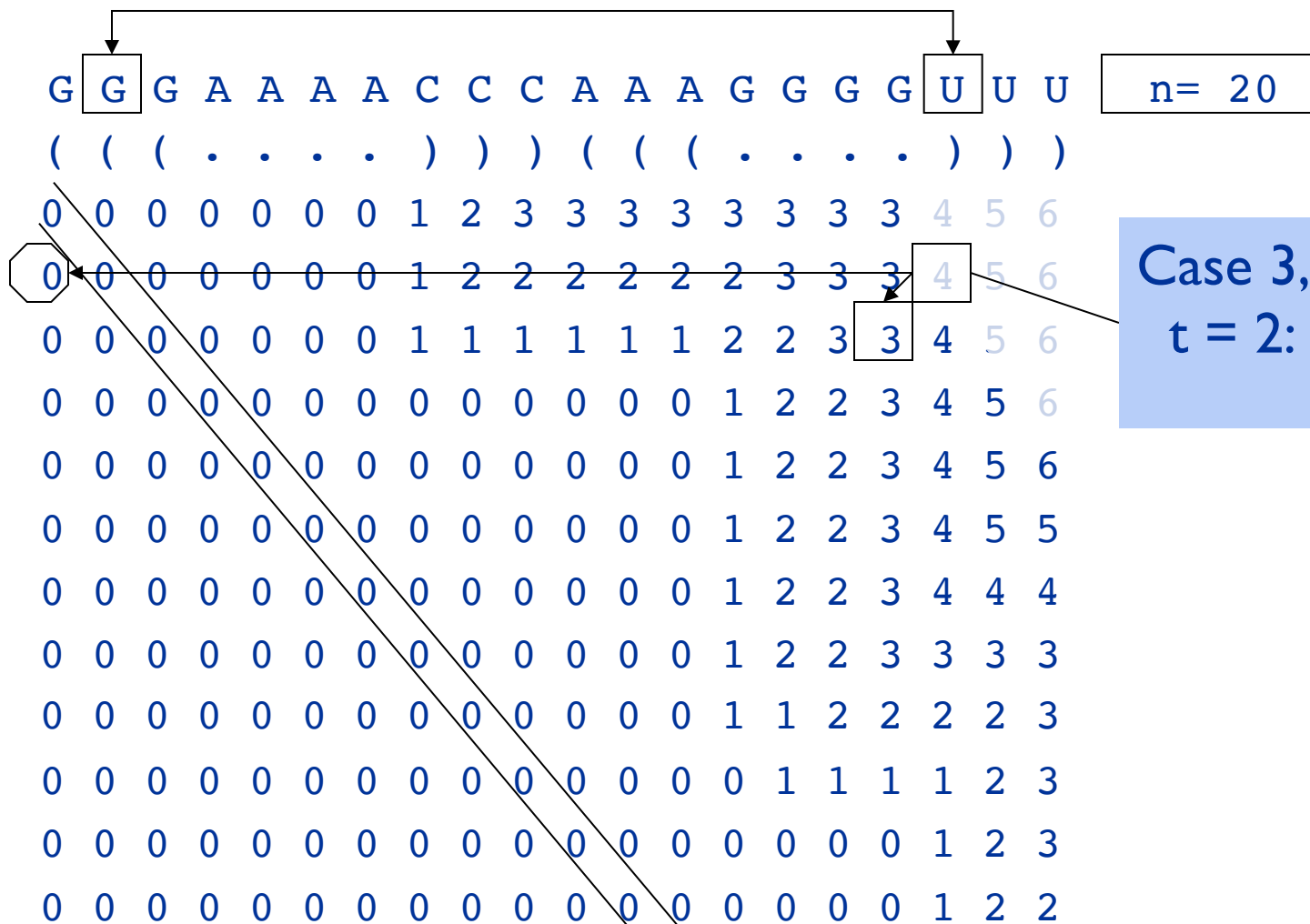
Case 2:
 B_{18} unpaired?
 Always a possibility;
 then $OPT[2,18] \geq 3$

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

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

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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



Case 3, $2 \leq t < 18-4$:
 $t = 2$: no pair

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

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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



Case 3, $2 \leq t < 18-4$:
 $t = 3$: no pair

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

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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



Case 3, $2 \leq t < 18-4$:
 $t = 4$: yes pair
 $OPT[2,18] \geq 1+0+3$

GGAAAACCCAAAGGGGU
 $\dots((\dots(((\dots))))))$

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

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Computing one cell: 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	3	4	5	6
0	0	0	0	0	0	0	1	2	2	2	2	2	2	3	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	1	2	2	3	4	5	6
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	1	2	2	3	4	5	5
0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	3	4	4	4
0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	3	3	3	3
0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	2	2	2	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	2	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2

Case 3, $2 \leq t < 18-4$:
 $t = 5$: yes pair
 $OPT[2,18] \geq 1+0+3$

GGAAACCCAAAGGGGU
 $\dots(\dots(((\dots))))$

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

0
 0

Computing one cell: 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	0	1	2	3	3	3	3	3	3	3	3	4	5	6
0	0	0	0	0	0	0	0	1	2	2	2	2	2	2	3	3	3	4	5	6
0	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	1	2	2	3	4	5	6
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	1	2	2	3	4	5	5
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	3	4	4	4
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	3	3	3	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	2	2	2	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	2	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2

Case 3, $2 \leq t < 18-4$:
 $t = 6$: yes pair
 $OPT[2,18] \geq 1+0+3$

GGAA**A**ACCCAAAGGGGU
(.((((.....))))

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

0 0

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



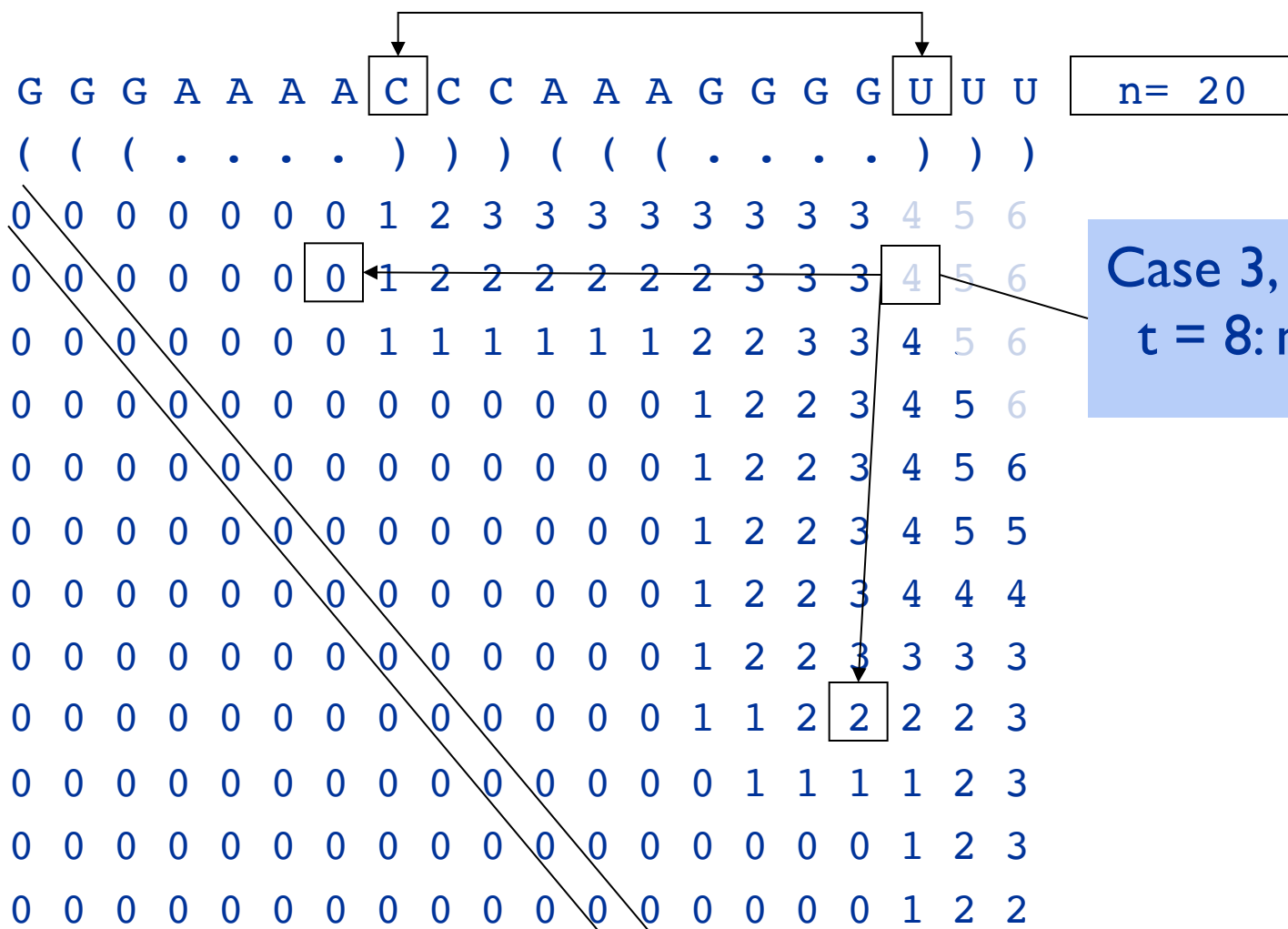
Case 3, $2 \leq t < 18-4$:
 $t = 7$: yes pair
 $OPT[2,18] \geq 1+0+3$

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

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



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



Case 3, $2 \leq t < 18-4$:
 $t = 8$: no pair

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

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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

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

Case 3, $2 \leq t < 18-4$:
 $t = 11$: yes pair
 $OPT[2,18] \geq 1+2+0$

GGAAAACCC**AA**AGGGGU
 ((.....))(.....)

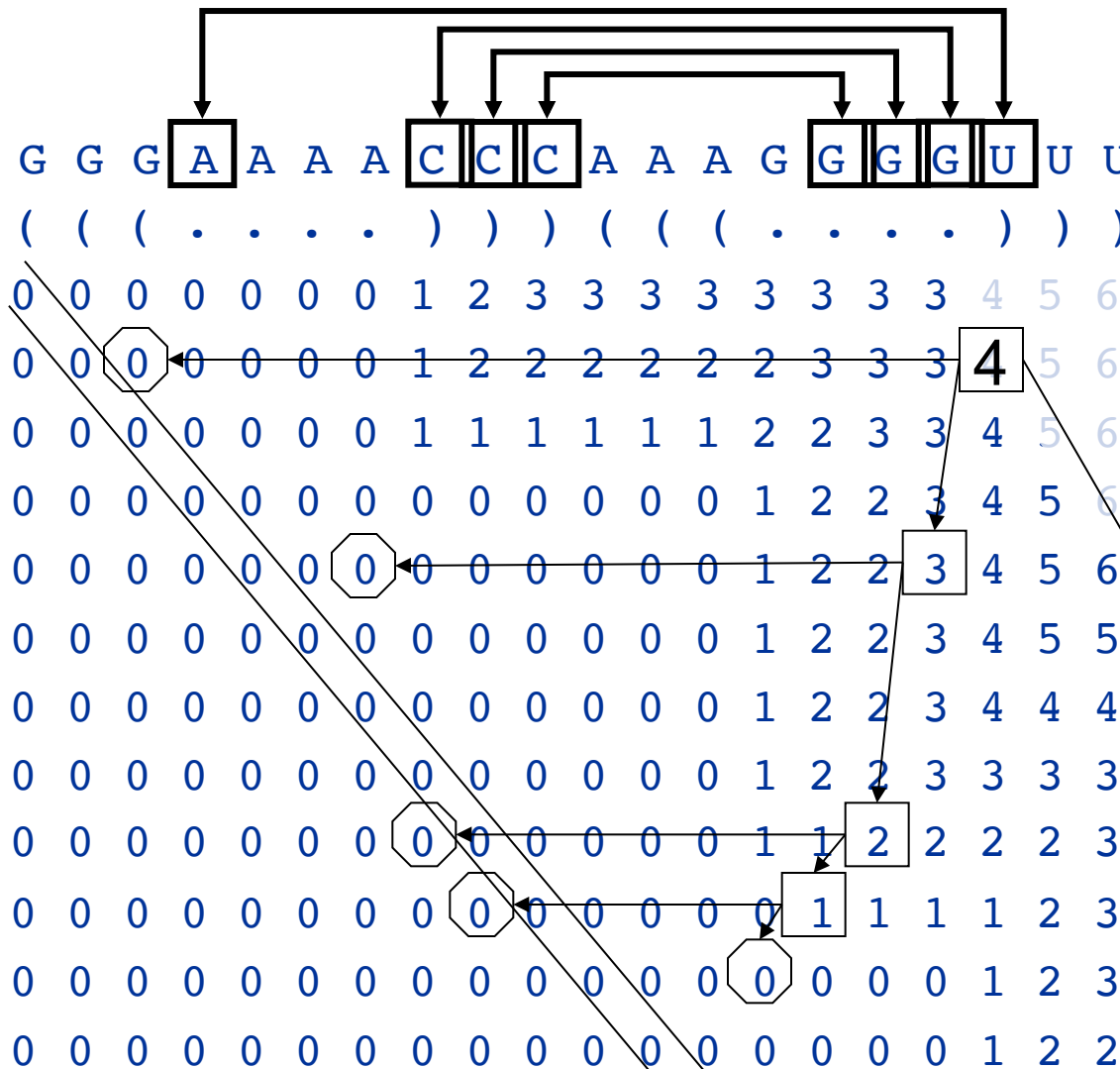
(not shown:
 $t=9,10,12,13$)

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

0 0

Computing one cell: $OPT[2,18] = 4$

$n = 20$



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

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

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

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

Approaches to Structure Prediction

Maximum Pairing

- + works on single sequences
- + simple
- too inaccurate

Minimum Energy

- + works on single sequences
- ignores pseudoknots
- only finds “optimal” fold

Partition Function

- + finds all folds
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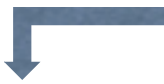
Pair-based Energy Minimization


$E(i,j)$ = energy of *pairs* in optimal pairing of $r_i \dots r_j$

$E(i,j) = \infty$ for all i, j with $i \geq j-4$; otherwise

$E(i,j)$ = min of:

$$\begin{cases} E(i,j-1) \\ \min \{ E(i,k-1) + e(r_k, r_j) + E(k+1,j-1) \mid i \leq k < j-4 \} \end{cases}$$

 energy of $k-j$ pair

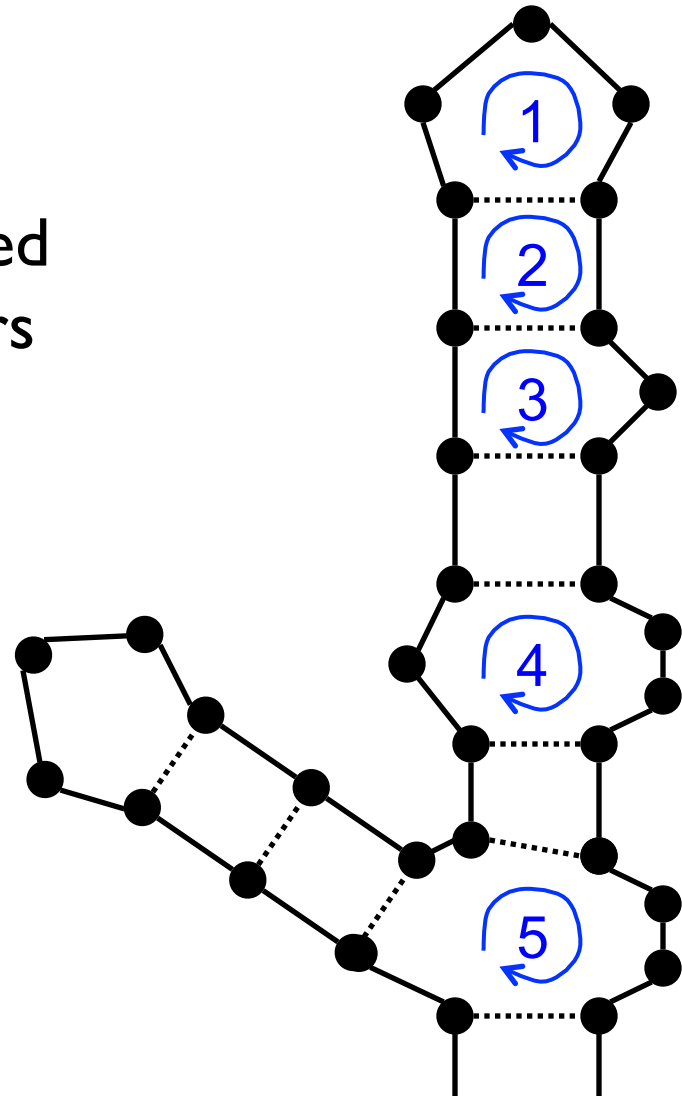
Time: $O(n^3)$ 

Loop-based Energy Minimization

Detailed experiments show it's more accurate to model based on *loops*, rather than just pairs

Loop types

1. Hairpin loop
2. Stack
3. Bulge
4. Interior loop
5. Multiloop



Zuker: Loop-based Energy, I

$W(i,j)$ = energy of optimal pairing of $r_i \dots r_j$

$V(i,j)$ = as above, but forcing pair $i \bullet j$

$W(i,j) = V(i,j) = \infty$ for all i, j with $i \geq j-4$

$W(i,j) = \min(W(i,j-1),$
 $\min \{ W(i,k-1) + V(k,j) \mid i \leq k < j-4 \}$
)

Zuker: Loop-based Energy, II

hairpin stack

bulge/
interior multi-
loop

$$V(i,j) = \min(\text{eh}(i,j), \text{es}(i,j)+V(i+1,j-1), \text{VBI}(i,j), \text{VM}(i,j))$$

$$\text{VM}(i,j) = \min \{ W(i,k)+W(k+1,j) \mid i < k < j \}$$

$$\text{VBI}(i,j) = \min \{ \text{ebi}(i,j,i',j') + V(i', j') \mid$$

$$i < i' < j' < j \ \& \ i'-i+j-j' > 2 \}$$

bulge/
interior

Time: $O(n^4)$

$O(n^3)$ possible if $\text{ebi}(\cdot)$ is “nice”

Energy Parameters

Q. Where do they come from?

A1. Experiments with carefully selected synthetic RNAs

A2. Learned algorithmically from trusted alignments/structures [Andronescu et al., 2007]

Single Seq Prediction Accuracy

Mfold, Vienna,... [Nussinov, Zuker, Hofacker, McCaskill]

Latest estimates suggest ~50-75% of base pairs predicted correctly in sequences of up to ~300nt

Definitely useful, but obviously imperfect

Approaches to Structure Prediction

Maximum Pairing

- + works on single sequences
- + simple
- too inaccurate

Minimum Energy

- + works on single sequences
- ignores pseudoknots
- only finds “optimal” fold

Partition Function

- + finds all folds
- ignores pseudoknots

Approaches, II

Comparative sequence analysis

- + handles all pairings (potentially incl. pseudoknots)
- requires several (many?) aligned, appropriately diverged sequences

Stochastic Context-free Grammars

Roughly combines min energy & comparative, but no pseudoknots

Physical experiments (x-ray crystallography, NMR)

Summary

RNA has important roles beyond mRNA

Many unexpected recent discoveries

Structure is critical to function

True of proteins, too, but they're easier to find from sequence alone due, e.g., to codon structure, which RNAs lack

RNA secondary structure can be predicted (to useful accuracy) by dynamic programming

Next: RNA “motifs” (seq + 2-ary struct) well-captured by “covariance models”