CSEP 590A
Summer 2006
Lecture 8

RNA Secondary Structure Prediction

Outline

Biological roles for RNA

What is "secondary structure?

How is it represented?

Why is it important?

Examples

Approaches

RNA Structure

Primary Structure: Sequence

Secondary Structure: Pairing

Tertiary Structure: 3D shape

RNA Pairing

Watson-Crick Pairing

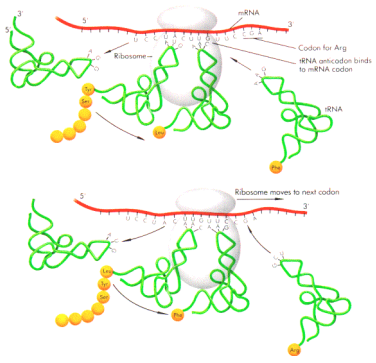
C - G ~ 3 kcal/mole

A - U ~ 2 kcal/mole

"Wobble Pair" G - U ~1 kcal/mole

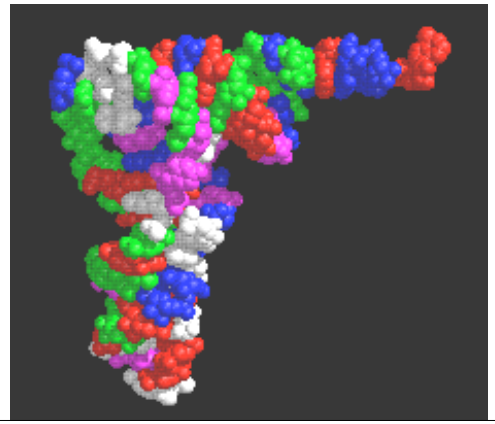
Non-canonical Pairs (esp. if modified)

Ribosomes

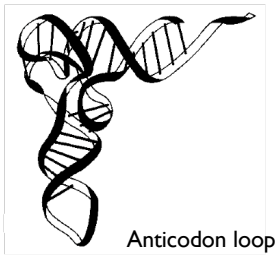


Watson, Gilman, Witkowski, & Zoller, 1992

tRNA 3d Structure



tRNA - Alt. Representations



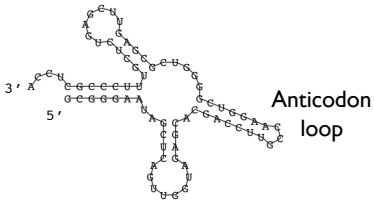
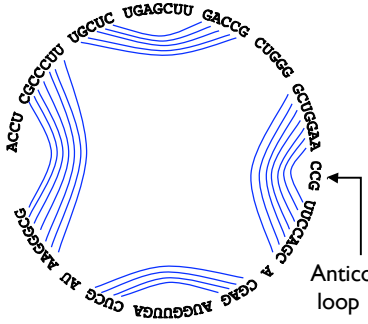
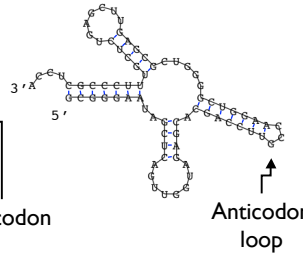


Figure 1: a) The spatial structure of the phenylalanine tRNA form yeast

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

tRNA - Alt. Representations





"Classical" RNAs

tRNA - transfer RNA (~61 kinds, ~ 75 nt)

rRNA - ribosomal RNA (~4 kinds, 120-5k nt)

snRNA - small nuclear RNA (splicing: U1, etc, 60-300nt)

RNaseP - tRNA processing (~300 nt)

RNase MRP - rRNA processing; mito. rep. (~225 nt)

SRP - signal recognition particle; membrane targeting (~100-300 nt)

SECIS - selenocysteine insertion element (~65nt)

6S - ? (~175 nt)

Semi-classical RNAs
(discovery in mid 90's)

tmRNA - resetting stalled ribosomes

Telomerase - (200-400nt)

snoRNA - small nucleolar RNA (many varieties; 80-200nt)

Recent discoveries

microRNAs

riboswitches

many ribozymes

regulatory elements

…

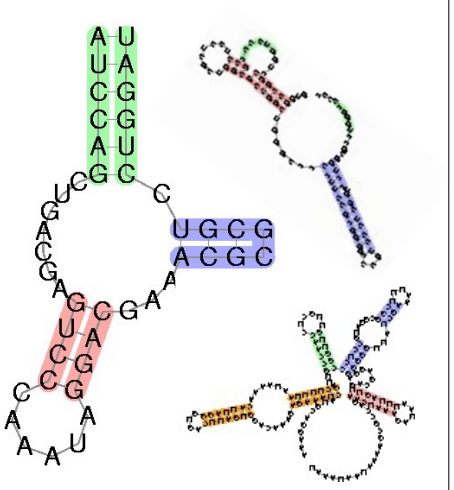
Hundreds of families

Rfam release 1, 1/2003: 25 families, 55k instances
Rfam release 7, 3/2005: 503 families, 300k instances

Why?

RNA's fold, and function

Nature uses what works

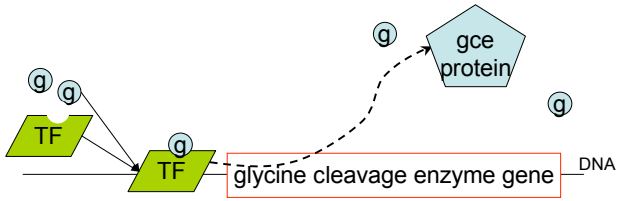


Noncoding RNAs

Example: Glycine Regulation

How is glycine level regulated?

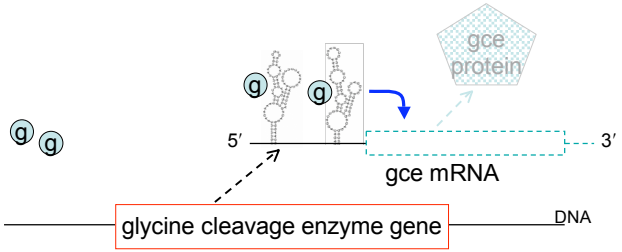
Plausible answer:



transcription factors (proteins) bind to DNA to turn nearby genes on or off

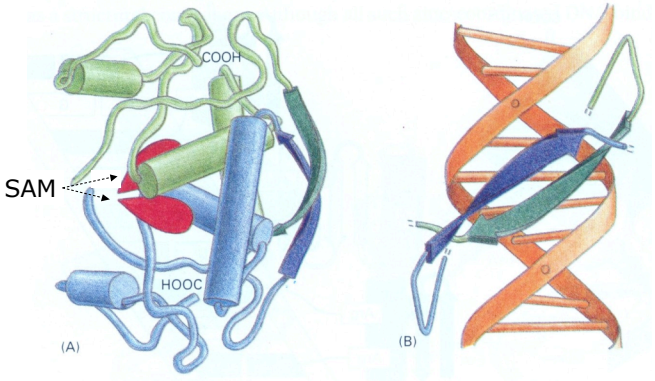
The Glycine Riboswitch

Actual answer (in many bacteria):



Mandal et al. Science 2004

Gene Regulation: The Met Repressor

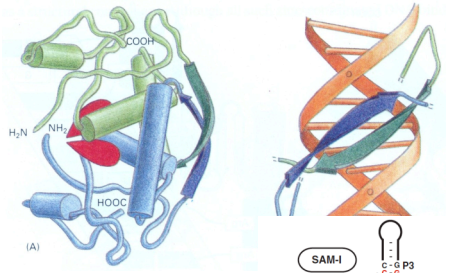


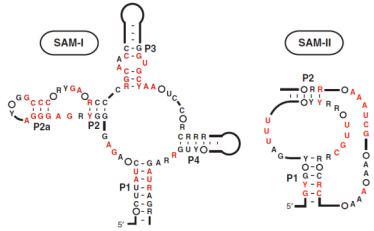
Protein

Alberts, et al, 3e.

DNA

Two SAM Ribo-switches

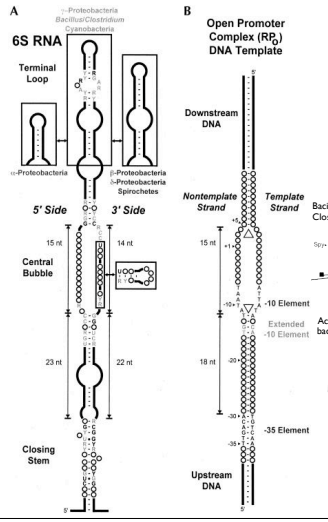


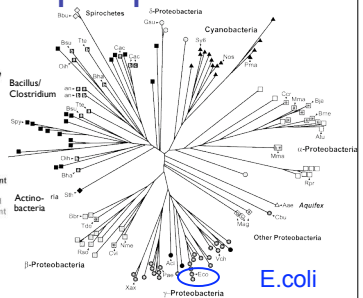


Alberts, et al, 3e.

Corbino et al., Genome Biol. 2005

6S mimics an open promoter

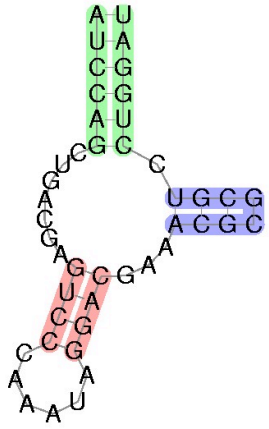




Barrick et al. *RNA* 2005
Trotochaud et al. *NSMB* 2005
Willkomm et al. NAR 2005

The Hammerhead Ribozyme

Involved in "rolling circle replication" of viruses.

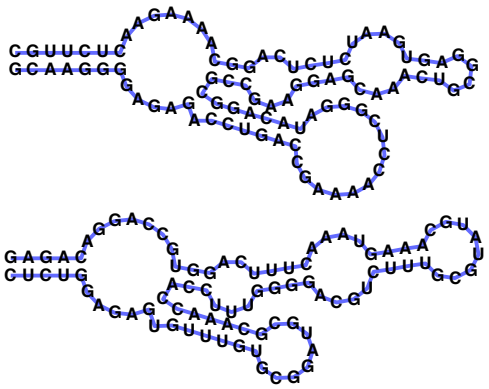


Wanted

Good structure prediction tools
Good motif descriptions/models
Good, fast search tools
("RNA BLAST", etc.)
Good, fast motif discovery tools
("RNA MEME", etc.)

Importance of structure makes last 3 hard

Why is RNA hard to deal with?



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

Task 1:
Structure Prediction

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)

Definitions

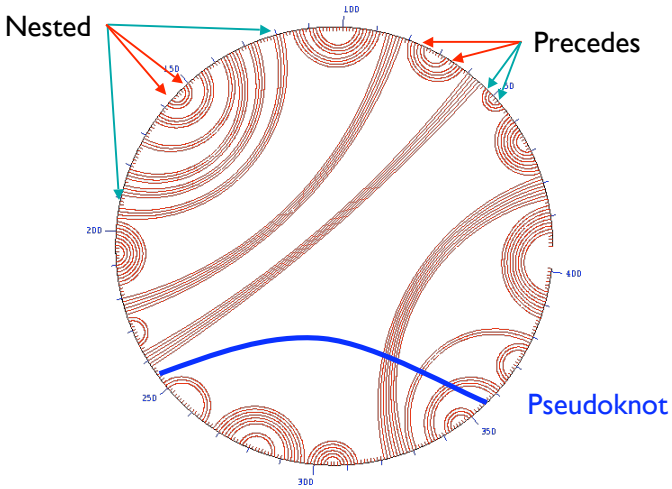
Sequence $^{5'}$ r_1 r_2 r_3 ... r_n $^{3'}$ in {A, C, G, T}

A Secondary Structure is a set of pairs i•j s.t.

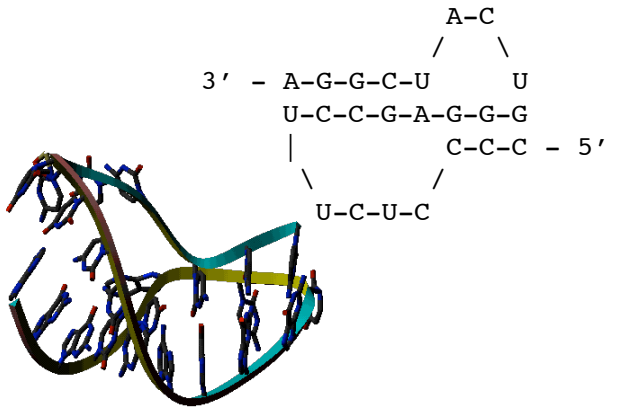
i < j-4, and } no sharp turns

if i•j & i'•j' are two different pairs with i ≤ i', then

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



A 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

Approaches, II

Comparative sequence analysis
- \+ handles all pairings (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 crystalography, NMR)

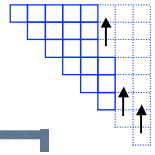
Nussinov: Max Pairing

B(i,j) = # pairs in optimal pairing of r_i ... r_j

B(i,j) = 0 for all i, j with i ≥ j-4; otherwise

B(i,j) = max of:

- B(i,j-1)
- max { B(i,k-1)+1+B(k+1,j-1) | i ≤ k < j-4 and r_k-r_j may pair}

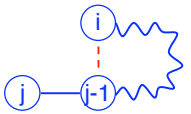


Time: $O(n^3)$

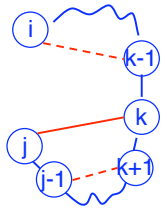
"Optimal pairing of r_i ... r_j"

Two possibilities

J Unpaired:
Find best pairing of r_i ... r_{j-1}



J Paired:
Find best r_i ... r_{k-1} +
best r_{k+1} ... r_{j-1} plus 1



Why is it slow?
Why do pseudoknots matter?

Pair-based Energy Minimization

E(i,j) = energy of pairs in optimal pairing of r_i ... r_j

E(i,j) = ∞ for all i, j with i ≥ j-4; otherwise

E(i,j) = min of:

- E(i,j-1)
- min { E(i,k-1) + e(r_k, r_j) + E(k+1,j-1) | i ≤ k < j-4 }

energy of j-k pair

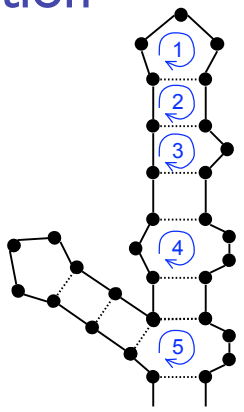
Time: $O(n^3)$

Loop-based Energy Minimization

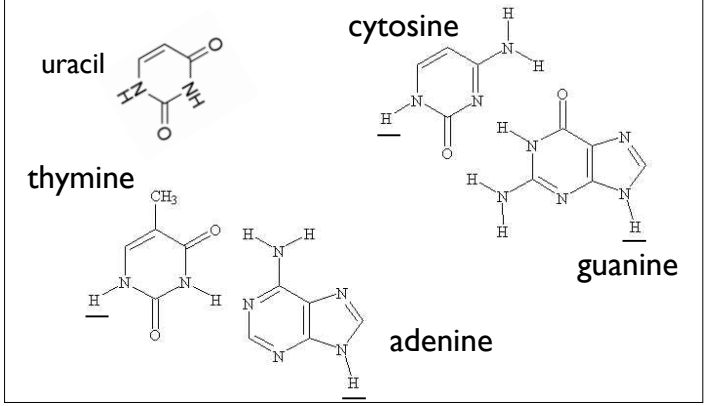
Detailed experiments show it's more accurate to model based on loops, rather than just pairs

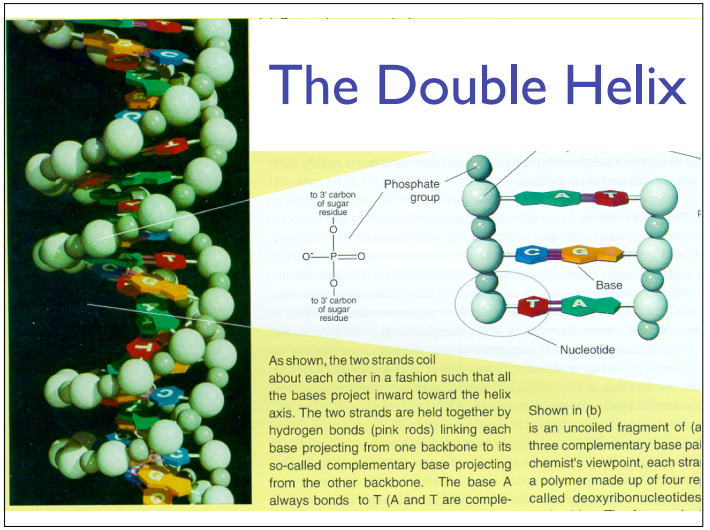
Loop types

- Hairpin loop
- Stack
- Bulge
- Interior loop
- Multiloop

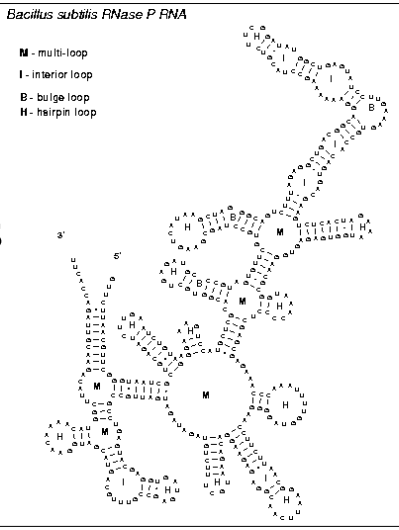


Base Pairs and Stacking





Loop Examples



Zuker: Loop-based Energy, I

W(i,j) = energy of optimal pairing of r_i ... r_j

V(i,j) = as above, but forcing pair i•j

W(i,j) = V(i,j) = ∞ for all i, j with i ≥ j-4

W(i,j) = min(W(i,j-1),
min { W(i,k-1)+V(k,j) | i ≤ k < j-4 }
)

Zuker: Loop-based Energy, II

hairpin stack bulge/ interior multi- loop

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

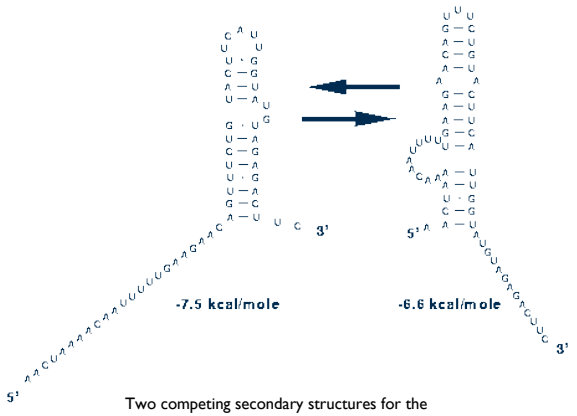
$VM(i,j) = \min \{ W(i,k)+W(k+1,j) \mid i < k < j \}$

$VBI(i,j) = \min \{ ebi(i,j,i',j') + V(i', j') \mid i < i' < j' < j \ \& \ i'-i+j-j' > 2 \}$

bulge/ interior

Time: $O(n^4)$

$O(n^3)$ possible if ebi(.) is "nice"



Two competing secondary structures for the Leptomonas collosoma spliced leader mRNA.

Suboptimal Energy

There are always alternate folds with near-optimal energies. Thermodynamics: populations of identical molecules will exist in different folds; individual molecules even flicker among different folds

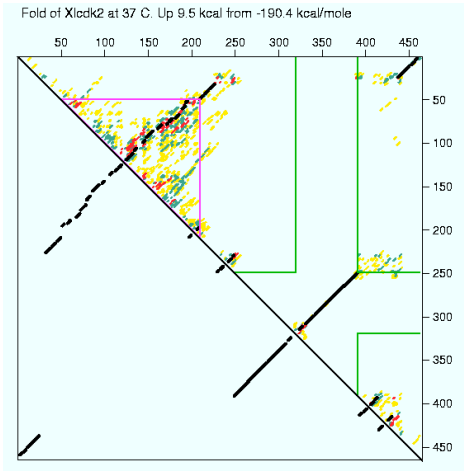
Mod to Zuker's algorithm finds subopt folds

McCaskill: more elaborate dyn. prog. algorithm calculates the "partition function," which defines the probability distribution over all these states.

Example of suboptimal folding

Black dots: pairs in opt fold

Colored dots: pairs in folds 2-5% worse than optimal fold



Accuracy

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

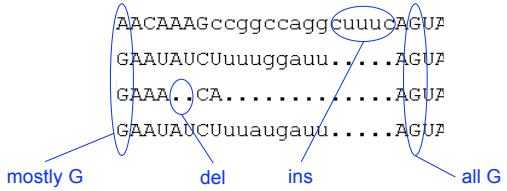
Definitely useful, but obviously imperfect

Task 2: Motif Description

How to model an RNA "Motif"?

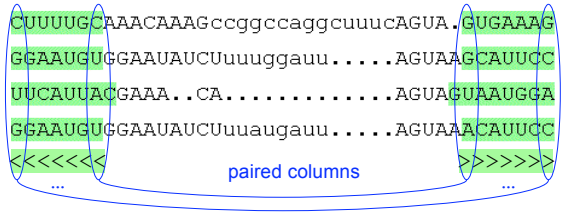
Conceptually, start with a profile HMM:

- from a multiple alignment, estimate nucleotide/ insert/delete preferences for each position
- given a new seq, estimate likelihood that it could be generated by the model, & align it to the model



How to model an RNA "Motif"?

Add "column pairs" and pair emission probabilities for base-paired regions



RNA Motif Models

"Covariance Models" (Eddy & Durbin 1994)
- aka profile stochastic context-free grammars
- aka hidden Markov models on steroids

Model position-specific nucleotide preferences *and* base-pair preferences

Pro: accurate

Con: model building hard, search sloooow

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, due, e.g., to codon structure, which RNAs lack

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

RNA "motifs" (seq + 2-ary struct) well-captured by "covariance models"