CSE 527
Lecture 17, 11/24/04

RNA Secondary Structure Prediction

Outline

- What is it
- How is it Represented
- Why is it important
- Examples
- Approaches

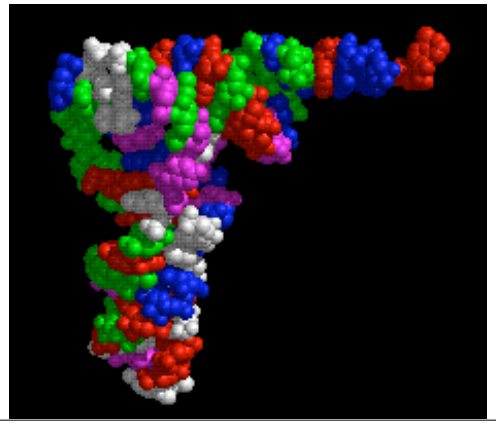
RNA Structure

- 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)

A tRNA 3d Structure



tRNA - Alt. Representations

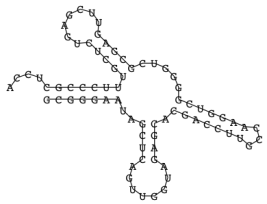


Figure 1: a) The spatial structure of the phenylalanine tRNA form yeast

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

A "Mountain" diagram

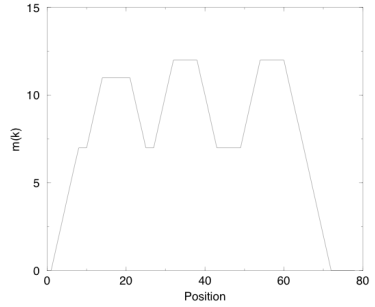
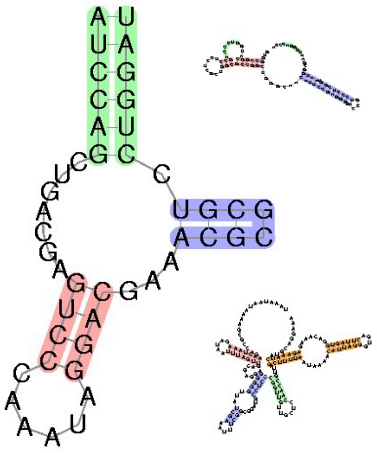


Figure 3: Mountain representation of the tRNA secondary structure shown in Figure 1. The three plateaus correspond to the three hairpin loops of the clover leave structure.

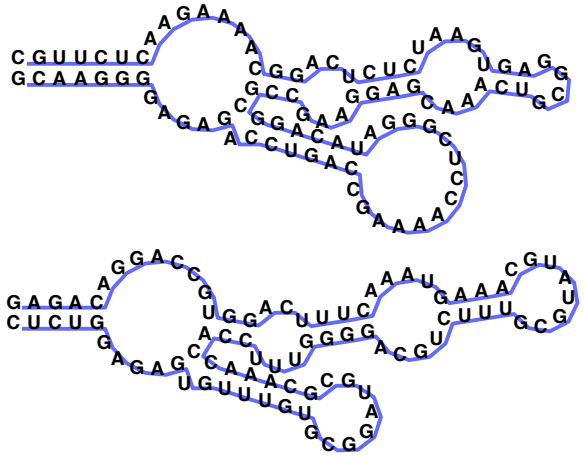
Why?

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



Importance

- Ribozymes (RNA Enzymes)
- Retroviruses
- Effects on transcription, translation, splicing...
- Functional RNAs: rRNA, tRNA, snRNA, snoRNA, micro RNA, RNAi, riboswitches, regulatory elements in 3' & 5' UTRs, ...



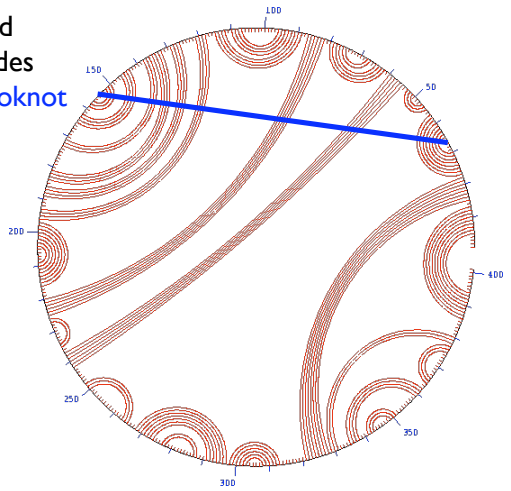
Definitions

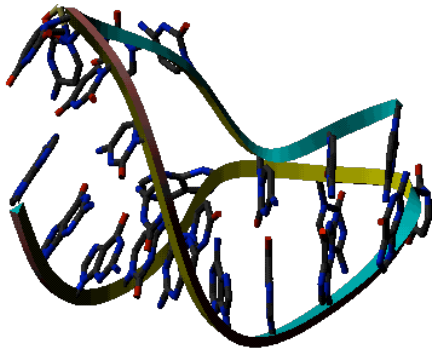
- Sequence $^{5'}\ r_1\ r_2\ r_3 \ldots r_n\ ^{3'}$ in {A, C, G, T}
- A Secondary Structure is a set of pairs i•j s.t.

1. $i < j-4$
2. if i•j & i'•j' are two pairs with $i \le i'$, then
   - A. $i = i'$ & $j = j'$, or
   - B. $j < i'$, or
   - C. $i < i' < j' < j$

} First pair precedes 2nd, or is nested within it. No "pseudoknots."

Nested
Precedes
Pseudoknot





The corresponding secondary structure is:

```
                A-C
3'- A-G-G-C-U/   U
    U-C-C-G-A-G-G-G
     U         C-C-C - 5'
      C--U--C/
```

A Pseudoknot

Approaches to Structure Prediction

- Maximum Pairing
  + 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
- 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 ri ... rj
- B(i,j) = 0 for all i, j with i ≥ j-4; otherwise
- B(i,j) = max of:

1. B(i+1,j)
2. B(i,j-1)
3. B(i+1,j-1) +(if ri pairs with rj then 1 else 0)
4. max { B(i,k)+B(k+1,j) | i < k < j }

Time: $O(n^3)$

Pair-based Energy Minimization

- E(i,j) = energy of pairs in optimal pairing of ri ... rj
- E(i,j) = ∞ for all i, j with i ≥ j-4; otherwise
- E(i,j) = min of:

  1. E(i+1,j)
  2. E(i,j-1)
  3. E(i+1,j-1) + e(ri,rj)
  4. min { E(i,k)+E(k+1,j) | i < k < j }

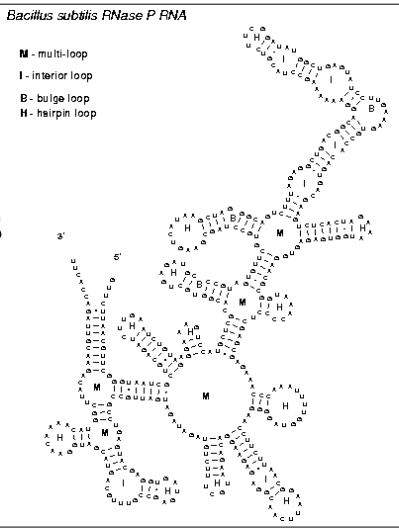
energy of one pair

Time: $O(n^3)$

Loop-based Energy Minimization

- Detailed experiments show that it's more accurate to model based on loops, rather than just pairs
- Loop types
  - Stack
  - Hairpin loop
  - Bulge
  - Interior loop

Loop Examples



Zuker: Loop-based Energy, I

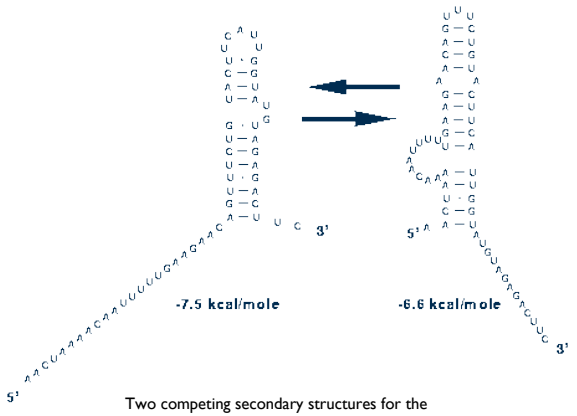
- W(i,j) = energy of optimal pairing of ri ... rj
- V(i,j) = as above, but forcing pair i•j
- W(i,j) = V(i,j) = ∞ for all i, j with i ≥ j-4
- W(i,j) = min(W(i+1,j), W(i,j-1), V(i+1,j-1), min { E(i,k)+E(k+1,j) | i < k < j })

Zuker: Loop-based Energy, II

- V(i,j) =min(eh(i,j), es(i,j)+V(i+1,j-1), VBI(i,j), VM(i,j))
  (hairpin, stack, bulge/interior, multi-loop)
- VM(i,j) = min { W(i,k)+W(k+1,j) | i < k < j })
- VBI(i,j) = min { ebi(i,j,i',j') + V(i', j') |
  i < i' < j' < j & i'-i+j-j' > 2 }

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 predicts that populations of identical molecules will exist in different folds; individual molecules even flicker among different folds
- Zuker's algorithm can be modified to find suboptimal folds
- McCaskill gives a more elaborate dynamic programming algorithm calculating 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