



RNA Secondary Structure

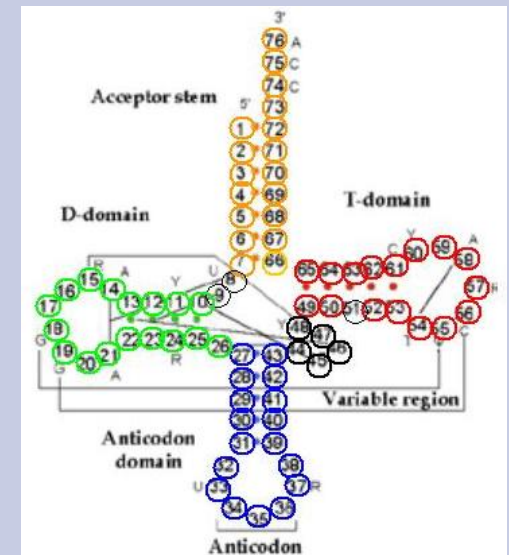
❖ RNA is a sequence of nucleotides

- Adenine, Guanine, Cytosine, Uracil

❖ Adenine pairs with Uracil, and Cytosine pairs with Guanine by a hydrogen bond

❖ The pairing makes the RNA sequence fold upon itself, resulting a secondary structure of RNA

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GCGGAUUUAGCUCAGUUGG
GAGAGCGCCAGACUGAAGA
UCUGGAGGUCCUGUGUUCG
AUCCACAGAAUUCGCACCA
```



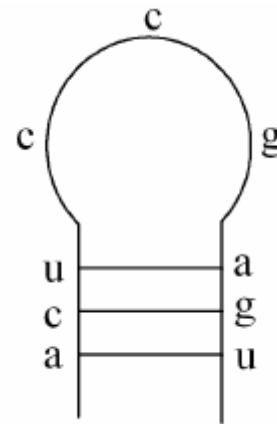
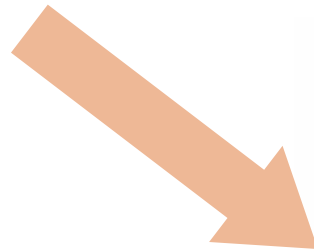


RNA Secondary Structure

A C U C C G A G U

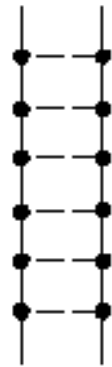
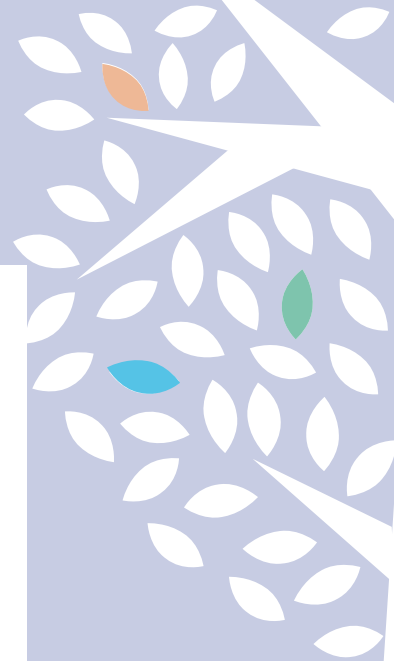


(((. . .)))

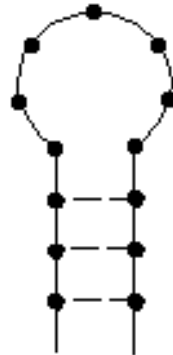




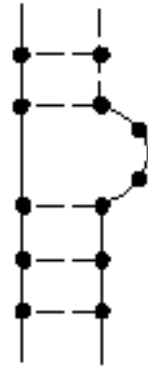
Various Substructures



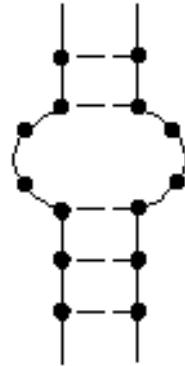
Stem



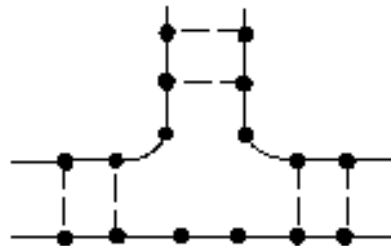
Hairpin loop



Bulge loop



Internal loop

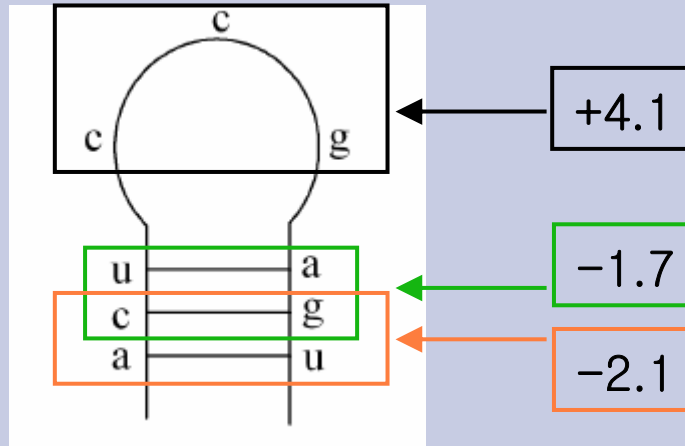


Branch loop



Secondary Structure and Energy

- ❖ Two pairs of nucleotides reduce the total free energy of RNA molecule by stacking on each other
- ❖ Loops increase the total free energy of RNA molecule



- ❖ Biologists want to predict the secondary structure with minimum free energy



HW3. RNA Secondary Structure Prediction

- ❖ **Write a Prolog program that**
 - given a sequence of RNA,
 - predicts the secondary structure with minimum free energy
- ❖ **The program should print**
 - The predicted structure
 - with ‘(’, ‘.’, and ‘)’
 - Free energy of the structure
- ❖ **Efficiency and correctness will be the measure**
- ❖ **Detailed energy data will be distributed**
- ❖ **Until 4/26 3:30pm**

