## RNA Secondary Structure

CSE 417
W.L. Ruzzo


The Double Helix


## 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...
1 1 1 1 1 1 1 1 11


## 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

"Central Dogma" "Central Chicken \& Egg"?


Was there once an "RNA World"?

### 6.5 RNA Secondary Structure

Algorithms

RNA Secondary Structure

Secondary structure. A set of pairs $S=\left\{\left(b_{i}, b_{j}\right)\right\}$ that satisfy:

- [Watson-Crick.]
- $S$ is a matching 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 $\left(b_{i}, b_{j}\right) \in S$, then $i<j-4$.
- [Non-crossing.] If $\left(b_{i}, b_{j}\right)$ and $\left(b_{k}, b_{1}\right)$ are two pairs in $S$, then we cannot have $\mathrm{i}<\mathrm{k}<\mathrm{j}<\mathrm{l}$.

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

Goal. Given an RNA molecule $B=b_{1} b_{2} \ldots b_{n}$, find a secondary structure $S$ that maximizes the number of base pairs.

## RNA Secondary Structure

RNA. String $B=b_{1} b_{2} \ldots b_{n}$ over alphabet $\{A, C, G, U\}$.
Secondary structure. RNA is single-stranded so it tends to loop back and form base pairs with itself. This structure is essential for understanding behavior of molecule.

Ex: gucgauugagcganuguancancguggcuacggcgaga

complementary base pairs: A-U, C-G

RNA Secondary Structure: Examples

Examples.


RNA Secondary Structure: Subproblems

First attempt. $\operatorname{OPT}(\mathrm{j})=$ maximum number of base pairs in a secondary structure of the substring $b_{1} b_{2} \ldots b_{j}$.


Difficulty. Results in two sub-problems.

- Finding secondary structure in: $\mathrm{b}_{1} \mathrm{~b}_{2} \ldots \mathrm{~b}_{+-1}$. $\leftarrow$ OPT(t-1)
- Finding secondary structure in: $b_{t+1} b_{t+2} \cdots b_{n-1}$. $\leftarrow$ need more sub-problems


## Bottom Up Dynamic Programming Over Intervals

Q. What order to solve the sub-problems?
A. Do shortest intervals first.

```
RNA (b
    for k=5,6,\ldots, n-1
        for i = 1, 2,
            j=1+k
    turn M[1,n] using recurrence
,
```

3

j

Running time. $O\left(n^{3}\right)$.


## Dynamic Programming Over Intervals

Notation. OPT $(\mathrm{i}, \mathrm{j})=$ maximum number of base pairs in a secondary structure of the substring $b_{i} b_{i+1} \ldots b_{j}$

- Case 1. If $\mathrm{i} \geq \mathrm{j}-4$

OPT $(\mathrm{i}, \mathrm{j})=0$ by no-sharp turns condition.

- Case 2. Base $b_{j}$ is not involved in a pair. $\operatorname{OPT}(\mathrm{i}, \mathrm{j})=\operatorname{OPT}(\mathrm{i}, \mathrm{j}-1)$
- Case 3. Base $b_{j}$ pairs with $b_{\dagger}$ for some $i \leq t<j-4$.
non-crossing constraint decouples resulting sub-problems $-\operatorname{OPT}(\mathrm{i}, \mathrm{j})=1+\max _{\mathrm{t}}\{\operatorname{OPT}(\mathrm{i}, \mathrm{t}-1)+\operatorname{OPT}(\mathrm{t}+1, \mathrm{j}-1)\}$

$$
\begin{aligned}
& \uparrow \\
& \text { take max over } t \text { such h hat } i \leq \subset<j-4 \text { and } \\
& b_{+} \text {and } b_{j} \text { are Watson-Crick complements }
\end{aligned}
$$

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


