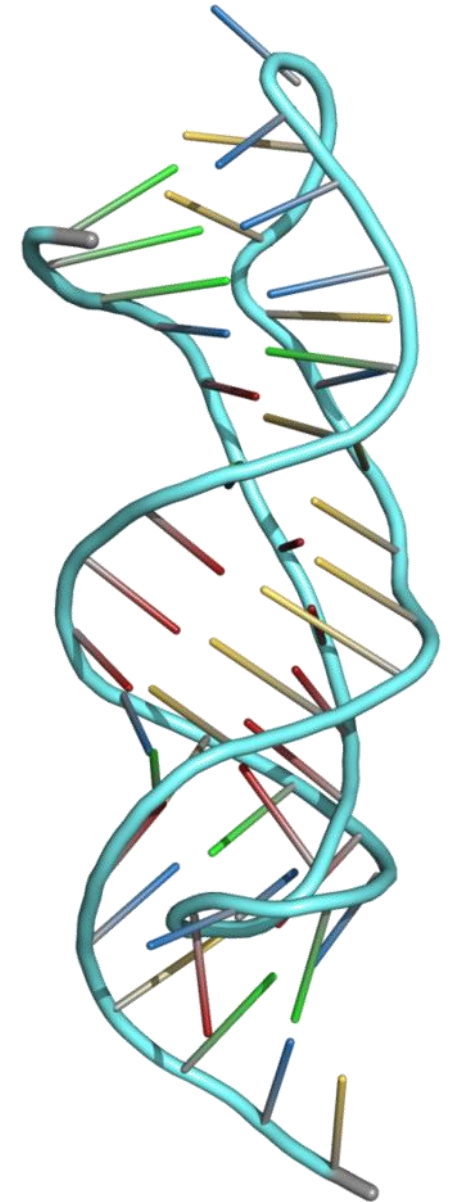


Pseudoknot Structures in RNA Molecules

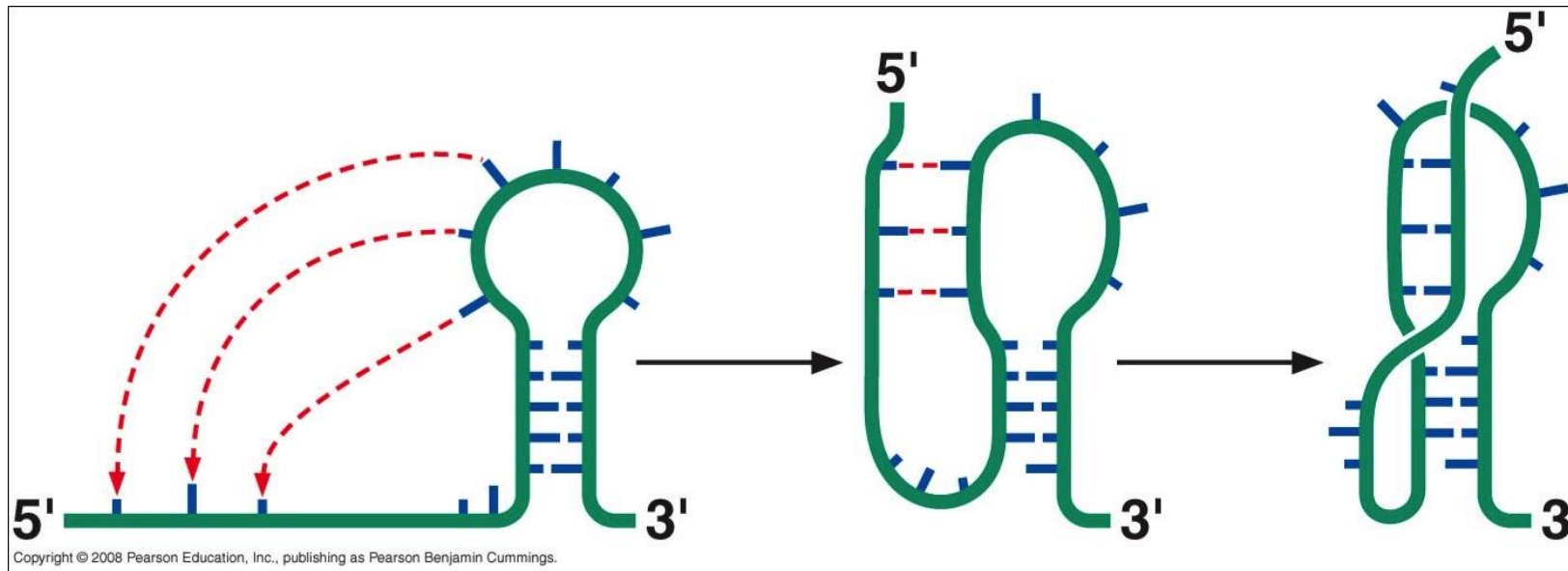
Anshu Patel

3D backbone structure
of pseudoknot from
human telomerase RNA



What are pseudoknots?

Structure formed by base-pairing between a single-stranded region of RNA in a hairpin loop with a complementary sequence of nucleotides elsewhere in the RNA chain



H-type pseudoknot

Use a system of “stems” (S1 and S2) and “loops” (L1 and L3) to name structures

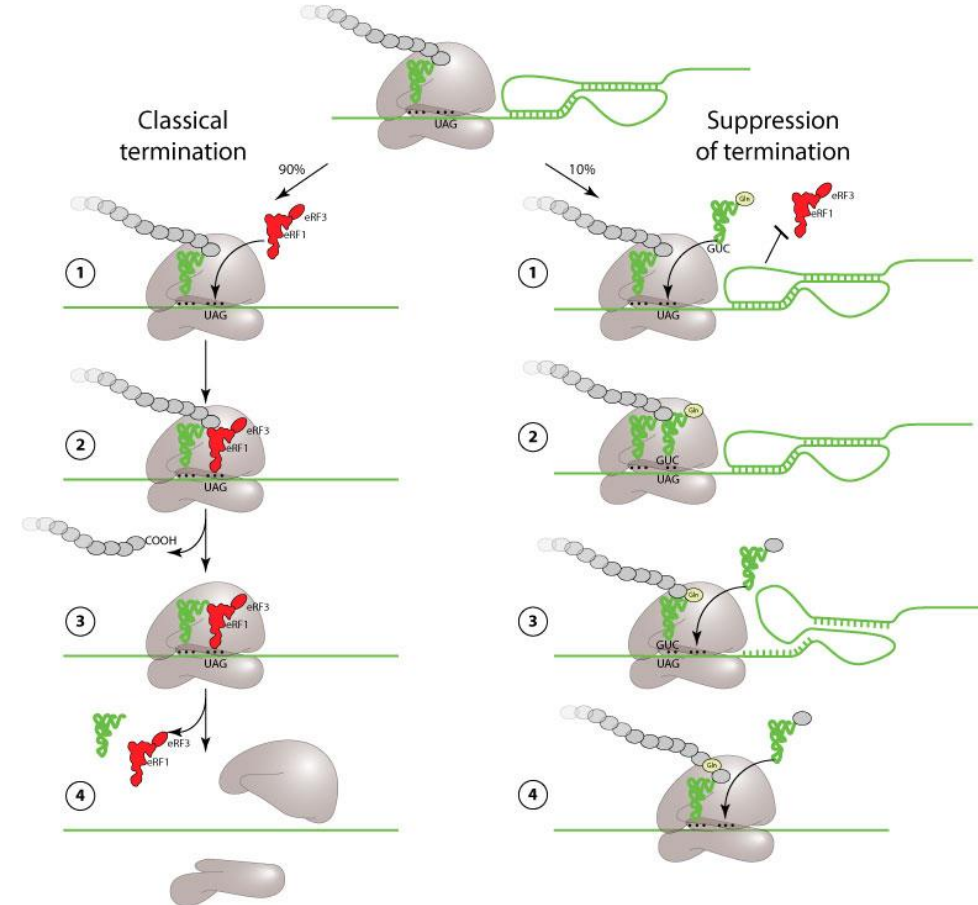
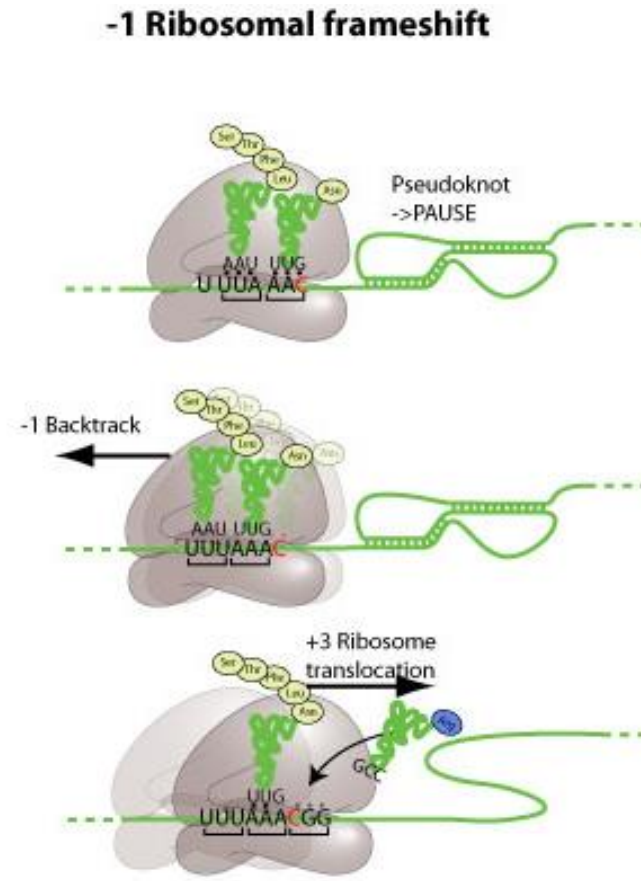
Why are they important?

Biologically significant:
Structure → Function

Examples:

- Autoregulation in translation
- Frameshifting
- Stop codon readthrough

*Prevalent in many viruses
such as SARS, Hepatitis C,
and HIV



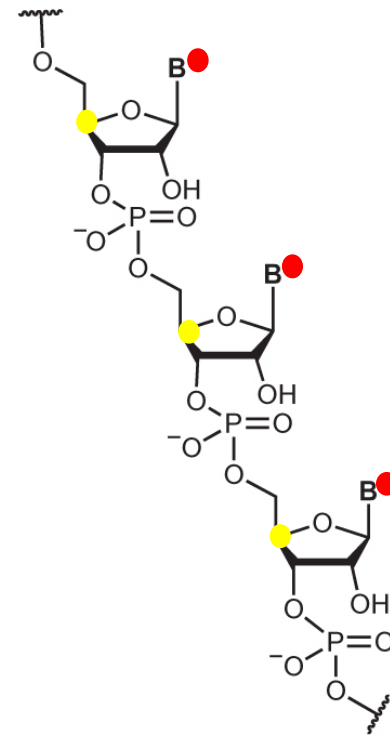
They are very difficult to study

- It is an open problem to build an algorithm that can correctly predict secondary structures that may contain pseudoknots
- Runtime for prediction software is often exponential as length of RNA molecule increases (have to use recursive methods)
- 3D interactions between nucleotides make it difficult to model and study using planar trees or diagrams

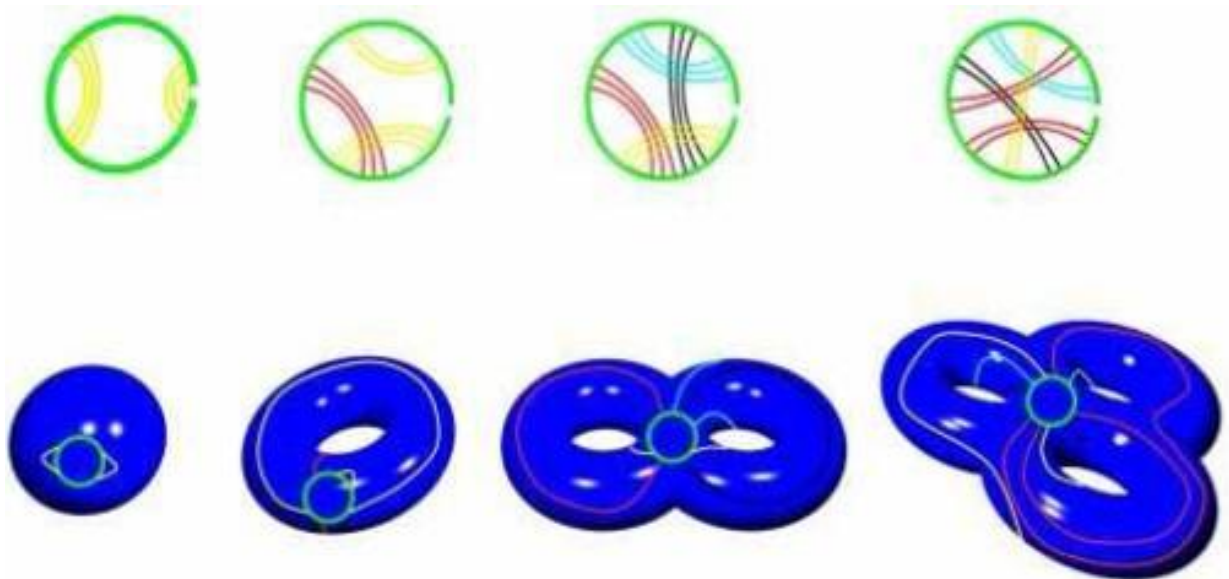
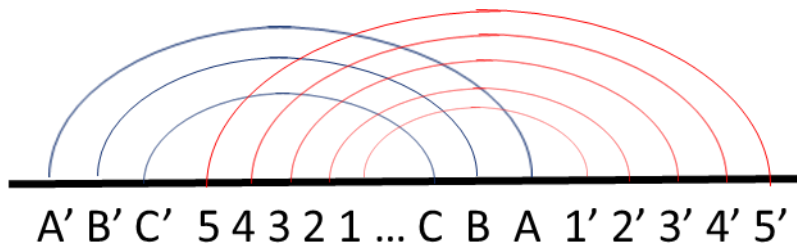
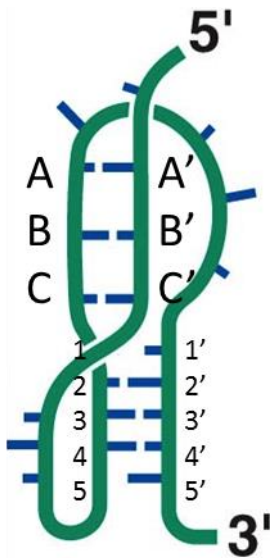
Understanding Pseudoknots

Can use mathematical quantities to determine properties about structure

- Studying RNA molecules as Graphs
- Genus of an RNA pseudoknot
- Linking Number, Writhe, and Twist



Selecting our atoms to define a “ribbon” that help us calculate linking number, writhe, and twist.



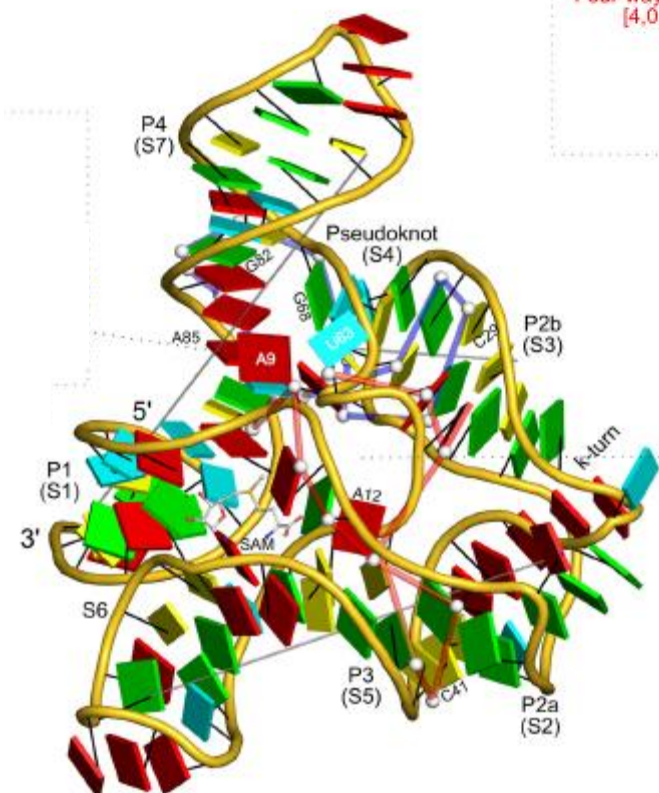
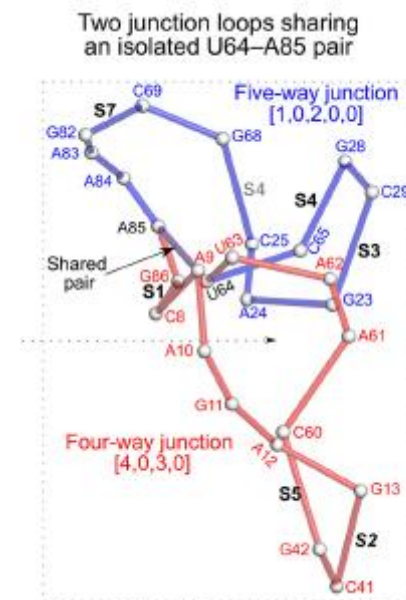
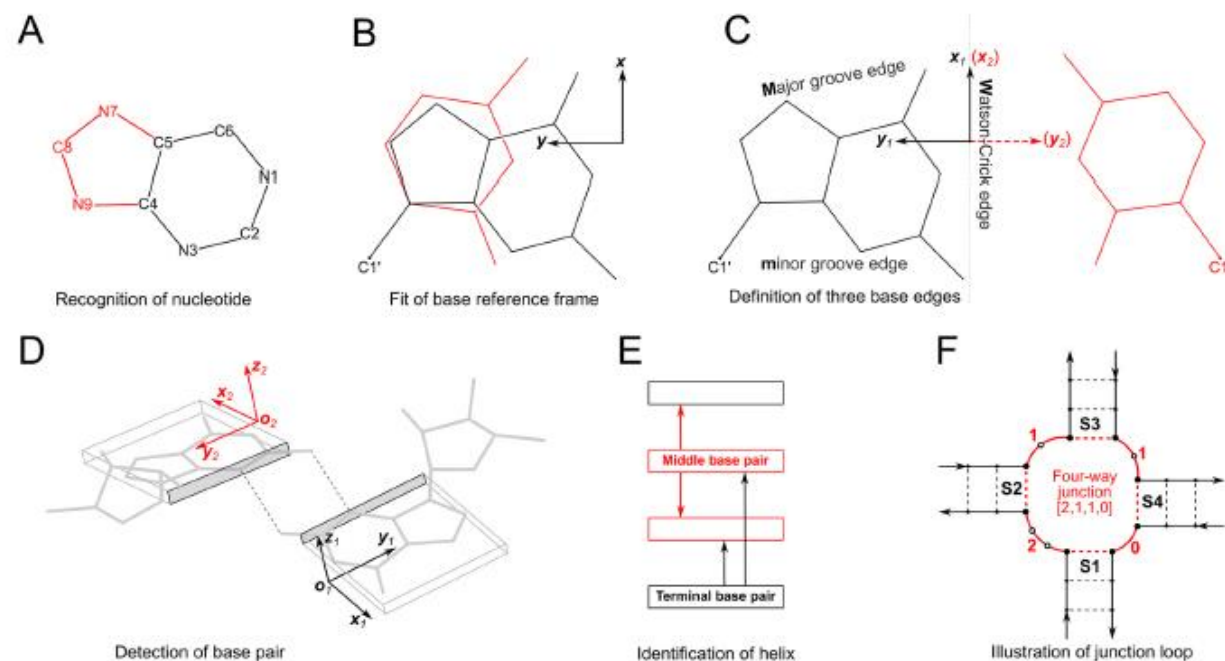
Using DSSR

DSSR: an integrated software tool for dissecting the spatial structure of RNA

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Sources

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Nicolas Clauvelin, Wilma K. Olson & Irwin Tobias

Pictures:

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- <http://nar.oxfordjournals.org/content/early/2015/07/15/nar.gkv716.full>