Construction of RNA 3D fragment database

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Objectives

- Construct database with RNA motifs from already known molecules

- Predict RNA motifs given the sequence (RNA design)
Geometric nomenclature of RNA base pairs
RNA secondary structure decomposition
Construct RNA 3D motifs database

RNAView -> Base pairs extraction -> 2d representation -> Motif extraction -> Writing to database
Base interactions networks

W: Watson-Crick edge
H: Hoogsteen edge
S: Sugar edge
Study the relationship between the sequence and the 3D motif of RNA

Aspects
Automatic annotation of motifs from pdb files
Motif prediction from RNA sequence

Putative features for prediction from pdb file:
- Number of interactions of each geometric family type
- Succession of base pair types in a motif – unigrams, bigrams, etc.

Feature for prediction given RNA sequence:
- Probability of forming pair of certain type between bases
Thank you for your attention