

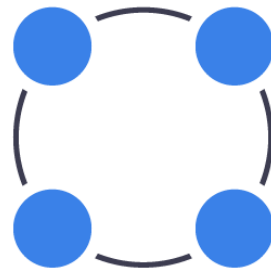
# Construction of RNA 3D fragment database

Alexander Ilin

Supervisor: Nikolay Dokholyan  
(University of North Carolina at Chapel Hill)



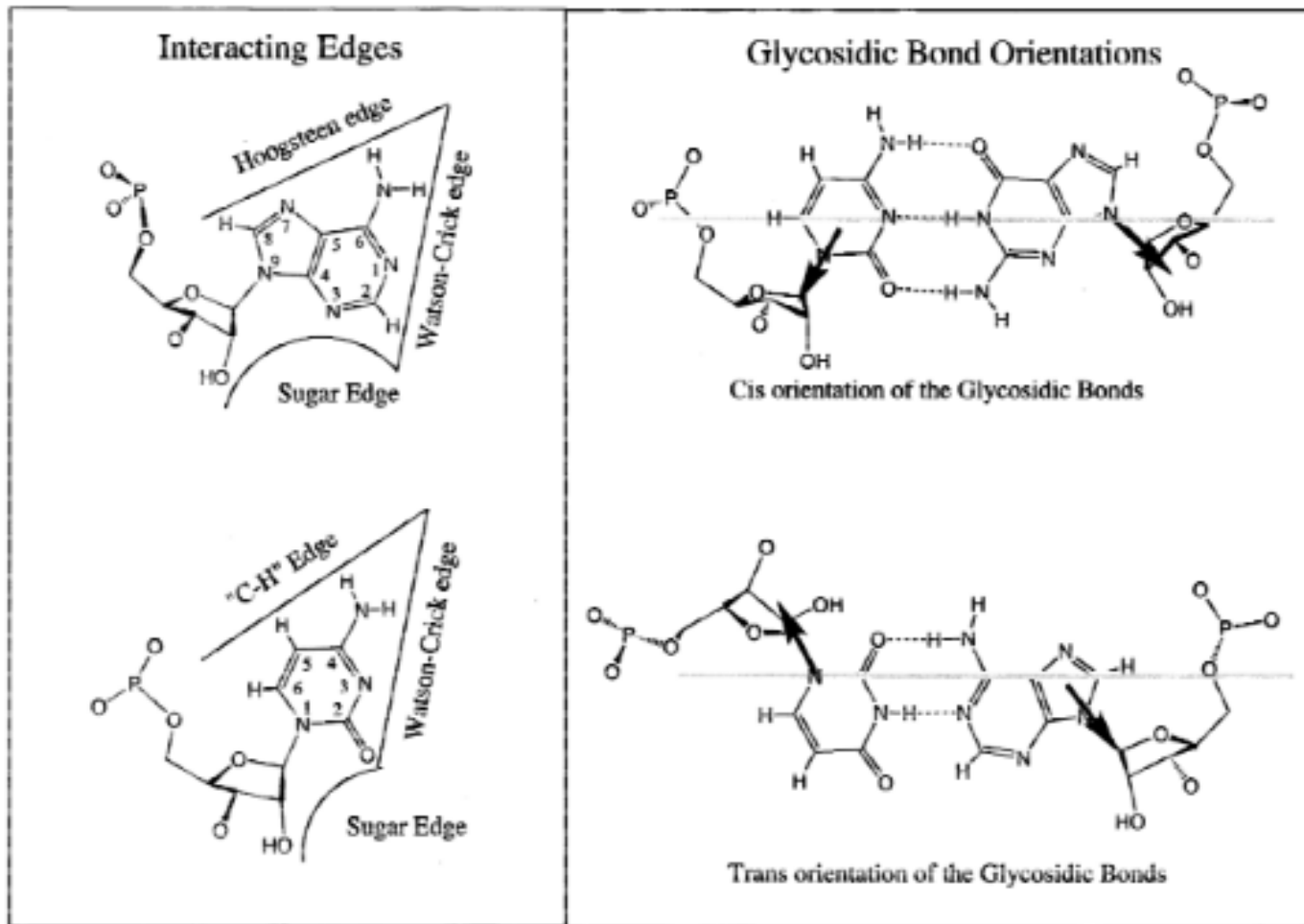
THE UNIVERSITY  
*of* NORTH CAROLINA  
*at* CHAPEL HILL



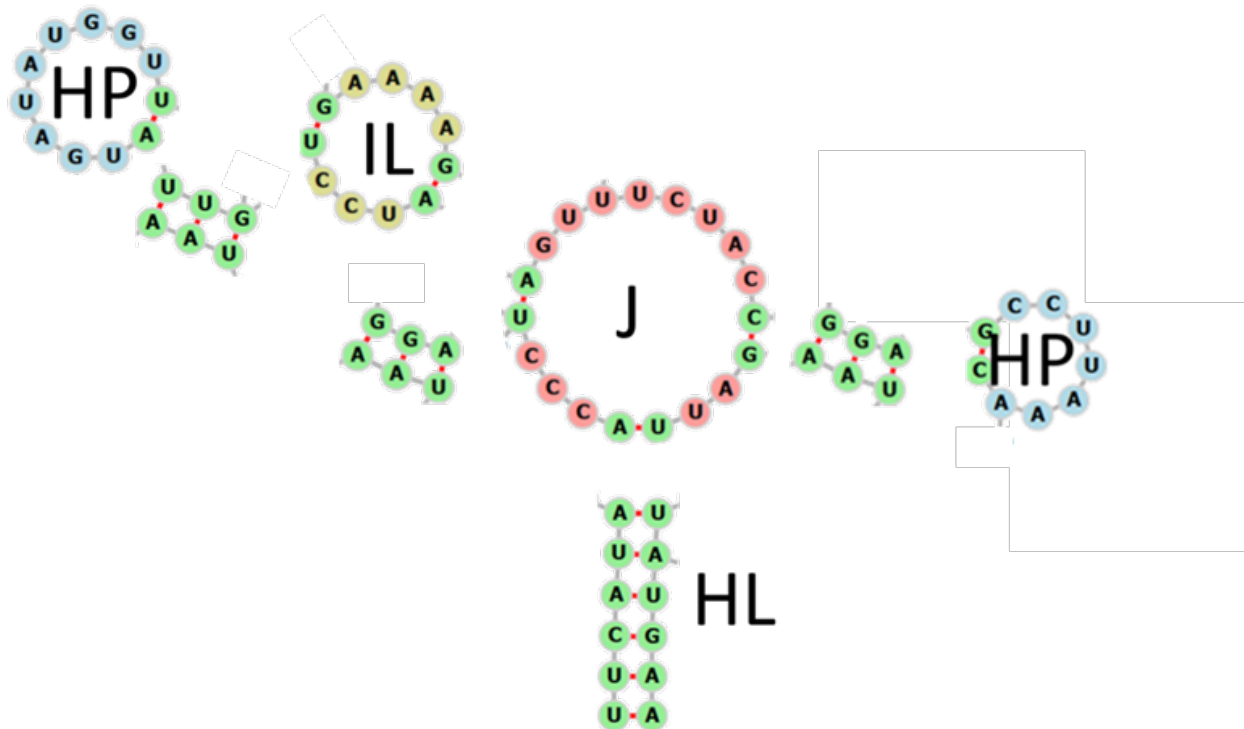
# Objectives

- Construct database with RNA motifs from already known molecules
- Predict RNA motifs given the sequence (RNA design)

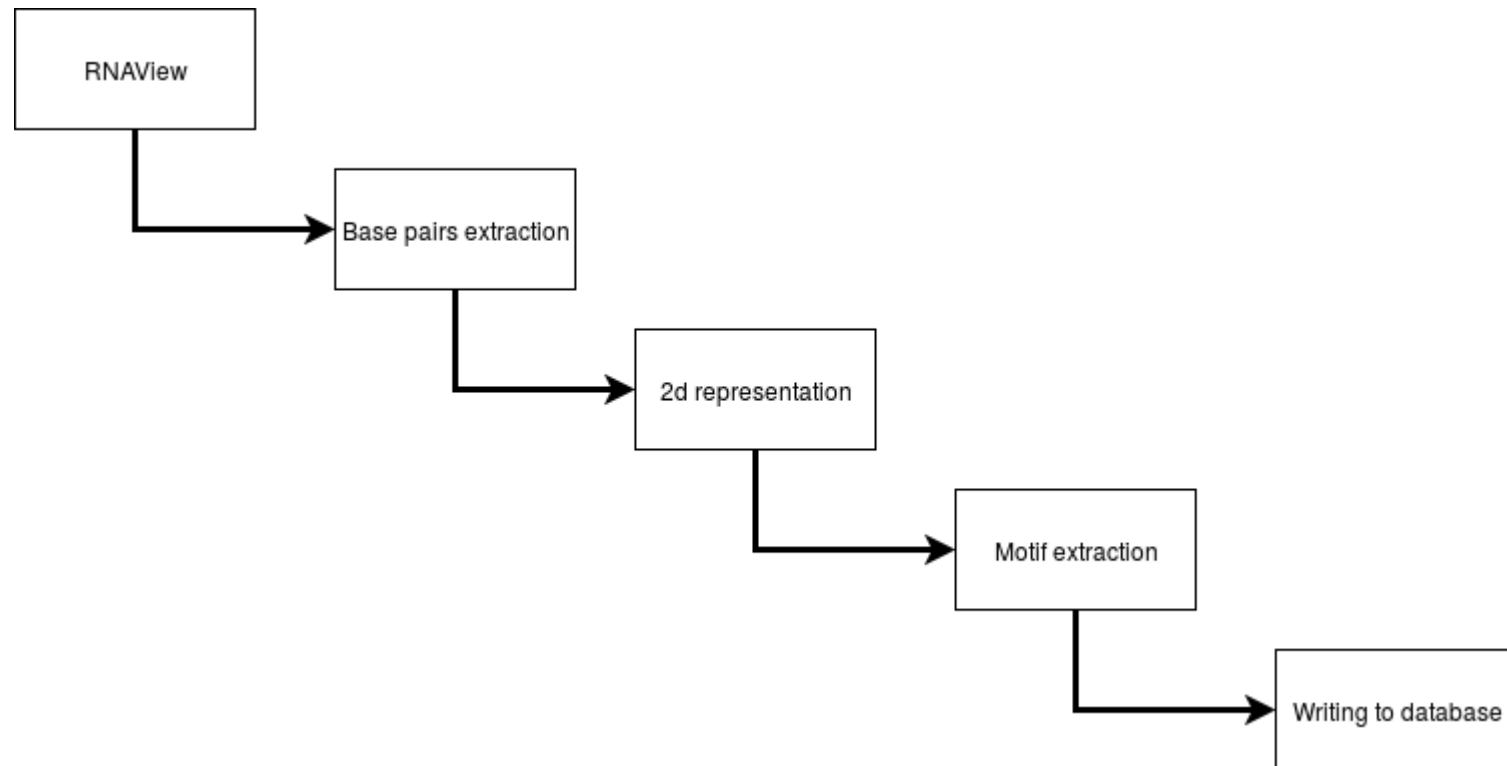
# Geometric nomenclature of RNA base pairs



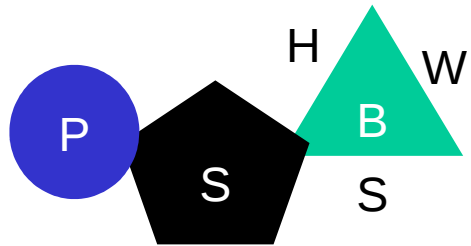
# RNA secondary structure decomposition



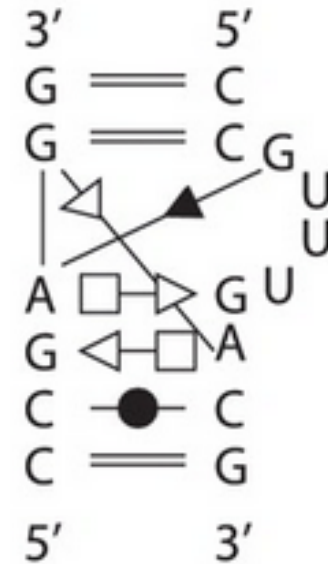
# Construct RNA 3D motifs database



# 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

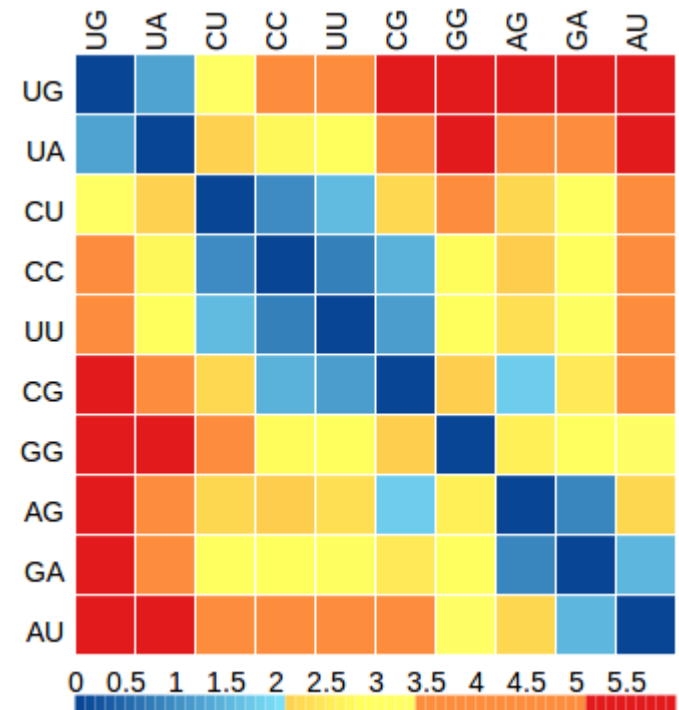
Automatic annotation of motifs from pdb files  
Motif prediction from RNA sequence

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