

RNA Structure Prediction and Protein Interactions

RNA Function

- Storage/transfer of genetic information
- Newly discovered regulatory functions - RNAi pathways especially
- Catalytic

RNA types & functions

Types of RNAs	Primary Function(s)
mRNA - messenger	translation (protein synthesis) regulatory
rRNA - ribosomal	translation (protein synthesis) <catalytic>
t-RNA - transfer	translation (protein synthesis)
hnRNA - heterogeneous nuclear	precursors & intermediates of mature mRNAs & other RNAs
scRNA - small cytoplasmic	signal recognition particle (SRP) tRNA processing <catalytic>
snRNA - small nuclear	mRNA processing, poly A addition <catalytic>
snoRNA - small nucleolar	rRNA processing/maturation/methylation
regulatory RNAs (siRNA, miRNA, etc.)	regulation of transcription and translation, other??

RNA Structure

- RNA forms complex 3D structures
- Mainly single stranded
- The single RNA strand can self-hybridize to form base paired regions

RNA Structure Prediction

- RNA tertiary structure is very difficult to predict
- Focus on predicting RNA secondary structure
- Given a RNA sequence, predict the secondary structure of the molecule
- Almost all methods ignore higher order secondary structures like psuedoknots

RNA Secondary Structure Prediction Methods

- Two main types of methods
- Ab initio - based on calculating the most energetically favorable secondary structure
- Comparative approach - based on evolutionary comparison of multiple related RNA sequences

Ab Initio Prediction

- Only requires a single RNA sequence
- Calculates minimum free energy structure
- Base pairing lowers free energy of the structure, so methods attempt to find secondary structure with maximal base pairing

Popular Ab Initio Prediction Programs

- Mfold
 - Combines DP with thermodynamic calculations
 - Fairly accurate for short sequences, less accurate as sequence length increases
- RNAfold
 - Returns multiple structures near the optimal structure
 - Computes a larger number of potential secondary structures than Mfold, so it uses a simplified energy function

Comparative Approach

- Uses multiple sequence alignment
- Assumes related sequences fold into the same secondary structure

Popular Comparative Prediction Programs

- Two main types:
- Require user to provide MSA
 - RNAalifold
- No MSA required
 - Foldalign
 - Dynalign

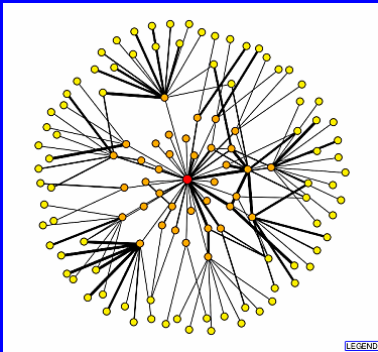
Protein Interactions

- Many experimental methods to determine protein interactions
- Vary in quality

Some terminology for networks

- Node - protein in a network
- Edge - an interaction between two nodes (proteins)

Graph Example



- <http://dabbslab.gdcb.iastate.edu/BCB590>