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Title: Computational methods for RNA secondary structure determination

Abstract:

RNA secondary structure is defined along with three different ways to display them. Two distinct approaches are presented for determining secondary structure from sequence data. The comparative method requires a multiple sequence alignment of a collection of homologous RNA sequences. It uses phylogeny to determine common, conserved base pairs that are more likely to be the result of evolution than to exist by chance. On the other hand, recursive algorithms may be used on single sequences to compute minimum free energy structures, partition functions and other biophysical quantities. These algorithms ignore evolution and use empirically derived energy parameters based on physical chemistry. Examples will be given for both methods.

The latter part of the lecture will include recent work on computing the entropy of the Boltzmann distribution of foldings and how this quantity may be used to judge the overall reliability of free energy based methods for particular molecules.