# RNA STRUCTURE PREDICTION : MODELING THE FOLDING KINETICS

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RNA folding is thought to proceed via well-defined "secondary structures" which solely involve the pairing of matching bases along the primary sequence. Beyond the well-known, topologically simple, tree-like structures (e.g. a tRNA clover leaf), these base-base pairings can also give rise to so-called "pseudoknotted" configurations arising from the hybridization between different branches in a secondary structure. Although such "non-nested" structures are believed to be common and essential in many natural RNA molecules (as demonstrated by their high conservation during evolution), there are, to our knowledge, still no secondary structure prediction programs that take into account the loss of entropy in these non-nested configurations. We have developed an algorithm that models the long time scale kinetics of RNA folding, assuming that it proceeds via a succession of partially folded secondary structures in quasi-equilibrium, in accordance with the slow folding processes observed experimentally. Our approach relies on a coarse grained description of the secondary structures based on the introduction of quasi-independent subdomains, which enables one to include pseudoknots. Beyond the prediction of secondary structures, a kinetic code can address a variety of physical effects of technological and biological interest such as the hybridization to DNA chip arrays and the results of micromechanical experiments on single stranded nucleic acids.