



# Asymptotic distribution of motifs in a stochastic context-free grammar model of RNA folding

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We analyze the distribution of RNA secondary structures given by the Knudsen-Hein stochastic context-free grammar used in the prediction program Pfold. We prove that the distribution of base pairs, helices and various types of loops in RNA secondary structures in this probabilistic model is asymptotically Gaussian, for a generic choice of the grammar probabilities. Our proofs are based on singularity analysis of probability generating functions. Finally, we use our results to discuss how this model reflects the properties of some known ribosomal secondary structures.

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