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Modeling nucleic acid structure in the presence of single-stranded binding proteins[1] ROBERT FORTIES, RALF BUNDSCHUH, The Ohio State University — There are many important proteins which bind single-stranded nucleic acids, such as the nucleocapsid protein in HIV, the RecA DNA repair protein in bacteria, and all proteins involved in mRNA splicing and translation. We extend the Vienna Package for quantitatively modeling the secondary structure of nucleic acids to include proteins which bind to unpaired portions of the nucleic acid. All parameters needed to model nucleic acid secondary structures in the absence of proteins have been previously measured. This leaves the footprint and sequence dependent binding affinity of the protein as adjustable parameters of our model. Using this model we are able to predict the probability of the protein binding at any position in the nucleic acid sequence, the impact of the protein on nucleic acid base pairing, the end-to-end distance distribution for the nucleic acid, and FRET distributions for fluorophores attached to the nucleic acid.

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