3.2 Probability Profiling for Specific Loop Types

A statistical sample of all possible secondary structures for a given RNA sequence can be used for sampling estimates of the probabilities of any structural motifs. Actually, probability profiling for unpaired bases within particular loop types can easily be applied for this purpose. In principle, for each nucleotide position $i$, $1 \leq i \leq n$, of a given sequence of length $n$, one computes the probabilities that $i$ is an unpaired base within a specific loop type. These probabilities are given by the observed frequencies in a random sample set.