Since this application is rather intuitive, we decided to use it as a starting point for our disturbance analysis. Particularly, we derived a number of statistical samples for the well-known Escherichia coli tRNA\textsuperscript{Ala} sequence by applying the sampling strategy from Section 2.3 on the basis of diverse sets of probabilistic parameters (inside probabilities disturbed according to several particular variants as defined in Section 2.2) for that sequence and calculated corresponding probability profiles. All relevant results are displayed in Figures 5 to 18 of Section 5m-11. Some of the potentially most interesting ones are presented in Figures 2 to 4.

![Figure 2: Hairpin loop profiles for E.coli tRNA\textsuperscript{Ala} calculated from a random sample of 1000 structures generated with the SCFG (figures on the left) and LSCFG (figures on the right) approach, respectively (under the assumption of the less restrictive grammar parameters \( \min_{hel} = 1 \) and \( \min_{HL} = 1 \)). The exact (undisturbed) results are displayed by the thin black lines, and the correct hairpin loops in E.coli tRNA\textsuperscript{Ala} are illustrated by the black points.](image)

### 3.2.1 Errors on All Values

Let us first consider the profiles displayed in Figure 2 (and in Figures 5 and 6). Obviously, even if large relative errors on all inside probabilities and hence on the needed conditional sampling probabilities are generated, the sampled structures still exhibit the typical cloverleaf structure of tRNAs, especially for the length-dependent sampling approach where relative disturbances seem to have no significant negative effect on the sampling quality (see Figure 2a). However, Figure 2b perfectly demonstrates that if the disturbances have been created by adding absolute errors to all inside values, then – even for rather small absolute error values – the resulting samples obtained with both the SCFG and LSCFG approach are useless.

Note that for any given input sequence, it seems to be usually much more important for the employed sampling strategy to be able to identify which ones of the (combinatorially) possible substructures can actually be (validly) formed on the considered sequence fragment rather than to know their exact probabilities (according to the conditional distribution for the respective fragment), for two contrary reasons: First, in order to avoid drawing practically impossible choices, which later forces it to leave the considered sequence fragment (at least partially) unpaired. Second, for ensuring that none of the actually valid choices is prohibited during the folding process, such that the sampling procedure might inevitably prefer other (potentially even impossible) substructures. Consequently, in order to prevent a decline in accuracy of generated structures and a reduction of the overall sampling quality, it seems to be of great importance that the sampling strategy is capable of

\[4\text{If those decisions are not revised by employing backtracking procedures, see the description of the modifications incorporated into the sampling algorithm in order to deal with such situations as given in Section 2.3.} \]