Supplementary material: RNA fast-folding paths

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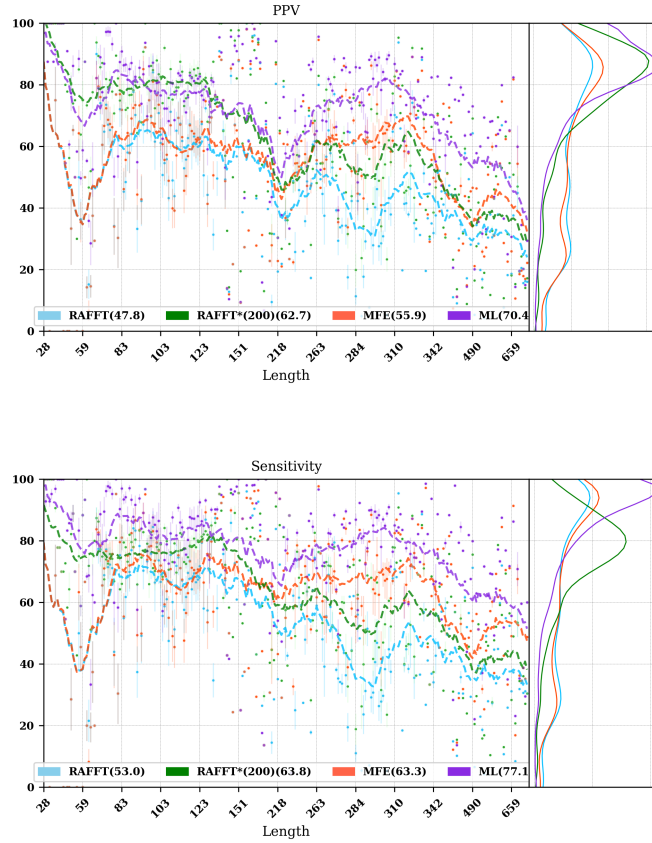
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Figure 1: **Predicted positive values and sensitivity results.** RAFFT (blue) displayed the best energy found. RAFFT*(200) shows the best score found among 200 saved structures. Left pans show the density (sequence-wise) of the accuracy measures.
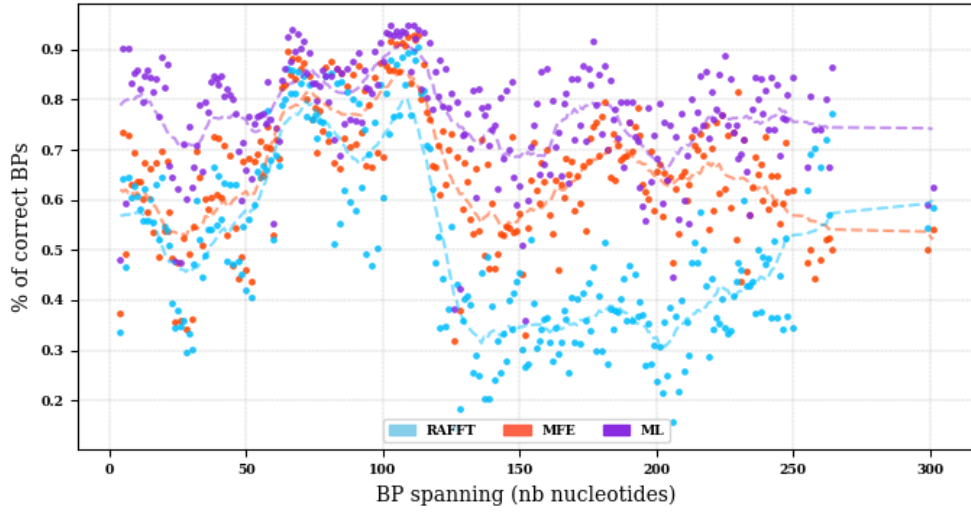
Figure 2: **Base pair spanning: It shows the percent of base pairs predicted found in the known structures per number of nucleotides between them.**
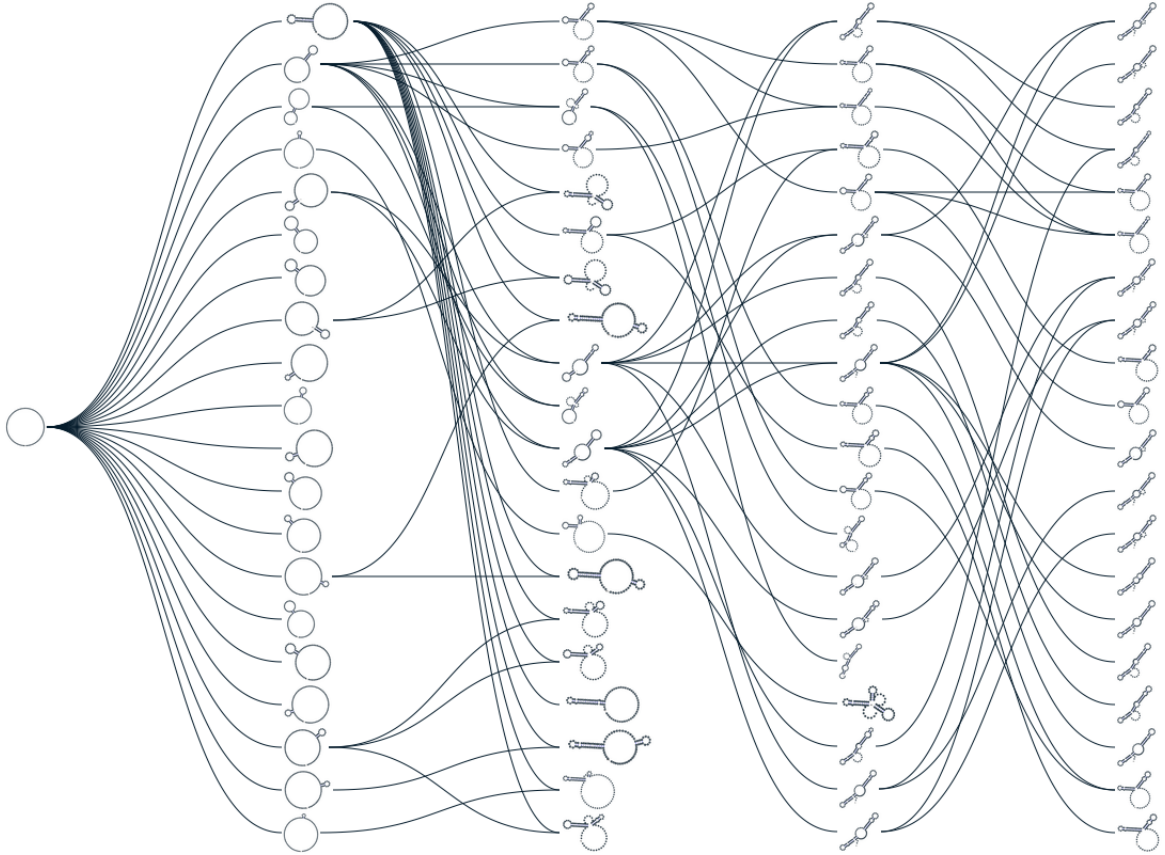

Figure 3: **Fast-folding paths with 20 saved structures for the Coronavirus frameshifting stimulation element.**