

Supplementary material: RNA fast-folding paths

Vaitea Opuu, Nono S. C. Merleau, and Matteo Smerlak

Max Planck Institute for Mathematics in the Sciences, Leipzig, Germany

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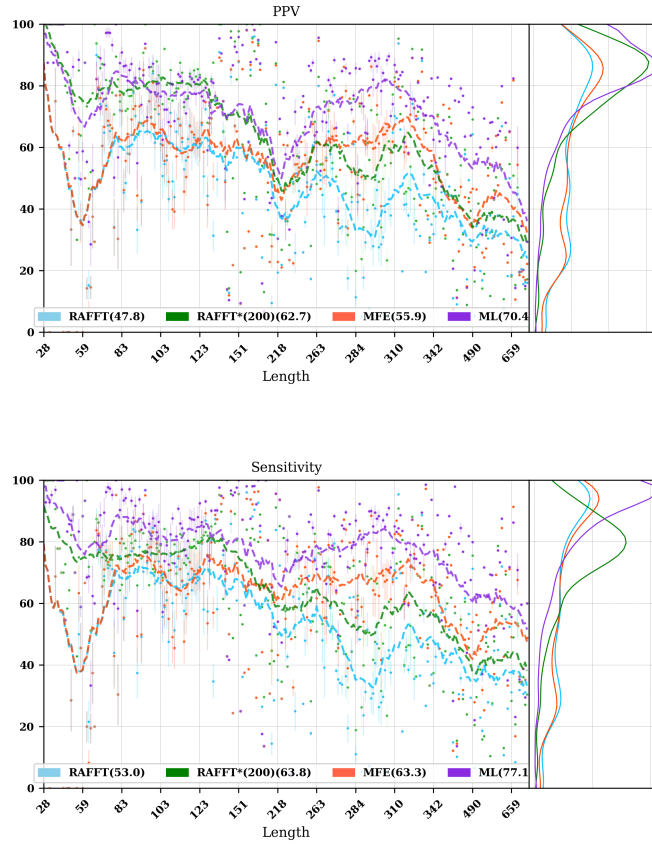


Figure 1: **Predicted positive values and sensitivity results.** RAFFT (blue) displayed the best energy found. RAFFT*(200) shows the best score found among 200 saved structures. Left pans show the density (sequence-wise) of the accuracy measures.

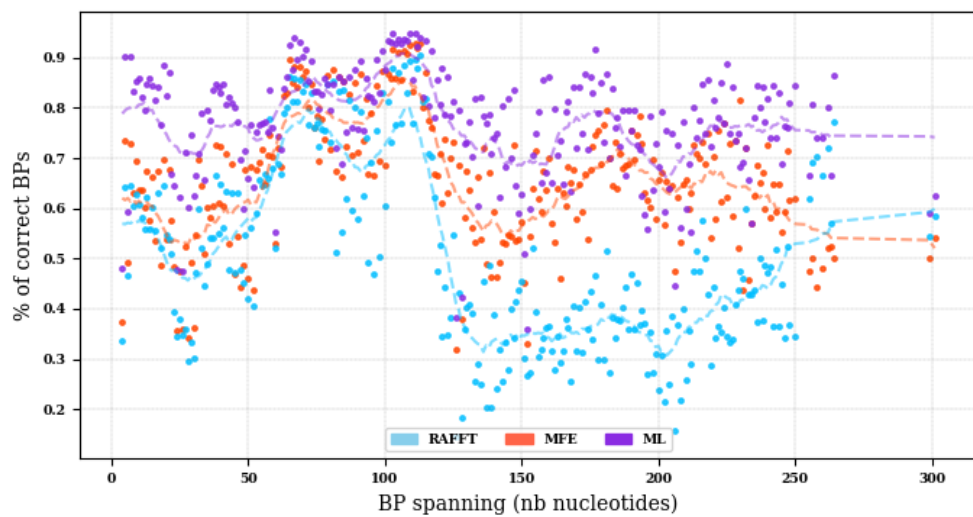


Figure 2: **Base pair spanning:** It shows the percent of base pairs predicted found in the known structures per number of nucleotides between them.