SUPPLEMENTARY INFORMATION

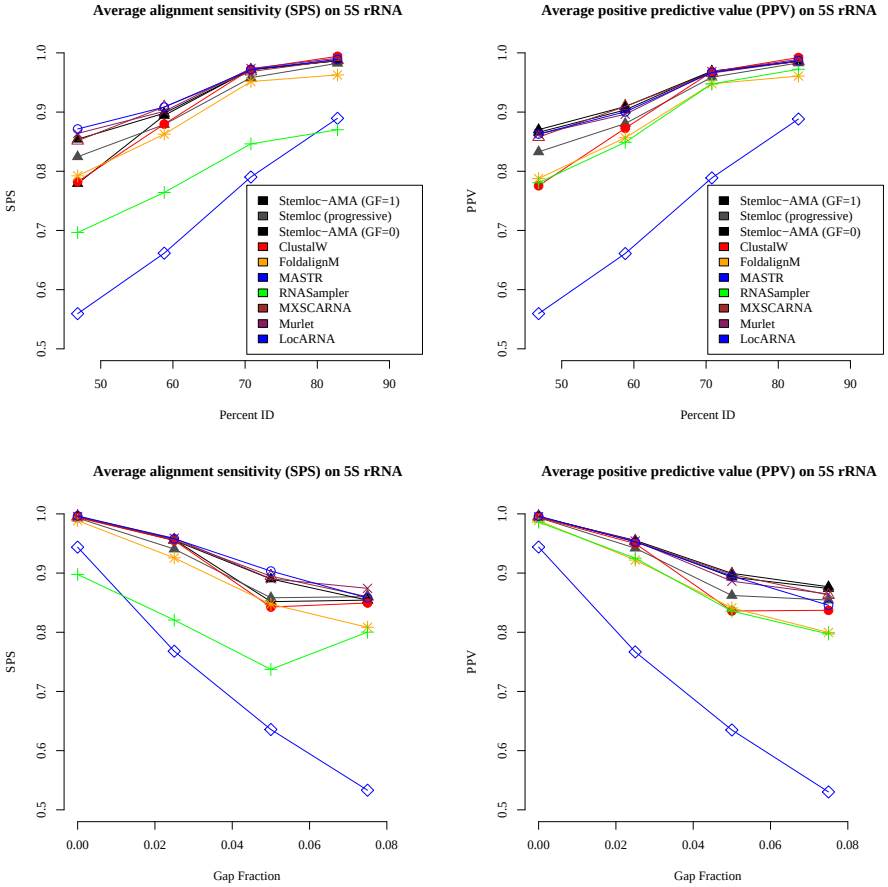

Fig. 1. Sensitivity (SPS) and positive predictive value (PPV) as functions of average pairwise sequence identity and fraction of gaps in the reference alignment. The gap fraction provides a measure of the structural divergence of the dataset. Ribosomal RNA is relatively easy to align; most programs perform similarly.

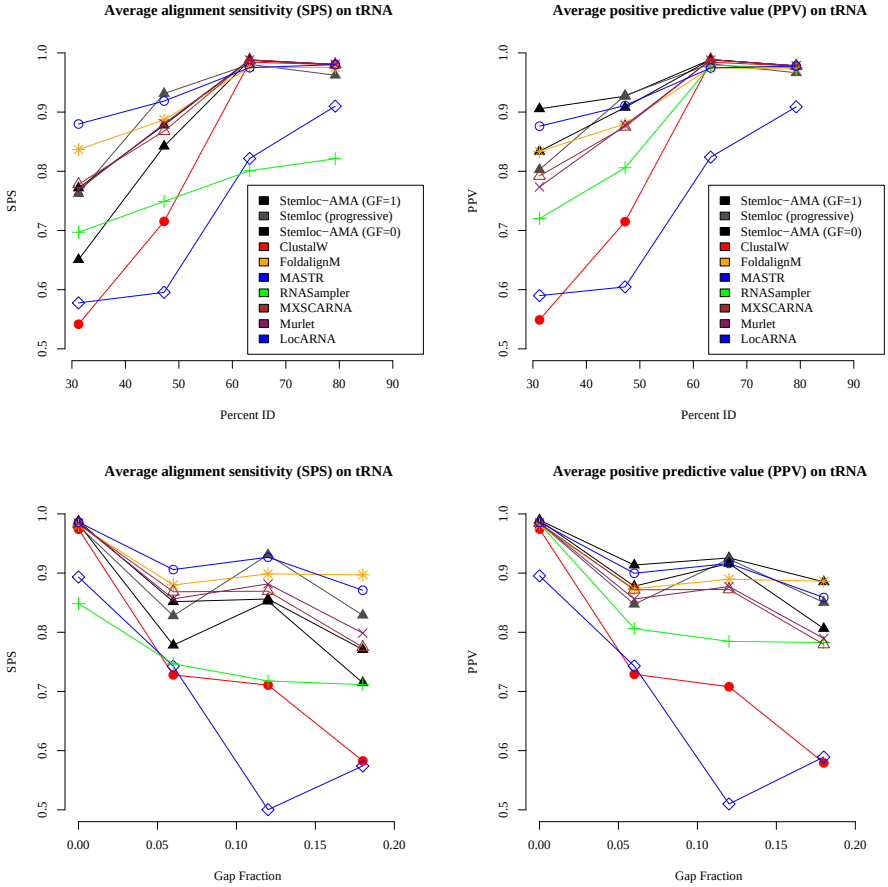

Fig. 2. At gap factor 1 (shown above) our sensitivity on tRNAs is $\sim 5\%$ less than `FoldalignM` or `Murlet`'s, although our PPV is better. Our sensitivity on tRNAs becomes comparable to `FoldalignM`and `Murlet`'s when we reduce the gap factor to 0 and our PPV remains superior).

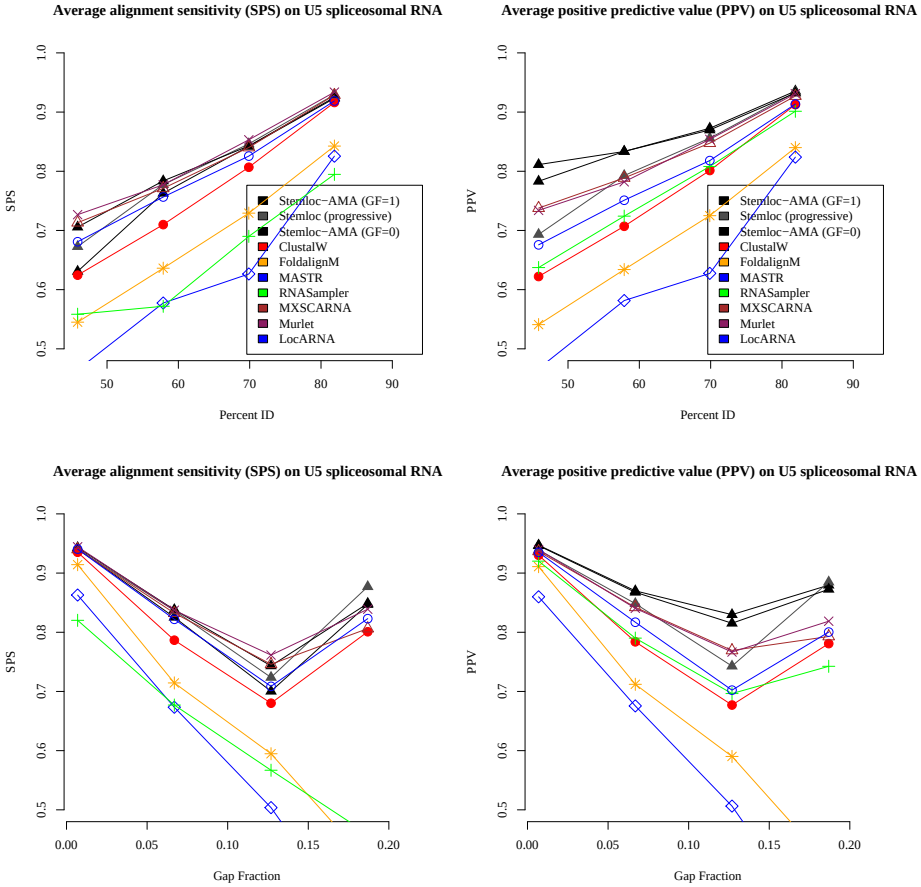

Fig. 3. The comparative advantage of our combined structural alignment and sequence annealing technique increases on more difficult datasets like U5. Note that the gap in PPV between our method and `Murlet`'s increases with decreasing sequence identity and increasing gap fraction.

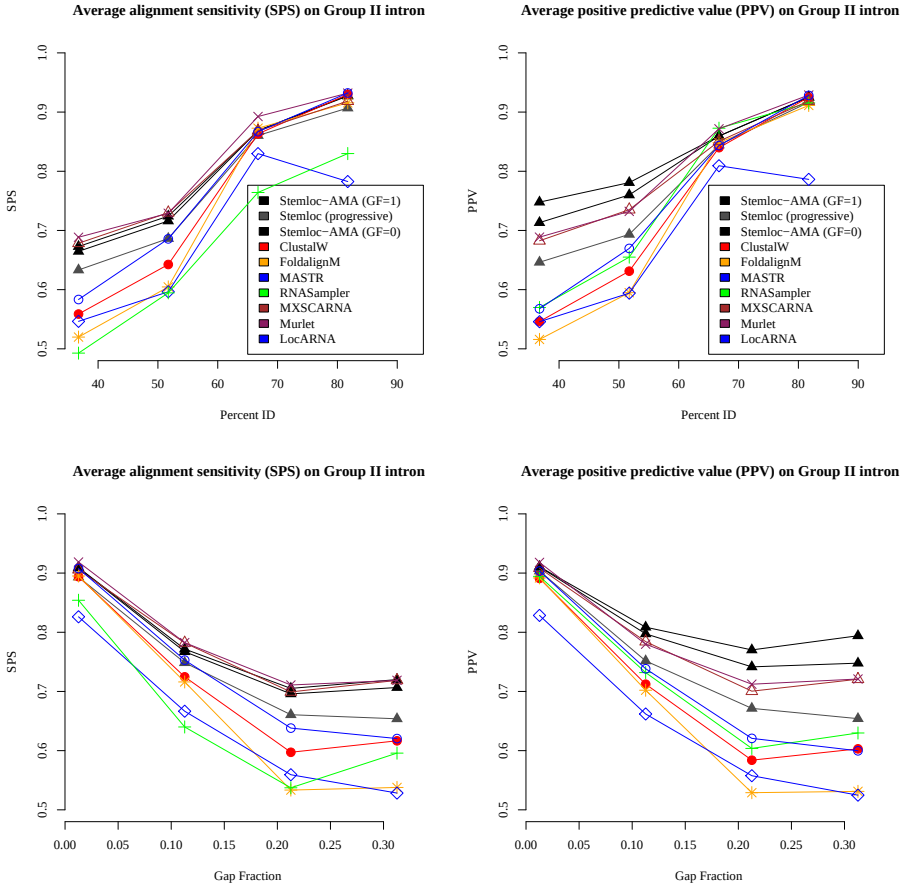

Fig. 4. Sequence annealing's robust handling of uncertainty helps `Stemloc-AMA` to significantly outperform `Stemloc` in progressive mode on Group II intron sequences, the most diverged dataset.