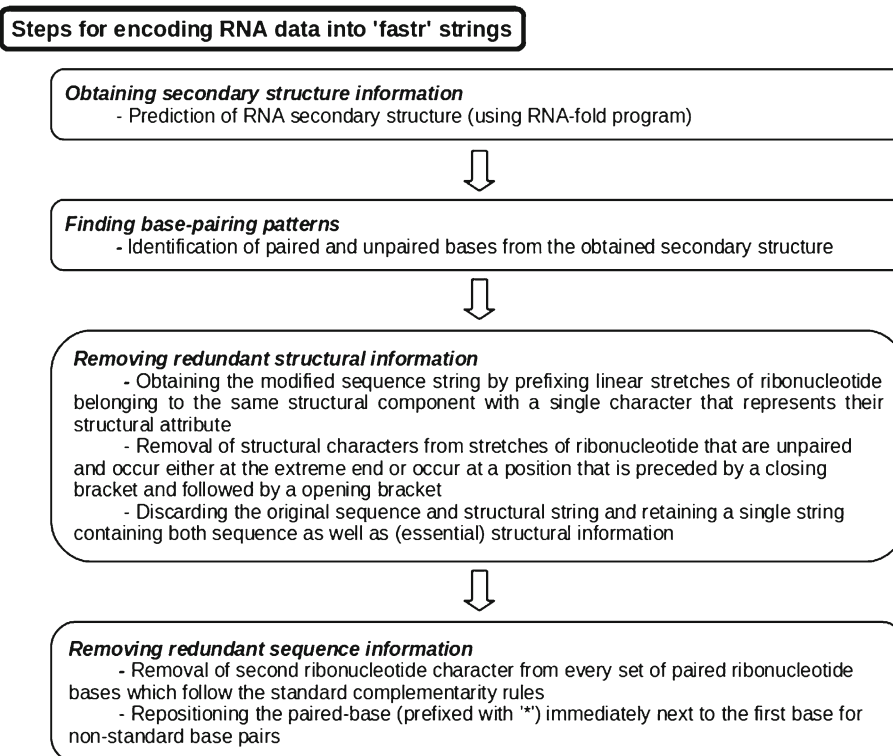


FASTR: A novel data format for concomitant representation of RNA sequence and secondary structure information

TUNGADRI BOSE, ANIRBAN DUTTA, MOHAMMED MH, HEMANG GANDHI and SHARMILA S MANDE

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Supplementary material



Supplementary figure 1A. Steps involved in encoding a RNA sequence data into a 'FASTR' string.

Steps for decoding RNA data from 'fastr' strings

Insertion of missing loop element

- Inserting structural characters for stretches of nucleotides that are unpaired and occur either at extreme end or occur at a position that is preceded by a closing bracket and followed by an opening bracket



Insertion of redundant sequence information

- Insertion of ribonucleotide characters (paired bases) which were removed during the formation of 'fastr' string



Insertion of redundant structural information

- Counting the number of ribonucleotide characters (immediately following each dot/bracket) and writing the same number of dots/brackets to the structure-string
- Removal of all structural elements from the (processed) 'fastr' string to obtain the sequence string

Supplementary figure 1B. Steps involved in decoding the 'FASTR' string to obtain RNA sequence and structure information.