

Input: miR(s) sequence and the 3'UTR sequence(s).

Output: the target positions (heads and ends), and the corresponding duplexes.

Scan the 3'UTR segment in 5' $\rightarrow$ 3' direction, and for each position i execute the following two steps:

Step1 Run the 2D-coding to obtain candidate duplexes.

Step2 Remove all pairs with gaps (“-”), and compute score of each candidate duplex by using the scoring function SF_i .

If $SF_i \geq 70$ then accept the duplex; otherwise reject the duplex.