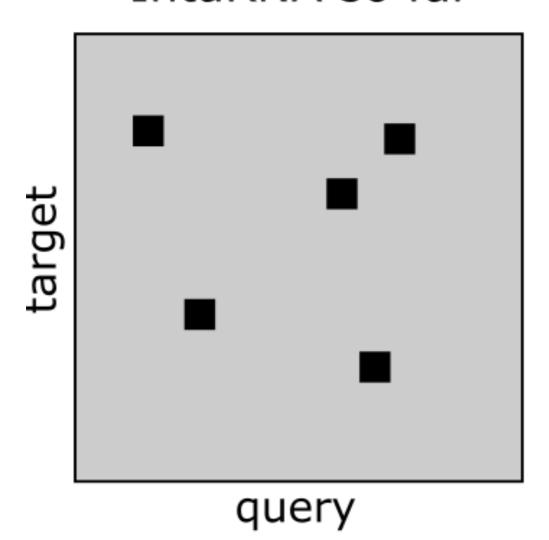
# RNA-RNA interaction prediction using seed extension

Frank Gelhausen

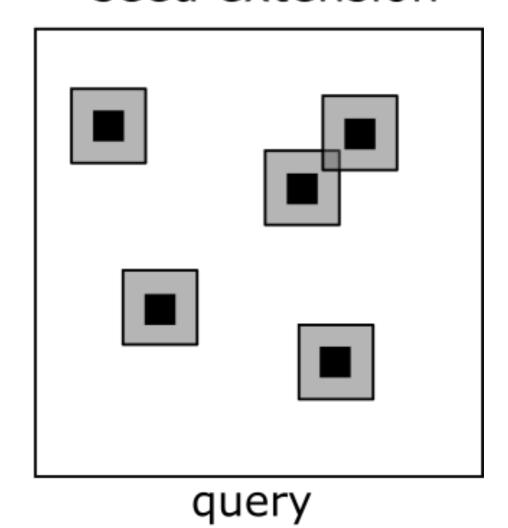
#### Motivation

IntaRNA so far



■ Seed

seed extension



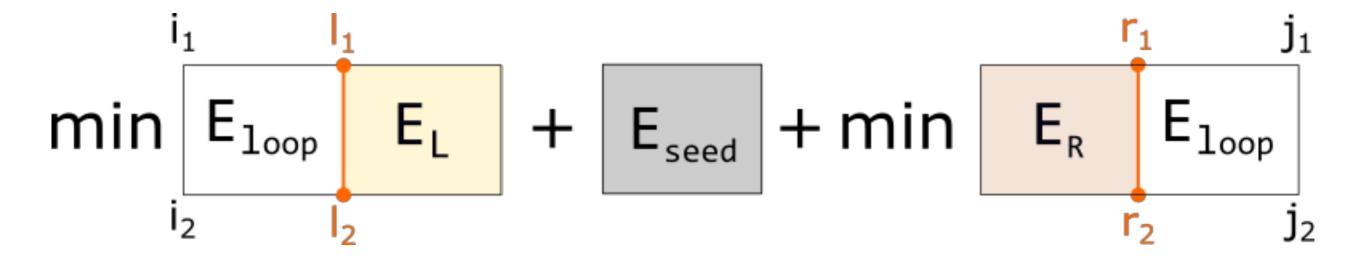
eg: sTarPicker

RiBlast

RiSearch2

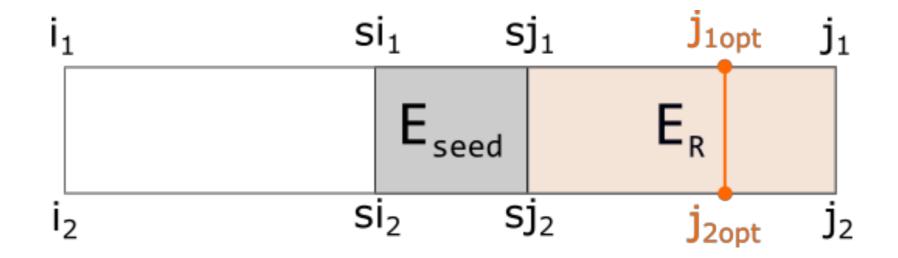
# Exact memory efficient method

Search minimum over all seeds using:

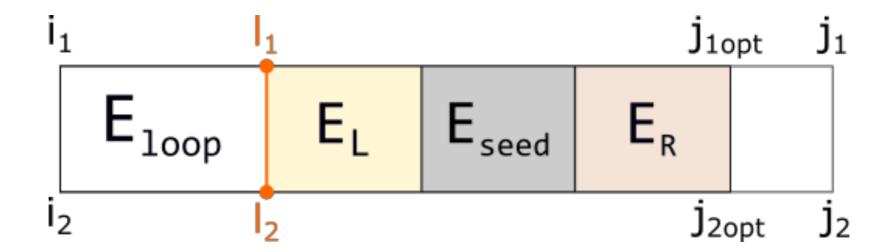


#### Heuristic method

First find j<sub>1</sub> and j<sub>2</sub> that minimize E<sub>R</sub>

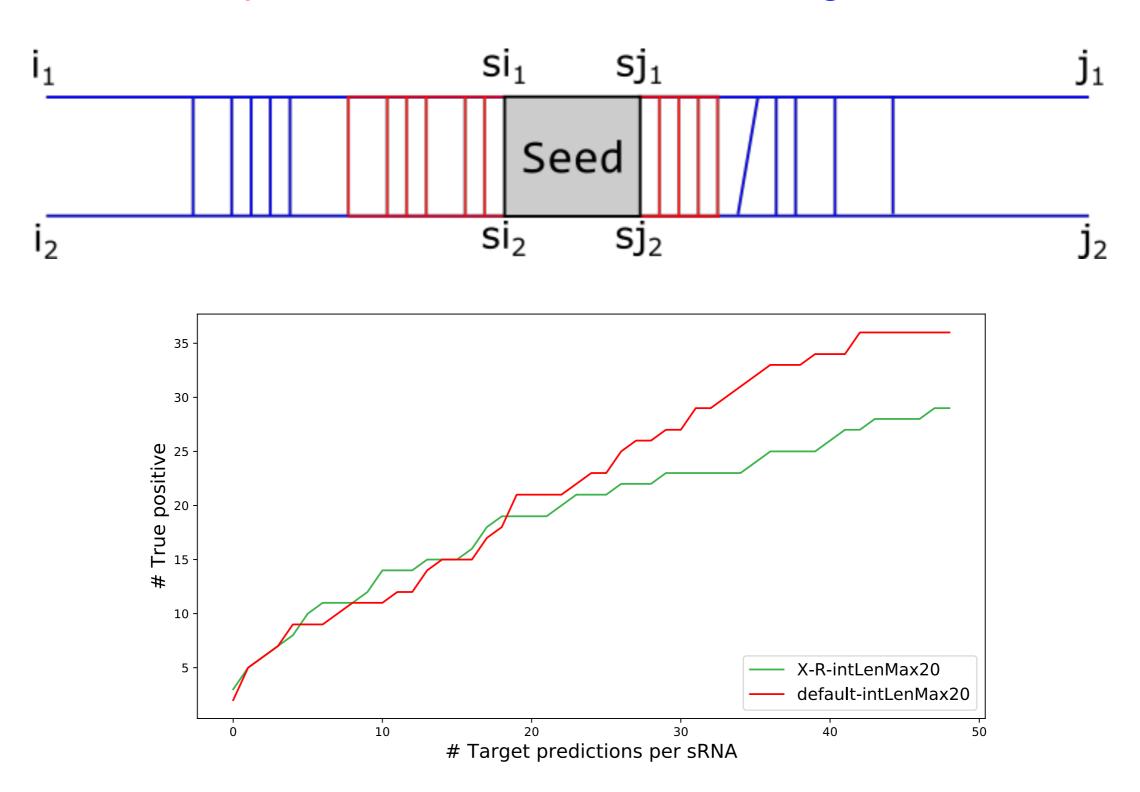


• Then minimize over entire interaction up to j<sub>1opt</sub>, j<sub>2opt</sub>

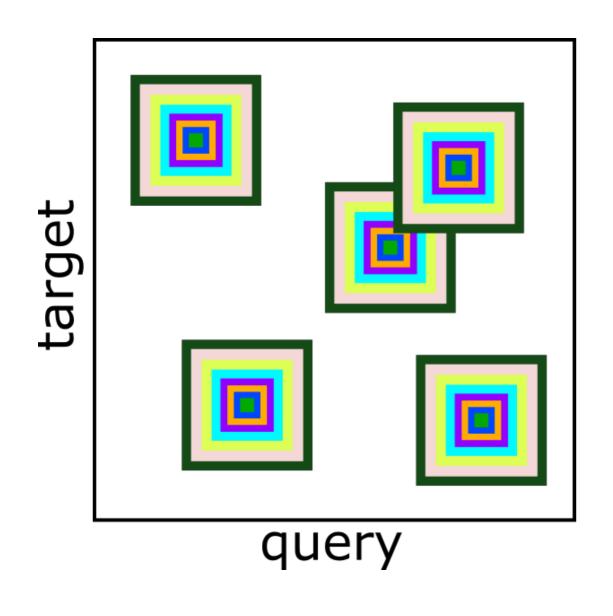


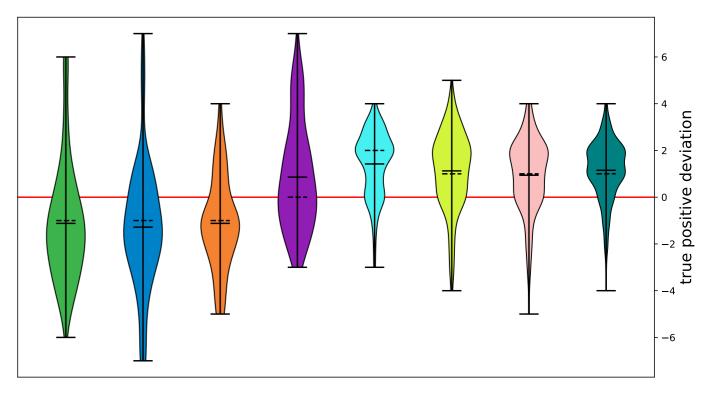
#### Riblast method

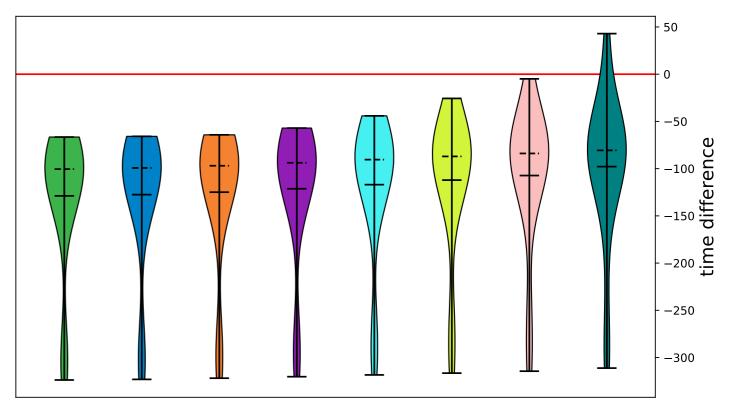
First do a parallel extension, then thorough extension



# Length-dependence







### Partition function

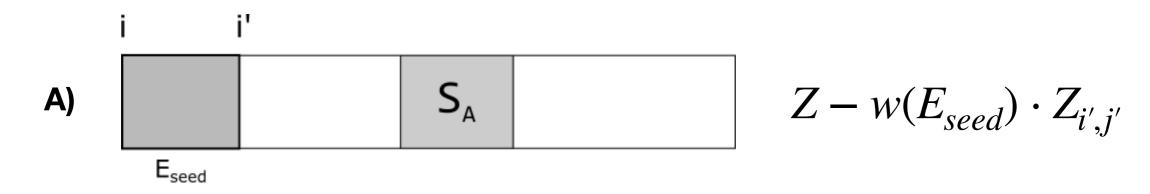
Goal: Find probabilities of interactions

$$Z = \sum Z_{i,j}$$

$$Z_{i,j} = \sum_{S_A} \left( \begin{array}{c|c} \mathbf{s} & \mathbf{s} & \mathbf{s} \\ \mathbf{s} & \mathbf{s} \end{array} \right)$$

Idea: remove seed for i

Cases:



B) 
$$S_A$$
  $Z-w(E_{left})\cdot Z_{i',j'}$