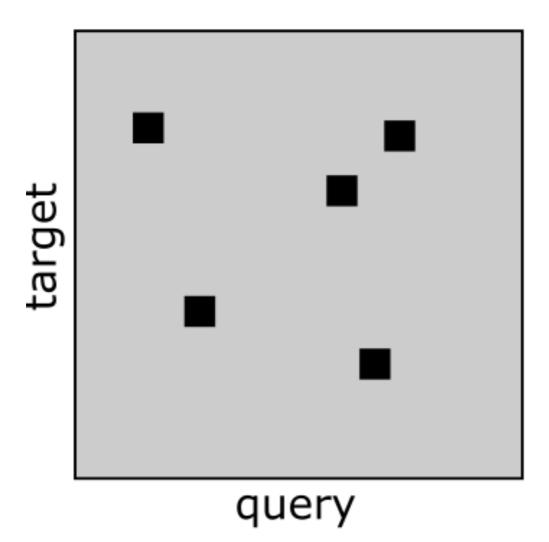
RNA-RNA interaction prediction using seed extension

Frank Gelhausen

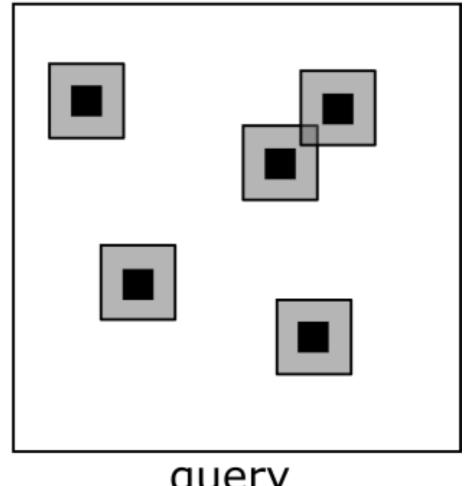
Motivation

IntaRNA so far



■ Seed

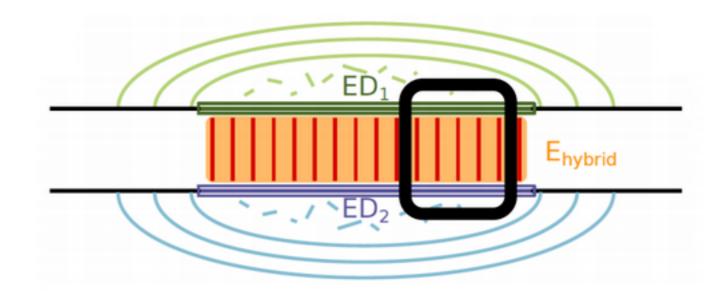
seed extension



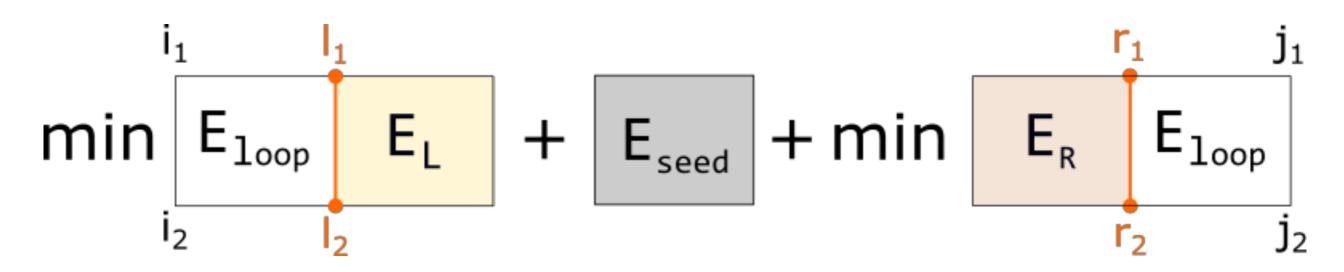
query

eg: sTarPicker RiBlast RiSearch2

Exact memory efficient method

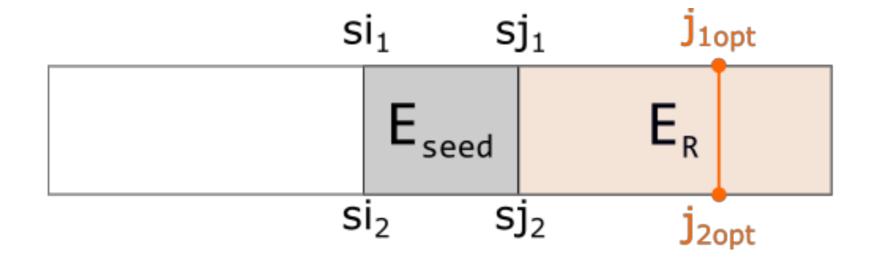


Search minimum over all seeds using:

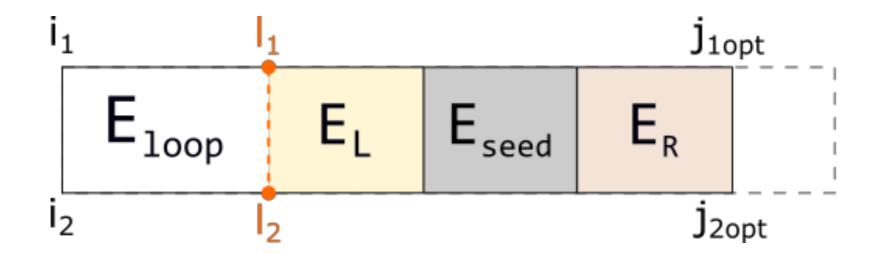


Heuristic method

First find j₁ and j₂ that minimize E_R

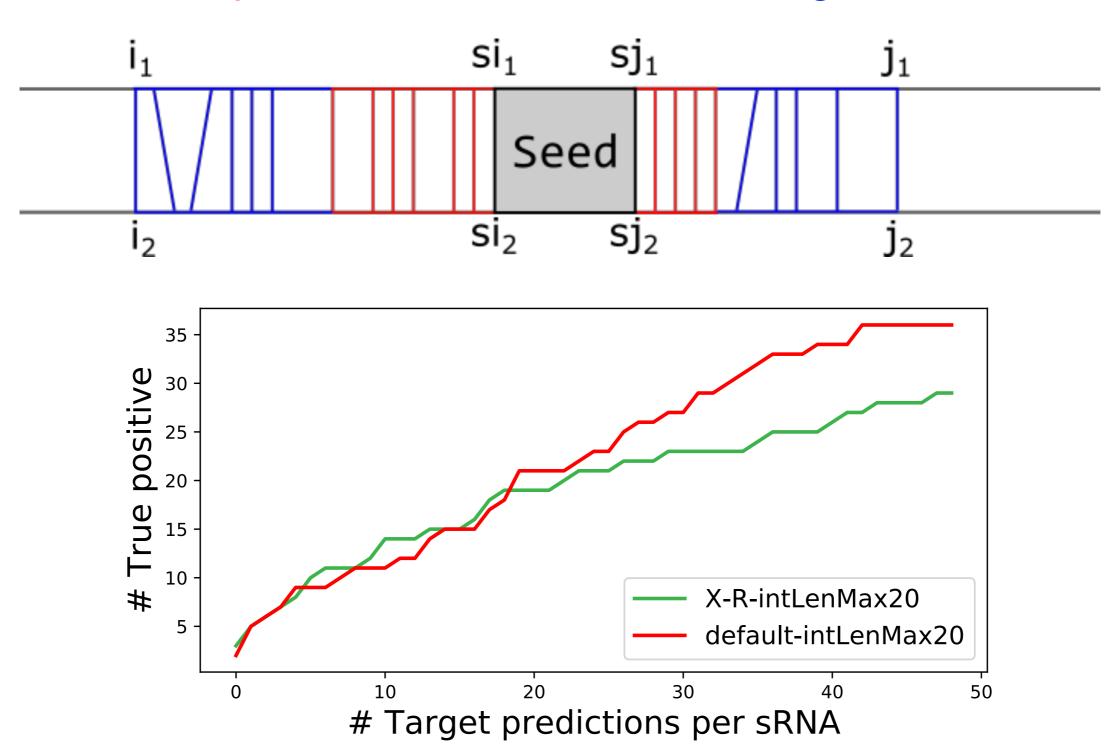


• Then minimize over entire interaction up to j_{1opt}, j_{2opt}

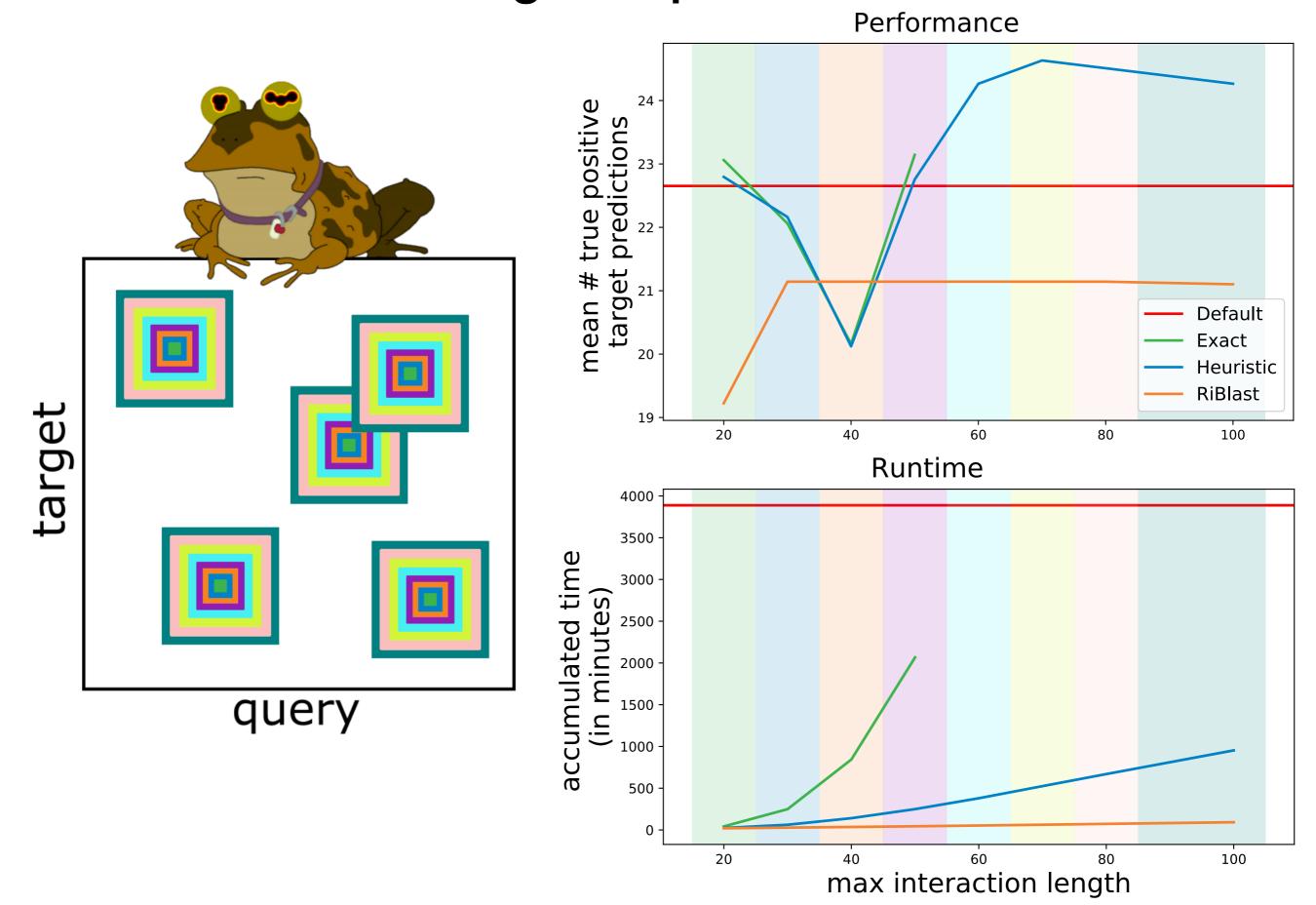


RiBlast method

First do a parallel extension, then thorough extension



Length-dependence



Partition function

Goal: Find probabilities of interactions

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

$$Z_{i,j} = \sum_{S_{A}} \left(\begin{array}{c|c} i & j \\ & \text{no seed} & S_{A} & \begin{array}{c} I \\ & S_{A} \end{array} \right)$$

Idea: remove seed for i

Cases:

