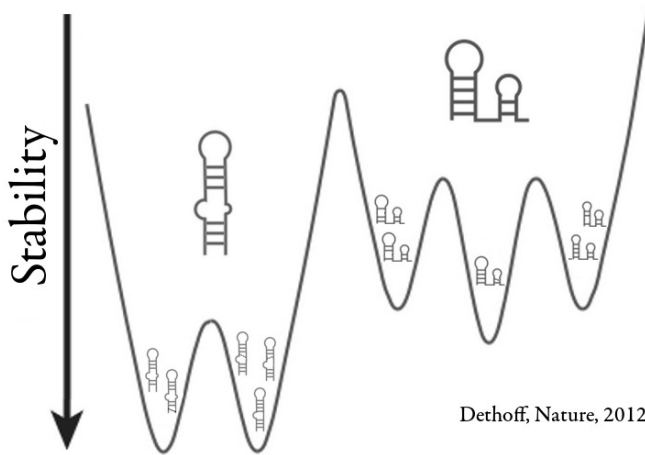


MC-Cons 2.0

by
Gabriel Parent

introduction

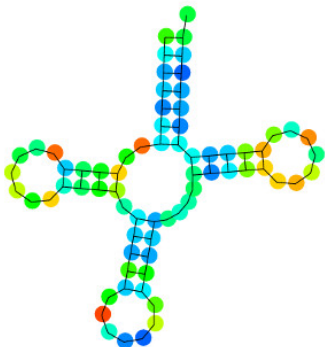
one RNA has many structures



softwares predict structure

- ❖ MC-Fold (Parisien, Major, Nature, 2008)
- ❖ Mfold (Zuker, NAR, 2003)
- ❖ many others

RNA families



tRNA (RF00005)



hammerhead ribozyme HH9 (RF02275)

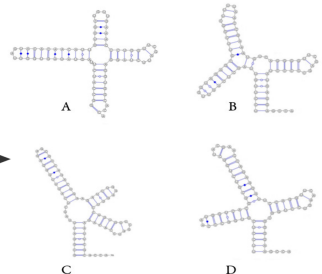
RFam (Nawrocki, NAR, 2014)

what has been done

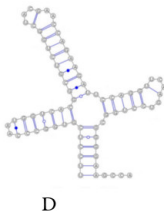
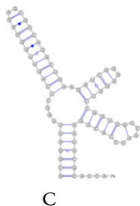
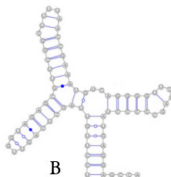
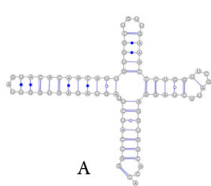
- ❖ MC-Cons (Parisien, Major, Nature 2008)
- ❖ uses fold then align strategy (Gardner, Giegerich, BMC Bioinfo, 2003)
- ❖ good only for small and similar structures

MC-Cons 2.0

RNA consensus



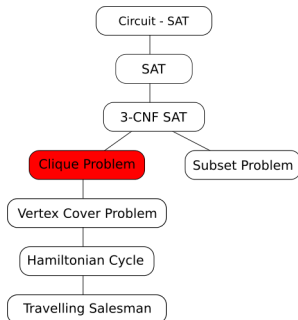
computational approach



	A	B	C	D
A	0	5	3	4
B		0	3	4
C			0	2
D				0

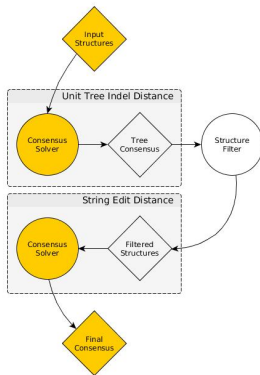
score = 42

it is very hard!



- result is the solution to max-clique
- exponential growth on input size

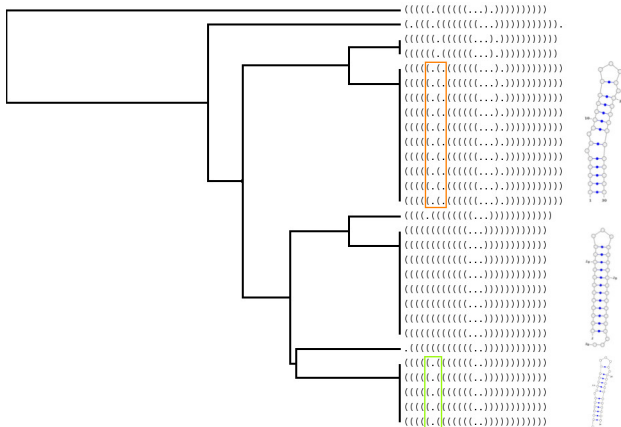
heuristic approach



- genetic algorithm (Barricelli, Methodos, 1954)
- local search

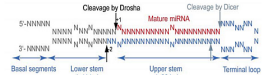
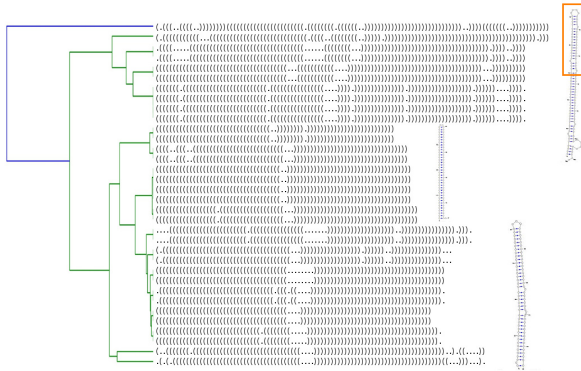
results

Iron Response Elements



RFam
(RF0037)
Nawrocki, NAR, 2014

microRNAs



Han, Cell, 2006

conclusion

summary

- ✦ MC-Cons was slow, now its fast enough.
- ✦ Useful for exploration of RNA families with computational tools.
- ✦ It is easily extensible.
- ✦ Still some tweaking to do with the workflow.

future work

- ❖ Devise and implement better distance functions
- ❖ Multi-objective optimization to explore those distance functions (NSGA2)
- ❖ Implement relevance feedback to score consensus

questions

