ALBERT LUDWIGS UNIVERISTY OF FREIBURG

Master Thesis

Multisite RNA-RNA Interaction Prediction

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Chapter 1

Introduction

RNA molecules play important roles in various biological processes.Their regulation and function are mediated by interacting with other molecules. Forming base pairs between two RNAs, called RNA-RNA interactions (RRI). There are fast and reliable single interaction site (S-RRI) prediction tools like IntaRNA, that often show the additional sites within their suboptimal list, ie. are capable of modelling all sites individually but not in a joint prediction. Many RNAs interact via multiple synchronous, non-overlapping subinteractions (M-RRI), e.g. OxyS-fhlA. The simultaneous prediction of both intra- and inter-molecular base pairing allowing for multiple sites is computationally expensive. Some known approaches are IRIS, piRNA, NUPACK. Here we use a S-RRI prediction tool (namely IntaRNA) for the prediction of M-RRI.

1.1 Biological Background of RNA

- 1.What is RNA
- 2.RNA representation a,c,g,u
- 3.classes of rna
- 4.base pairs of RNA
- 5.RNA secondary structure
- 6.types of rna secondary structure
- 7.nearest neighbor model
- 8.unpair probabilities

1.2 RNA-RNA Interaction

Computational prediction of RNA-RNA interactions (RRI) is a central methodology for the specific investigation of inter-molecular RNA interactions and regulatory effects of non-coding RNAs.RNA–RNA interactions are fast emerging as a major functional component in many newly discovered non-coding RNAs.

- Why RRI

1.3 RNA-RNA Interaction Prediction Approaches

There are several available methods, that can be classified according to their underlying prediction strategies, each implicating unique capabilities and restrictions often not transparent to the non-expert user.
Most computational methods for RNA structure or RNA-RNA interaction prediction are based on thermodynamic models and provide an efficient computation since Richard Bellman's principle of optimality [1] can be applied.

- 1. Approaches that predict RRI

1.3.1 Hybrid

1.3.2 General

1.3.3 Concatenation

1.3.4 Accessibility

- 1. S-RRI, M-RRI
- 2. problems with S-RRI

1.3.5 Adv. and disadv.

Hence we go for, Multi-site RRI optimization based on single-site IntaRNA predictions.

Chapter 2

Multisite Accessibility Based

Chapter 3

Results

Chapter 4

Discussion and conclusion

Bibliography

[1] Martin Raden, Mostafa Mahmoud Mohamed, Syed Mohsin Ali, and Rolf Backofen. Interactive implementations of thermodynamics-based rna structure and rna–rna interaction prediction approaches for example-driven teaching. *PLoS computational biology*, 14(8):e1006341, 2018.