

Non-Coding RNAs: How to find them and how to find targets.

During the last few years, a multitude of regulatory non-coding RNAs (ncRNAs) have been discovered. Many of these act as post-transcriptional regulators by base pairing to a target mRNA, causing mRNA cleavage or translational repression or activation. We will discuss two problems related to ncRNA.

The first is related to the problem of detecting and classifying ncRNAs. Here, one of the main bases are comparison methods that are based on both sequence and structure to determine conserved RNA-motifs, and our LOCARNA tool is currently one of the best systems to perform this task.

The second is the computational detection of possible targets since experimental verification of targets is difficult. Many existing target prediction programs neglect intra-molecular binding, while other approaches are either specialized to certain types of ncRNAs or too slow for genome-wide searches. We introduce INTARNA, a new general approach to the prediction of RNA-RNA interactions incorporating accessibility of target sites as well as the existence of a user-definable seed. INTARNA has a drastically reduced runtime compared to the best available program for the prediction of general RNA-RNA interactions so far.