

In the past years, the common view of RNA has evolved from a more or less boring intermediate in protein translation to a very important player in cell regulation. The changed role was primarily the result of the detection of thousands of non-coding RNAs with many different regulatory functions in post-translational regulation.

The detection of new functional RNAs requires new comparative methods for motif detection since the RNA sequence is much less conserved than the RNA structure. Hence, purely sequence-based methods for finding RNA-motifs such as multiple sequence alignment will fail, and we will discuss various approach (e.g. MARNA, LocaRNA) to sequence-structure alignment developed in our group. Beside finding structural RNAs, we will also discuss the importance of the RNA secondary structure for the regulation of the binding efficiency of RNA-binding proteins like splice enhancers/silencers.