“Computational detection of DNA binding long noncoding RNAs”

RNA sequencing indicates that a majority of transcripts expressed in one cell type is non-coding. Particularly interesting are the long non-coding RNAs (lncRNA), which can combine a myriad of functional domain characteristics of RNA molecules to act as modular scaffolds promoting the interaction of several proteins, RNA and DNA molecules. We are particularly interested in the triple helices—the interaction of RNA with DNA double helices. We currently develop algorithms for detection of triple helices and investigate regulatory roles of lncRNAs differentially expressed during cell differentiation and diseases.