

Silencing has taken biology scientists by storm in the last few years. It is a mechanism by which small RNA molecules control the faith of gene expression, DNA arrangement and specific RNA half life in the cytoplasm. The most important class of molecules in this fabulous story is called microRNA, and the more research is done the more these microRNAs show up in every aspect of molecular biology.

MicroRNAs are deeply involved in development. Their deregulations are most probably involved in (if not responsible for) many cancers. Many believe that a large fraction of the genome is regulated by miRNAs. Viruses encode microRNAs as attack mechanism against the cell, cells respond using microRNAs and siRNAs against viruses (external parasites) infections and transposon replication (endogenous parasites) is limited by microRNAs. MicroRNAs are everywhere and could even be involved in schizophrenia. Therapies based on silencing RNAs could well help in cures to many diseases and could be our very best hope for antiviral agents in any foreseeable future. RNA bioinformatics is in the eye of this storm and if the proper solutions are put forth, these will certainly benefit society as a whole.

MicroRNAs are synthesized from genomic DNA and act as inhibitor of gene function in a sequence specific manner. Three RNA bioinformatics problems are immediately suggested by this statement: (a) which segments of DNA exactly encode the microRNAs, (b) which genes are the targets of specific microRNAs and its converse (c) given a set of targeted genes, which RNA could be targeting them.

In the literature, problem (a) is known as the gene prediction problem, (b) is known as the target recognition problem and (c) has not yet been named because it is described by us for the first time, and we decided to call it the multi-specific oligonucleotide problem. No satisfying solution to any of these problems has yet been given and this thesis is about solving them.