Implementation of K-Factor Algorithm and Its Application to the Identification of microRNA Regulatory Elements

Ji W. Lee[1,2] and Bino John[3]

1 Bioengineering and Bioinformatics Summer Institute, Center for Computational Biology and Bioinformatics, University of Pittsburgh, Pittsburgh, PA 15261
2 Department of Bioengineering, Pennsylvania State University, University Park, PA 16802
3 Department of Computational Biology, University of Pittsburgh School of Medicine, Pittsburgh, PA 15261

MicroRNAs (miRNAs) are endogenous non-protein-coding RNAs that are thought to negatively regulate gene expression. We have developed the K-Factor computational method to accurately identify sequence elements that regulate the expression of miRNAs. Our results indicate that the biogenesis of miRNAs is regulated by numerous regulatory elements that frequently occur in multiple copies in the upstream sequences of miRNAs. The number of transcription factors that regulate human miRNAs also appears to be significantly large. We have also developed an extensible implementation of the K-Factor algorithm within a desktop application written in Java. The framework of the application is constructed to provide extensibility of functionality in the form of plug-ins. The software will be generally useful in the identification of sequence motifs that regulate the expression of gene sets of interest.