RANK AGGREGATION OF PUTATIVE microRNA TARGETS

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MicroRNAs (or miRs) are noncoding RNAs whose role is to repress translation by regulating gene expression through binding to mRNA targets. There are computational algorithms for miR target predictions, but their results vary. Thus, it would be useful to consolidate these results to have a greater degree of certainty before engaging in costly experiments. We studied three popular algorithms, miRanda, TargetScan, and PicTar, systematically through the use of three measures of similarity and a statistical test on the gene ontology categories. Two composite statistics were also devised to combine and rank the composite target list. In addition, a cross-entropy Monte Carlo method is also explored for solving this combinatorial optimization problem. We applied these methods to all human miRs. Our results indicate that TargetScan and PicTar tend to have a greater degree of similarity. We also demonstrate that our rank aggregation methods can be useful tools for short listing genes for downstream experiments. This is joint work with Jin Zhou.