Systematic study on microRNA regulation network from next generation sequencing

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MicroRNAs (miRNAs) are small non-coding single-stranded RNAs that regulate gene expression at post-transcriptional level through translational inhibition and mRNA degradation. Accumulated evidence demonstrates that miRNAs play significant roles in regulating genes that drive cancer progression and drug resistance.

Next generation sequencing technology has more advantages on the discovery of non-coding and small RNA than microarray without the limitations of probes and is also able to discover novel miRNAs when aligning reads to the genome. Here, we present an approach for the integration study of miRNAs and RNA sequencing data. This pipeline includes general sequencing data analysis pipelines for miRNA-seq and RNA-seq, and also an integration module, which are all implemented in a data analysis and integration framework, Anduril [Ovaska et al. Genome Medicine 2010].

Our objective in this study is to identify candidate miRNA-gene pairs that are highly correlated at expression level and also from micro-RNA target prediction. In addition, we include exome-sequencing data to study the effects of variants in miRNA-mRNA binding regions on their binding affinities. Candidate pairs are visualized at biological networks in a personalized mode.

We report here the candidate pairs with survival association in vivo breast cancer samples and personalized miRNA regulation networks. Our results show this approach is useful and efficient in finding miRNA regulation behavior which has survival effects in breast cancer and also discovering the impact on its regulation from genetics variation.