



Integration of high throughput miRNA and mRNA data through weighted gene co-expression network analysis



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ABSTRACT

miRNA regulates mRNA levels through base-pairing, by inducing transcript degradation or by inhibiting translation. Many high throughput biological experiments simultaneously assess global miRNA and mRNA profiles and seek to find coordinate expression modifications in both types of data. There are many computational algorithms to integrate miRNAs with their putative gene targets. We developed a method using weighted gene co-expression network analysis to identify gene targets for each miRNA. This method is illustrated with an example in a renal carcinoma dataset from patients with matched normal and tumour samples. We also find that by using WGCNA to define highly correlated genes into a number of modules greatly alleviates the multiple testing problems that plague standard gene-centric methods and it provides a novel integrative view of miRNAs and their putative genes.

Host: Van Savage, Ph.D.

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