Public Abstract
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In this present era of high-throughput technologies, meta-analysis is being widely used to integrate multiple similar high throughput studies. Here we propose a novel framework for applying meta-analysis techniques on expression data for gene function characterizations and biological networks construction like the gene regulatory network. In particular, we developed a prototype for gene function annotation using multiple microarray datasets and tested the performance of our model using yeast and human microarray datasets. Our results show significant improvement in functional annotation in general. We further applied the same meta-analysis method on the Arabidopsis plant in a collaborative project with Monsanto Company to construct regulatory network for Arabidopsis. Our method shows significant improvement than any other existing methods for inferring gene regulatory network.

Beside meta-analysis, I have invested a great deal of efforts in developing PRIMEGENS, an open source software, which could be used for large-scale primers and probe design for PCR, DNA synthesis, qRT-PCR (gene expression), and targeted next-generation sequencing (454, Solexa, Agilent sure-select technology etc.) for normal or bisulfite-treated genome. We recently extended its functionality including microarray probe design to cover genome-wide CpG islands in human, Taqman probes and discriminating transcripts from its multiple homologs or splice variants based on gene-specific unique fragment in soybean genome.