

## Genome-Wide Discovery of cis-Elements in Promoter Sequences

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Gene expression is regulated by transcription factors interacting with specific functional sequence motifs in promoters, UTRs and introns. Identifying functional motifs is essential for understanding the effect of genetic variations in rice lines, engineering of plants with specific expression pattern and for systematic reconstruction of the gene network. The problem of regulatory motif discovery is a classic bioinformatics challenge and many solutions have been proposed. We proposed a simple and robust method discovering motifs in DNA sequences using gene expression data. To assess the accuracy of the predictions we designed a benchmark which was used to compare our method with other approaches. The method is illustrated with examples of tissue specific and stress-related motifs in rice genome.

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New technologies produce terabytes of valuable information about rice: genome sequences of thousands varieties and cultivars, gene expression in different tissues, developmental stages and environments and automated phenotyping measurements. In addition, the rice knowledgebase is enriched by studies in other species using orthologous relationships between genes. Integration of such diverse pieces of data will enable many discoveries of gene-trait associations and will lead to new hypotheses on the mechanism of gene function. Organizing this information into proper data structures, providing visualization and basic analysis tools are challenging tasks due to the volume and complexity of the data. The International Rice Informatics Consortium (IRIC) aims to facilitate access to information for the broad rice scientific community by developing an IRIC information portal. The initial phase of development will be discussed.