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*Comparative Analysis of Clustering Techniques for RNA-seq Data*

RNA sequencing (RNA-seq) is a deep sequencing-based approach for transcriptome profiling. RNA-seq provides counts of transcripts, offering a method to quantify gene expression. Despite the vast availability of RNA-seq data, interpreting these data in their biological context remains a challenge. Using clustering algorithms, a systematic investigation of relationships between genes can be carried out to identify genes sharing similar expression patterns. A comparative study of three clustering techniques is presented using RNA-seq data obtained from a gene expression study looking at the response of maize to nitrogen limitation. Clusters of genes identified by each method are analyzed for biological significance.