A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in Saccharomyces cerevisiae

RNA-seq, has recently become an attractive method of choice in the studies of transcriptomes, promising several advantages compared with microarrays. In this study, we sought to assess the contribution of the different analytical steps involved in the analysis of RNA-seq data generated with the Illumina platform, and to perform a cross-platform comparison based on the results obtained through Affymetrix microarray. As a case study for our work we, used the Saccharomyces cerevisiae strain CEN.PK 113-7D, grown under two different conditions (batch and chemostat). Here, we assess the influence of genetic variation on the estimation of gene expression level using three different aligners for read-mapping (Gsnap, Stampy and TopHat) on S288c genome, the capabilities of five different statistical methods to detect differential gene expression (baySeq, Cuffdiff, DESeq, edgeR and NOISeq) and we explored the consistency between RNA-seq analysis using reference genome and de novo assembly approach. High reproducibility among biological replicates (correlation ≥0.99) and high consistency between the two platforms for analysis of gene expression levels (correlation ≥0.91) are reported. The results from differential gene expression identification derived from the different statistical methods, as well as their integrated analysis results based on gene ontology annotation are in good agreement. Overall, our study provides a useful and comprehensive comparison between the two platforms (RNA-seq and microarrays) for gene expression analysis and addresses the contribution of the different steps involved in the analysis of RNA-seq data.

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