Summary: In this chapter, we discuss the Transcriptogram method for statistically analyzing differential gene expression in a genome-wide profile. This technique suggests a method to hierarchically interrogate the data and, subsequently, narrow down to gene level. We present the method, discuss its reproducibility and enhanced signal-to-noise ratio, and discuss its application in investigating time series data as in cell cycle, therapy gene target identification, lineage and tissue classification and as a powerful test to identify error and assess the quality of normalization procedures. We finally present the software ready for download and discuss the R-plugin for BioConductor.

For the entire collection see Zbl 1470.92007.

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92-XX Biology and other natural sciences
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References:


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