Explaining the Sources of Discrepancies in Gene Expression Profiles Generated on three Whole-Genome Gene Expression Microarray Platforms

Maouche Seraya
(maouche@chups.jussieu.fr)

INSERM UMR S525, Faculté de Médecine Pitié-Salpêtrière, 91 Boulevard de l'Hôpital, Paris, 75013, France

Previous small-scale cross-platforms comparative studies have discussed several issues of microarraybased gene expression data, including comparability between platforms, repeatability between labs, performance, and concordance to non-array based gene expression. Recently, results of the MicroArray Quality Control (MAQC) project (**1**), the first large-scale crossplatforms study conducted with the goal of establishing quality control metrics for microarray data and of assessing the reliability of gene expression profiles generated on different platforms, showed that using standardized procedures, microarray results from different platforms are reproducible. We conducted a study to compare gene expression data generated on three platforms: Illumina Bead Chip Human-6 V1, Affymetrix HGU133plus 2.0, and the academic RNG/MRC two-color chip. 10 RNA samples from human monocyte and monocyte-derived macrophage were hybridized in parallel to the 3 platforms. In addition, a list of differentially expressed genes generated using a larger number of hybridizations to the RNG/MRC platform was included in the cross-platforms comparisons and used as a reference to assess the 3 platforms.