Handling global expression data from multiple microarray platforms

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Concordance between genomic expression profiles obtained on different DNA microarray platforms may be impaired by multiple concomitant factors, including non-homogeneity in data analysis procedures. To address this issue, we explored growth factor-induced transcriptome changes using the same series of mRNA samples with two types of DNA microarrays, respectively spotted cDNAs and high-density oligonucleotides (HDO).
Unigene database matching allowed us to estimate a total of over 25'000 genes explored, of which 6000 covered by both platforms, thus providing a wide basis for comparison and systematic cross-validation. A common procedure was specifically developed to minimize differences in data analysis between the two platforms. In particular, regulated genes were identified by a 'tunable' statistic test weighing expression change and duplicate variability across the whole experiment.
Data permutations and extensive false discovery analysis allowed accurate, platform-specific optimization of the test. Cross-validation was observed as a generally good correlation coefficient between the time-course responses observed in the two platforms. Interestingly, a similar extent of correlation was observed for genes redundantly explored within the same microarray, which provides evidence of substantial homogeneity between the microarray platforms examined.