Quantifications of Cross Hybridization on Oligonucleotide Microarrays

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Cross hybridization on microarrays generates signals from unintended genes, which presents a special challenge in gene expression profiling studies since it directly leads to false positives. However, little is known about the extent of cross hybridization and why certain probes are particularly prone to cross hybridization. Recently, we have developed a free-energy model of binding interactions on oligonucleotide arrays that can decompose the observed probe signals in terms of the effects of gene-specific and generic non-specific binding. We analyzed the data set provided by Affymetrix Inc., which followed a Latin square design with 14 genes spiked-in at various concentrations. Around 31 probesets show reproducible response to the spiked-in genes. In most cases, we were able to extract the amount of cross hybridization signals and identify the source, i.e., the fragments of spiked-in genes that matches the cross hybridizing probes. These findings demonstrate the utility of our model for identifying spurious cross-hybridization signals and obtaining robust measure of gene expression levels.