

*Assessing Effect of Cross-Hybridization on Oligonucleotide Microarrays*

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A prediction method that assess non-specific binding based on sequence similarity between probe and target sequences would aid in understanding and interpreting of global expression profile analysis. In this work we consider a linear hybridization model, and estimate the binding coefficients using the quadratic programming technique. We demonstrate that the estimated binding coefficients are correlated with the similarity of nucleotide sequences between probes and targets. We show that cross-hybridization can be detected for the probes that have 7 or more nucleotide similarity with target. We introduce binding patterns technique for predicting the binding coefficients. Our results suggest that further development based on nucleotide sequence can be fruitful.