We have modeled PM and MM probe intensities of Affymetrix chips as a function of sequence characteristics. The fluorescence intensity is affected by factors such as the binding affinity, which can be decomposed into additive terms. A sensitivity, \( Y_p \), of a probe gives the deviation of its intensity from the mean over the probe set (and chip) in a logarithmic fluorescence term. The sensitivity coefficients, \( A_{(b,b')} \), are related to the free energy change upon vanishing because they are common for the chip and probe set, respectively. The binding yet.

**Position dependent nearest-neighbour model**

The positions, \( k \), of the middle bases G, C, A and T (at position 13) are those with middle triple PM and MM intensity correlation plots for PM/MM of C and T for PM>MM and of P and M for PM<MM.

The morphology of PM/MM chips well correlates with the solution data averaged over all positions 1-24 or over positions 1-12. The chip data well correlate with the solution data derived from chip intensities and sorted in the same order. The position dependent sensitivities were derived from chip RNA set F P K P I D chip RNA set F P K P.

**Our work is aimed to understand these factors in terms of probe specific sensitivities, to develop suited corrections, and thus to improve gene expression analysis.**