BIOL 6930/Assignment #2: Microarray Normalization

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Multiple factors contribute to the variation in sample processing, such as diverse protocols, different labeling efficiencies. These factors can result in artificial differences between replicate samples. Proper normalization methods are necessary to reduce these systematic effects while maintaining true biological variability. In other words, normalization adjusts the individual hybridization intensities to balance them appropriately so that meaningful biological comparisons can be made.

There are many approaches to normalizing expression levels, such as total intensity normalization, linear regression analysis, log centering, and Chen’s ratio statistics, etc. Three techniques of normalization addressed here are MAS 5.0, Robust multi-chip normalization (RMA), and probe logarithmic intensity error estimation (PLIER). GeneChip MAS 5.0 normalization average difference with biweight calculation. Region-based scaling of intensity values by dividing the regions and scaling each to identical intensity value. RMA normalization use a chip background estimate and subtract from the PM probes normalized values are log transformed because probe effects are additive on a log scale. PLIER operates by finding target responses for each experiment I and feature responses for each feature j that minimize the function. MAS 5.0 normalization is scaling-based, while RMA and PLIER normalization are quantile-based.