Robust multiarray average (RMA) normalization is a method for microarrays that performs background subtraction and correction, quantile normalization across arrays, averaging of probe-level feature intensities extracted from .CEL files using the Affymetrix platform, and quality assessment. The RMA background correction step includes a convolution model in which the observed signal for each probeset is broken into components of true signal and noise. RMA normalizes and summarizes the probe level information without the use of the information obtained in the Mismatch (MM) probes. RMA does not use the Mismatch (MM) probes, because their intensities are often higher than the match probes, making them unreliable as indicators of non-specific binding. RMA values are in log2 units.

GeneChip RMA (GC-RMA) is an improved form of RMA that can use the sequence-specific probe affinities of the GeneChip probes to attain more accurate gene expression values. GC-RMA further introduces an adjustment for the presence of nonspecific hybridization that improves accuracy (relative to RMA) while maintaining large gains in precision.

Microarray Suite v 5,.0 (MAS5.0) normalization is a method which normalizes each array independently and sequentially. MAS5.0 calculates the difference between Perfect match (PM) and Mismatch (MM) probe values to obtain a “robust average”. Robust average is insensitive to small changes from any assumptions made. PM probes consist of oligonucleotides affixed to the array surface that bind the fluorescently labeled sample if transcripts corresponding to probes are expressed. Mismatch (MM) oligos are designed with an intentional mismatch and are used to define background signal.

RMA is more accurate and precise than MAS5.0 but may result in false negatives at low expression levels, a situation that is improved by the GCRMA algorithm. MAS 5.0 software yields a high standard deviation, particularly for transcripts expressed at low levels, while RMA has a dramatically improved measurement across a broad range of signal intensities.

References

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