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Normalization is the technique of reducing (or limiting) nonbiological variation in signal intensity levels in order to detect biological changes in gene expression correctly. Normalization aims to eliminate global effects, which are visible in plots that show all of the data for a slide or slides. Regarding microarray data, one form of normalization is the RMA (Robust Multi-array Average) normalization. This method of normalization acquires all chips that have the same background and value distribution. Another method of normalization is the MAS5.0 normalization, which is the Affymetrix Microarray Suite (MAS). Affymetrix GeneChips are made up of a number of probes, each of which is designed to quantify the amount of expression of a certain genomic sequence. Each probe is made up of hundreds of small 25-mer oligonucleotide strands that exactly match the sequence of the target mRNA. Opposing RMA normalization, MAS5 compares perfect match probes instead of mis match probes to obtain the true signal value. The true signal value is equivalent to the Tukey biweight, which is a procedure that consists of an outlier rejection as well as weights. This procedure uses the median weights and outlier rejections.