Kinlyn Williams

Bioinformatics

Dr. Pawar

Taesung Park et. al describe normalization as the process of removing some sources of variation which affect the measured gene expression levels. Normalization is used in microarray technology. This form of technology simultaneously monitors the expression levels for thousands of genes. Robust Multi-array Average (RMA) is a normalization procedure that assumes all chips have the same background as well as distribution of values. By iteratively reweighting least-squares or median polish, RMA fits the additive model.

MAS5.0 is another form of normalization which gives p-value for expression data. MAS5.0 compares PM and MM probes as well as normalizes each array sequentially and independently. This form of normalization uses data from mismatch probes that calculate a “robust average”. MAS5 model uses a measured value or N+P+S where N is noise, P is probe effect and S is signal. The MAS5.0 is most commonly used method for Affy chips.