Laura Cortes

**Overview:** Microarray data must be normalized to account for non-biological differences between samples (differences in RNA, differences in labeling). MA plots can be used to determine how well normalized data sets are.

**Background Correction for Microarrays (within chip)**

**Mas 5.0:** Normalizes each array independently and sequentially and uses both perfect match and mismatch probes (these are used to create robust average by subtracting MM from PM). May ignore a gene signal even if it is strong if it is normally distributed. The chip is broken up into rectangular regions and the lowest 2% is chosen as background for that region and the SD for the lowest 2% is chosen as noise. The background and noise are the weighted average of that zone. This method has been mostly replaced by RMA or LOESS.

**Robust Multi-array average (RMA):** depends on linear statistical model and parameters are estimated ad-hoc using perfect matched probes (PM). Noise is modelled normally while the signal is exponential, and the observed signal is assumed to be the result of both. The correction is signal divided by observed value.

**Quantile:** Fast. Assumes all histograms of probe intensities are made identical and uses median-centering to normalize all quantiles.Normalization is performed by averaging quantiles across chips, thus reducing expression variability. Performs well compared to other methods and accounts well for bias.

**Reference:**

bmbolstand.com