**Robust multiarray averaging (RMA)** is an expression matrix creation algorithm based on Affymetrix data, it converts AffyBatch object to an ExpressionSet. Normalization in microarray is the adjustment of microarray data for effects which arises from variations in technology rather than biological differences between the printed probes and RNA samples. Microarray needs to be normalized to account for technical variation between the arrays. Robust multiarray averaging (RMA) initial value is based on a simple moving average, RMA values are in log2 units, it is a microarray normalization which normalizes, corrects the background and reports probe level data without relying on the information gained from Mismatch probe (MM probe).

**Mas5.0 Normalization** normalizes each array independently and sequentially,

calculates a robust average of the (logged) Perfect Match PM- Mismatch MM values; the variation is observed as it increases at low signal strengths and generating extra noise by subtracting the MM values from their PM partners. It provides an algorithm that integrates the signals from the various Perfect-Match (PM) and Mismatch (MM) probes that target each transcript into a single value that precisely depicts its concentration. The result is referred to as the "detection p-value" and is utilized to generate a recognition call that marks the transcript as Present, Marginal, or Absent (P/M/A) may cause some confusion. MAS5 values are not directly comparable.

Reference

Robson, S. (2008, July 30). *RMA and GC-RMA Normalisation*. Retrieved February 14, 2022.

Bolstad,B., Irizarry,R., Åstrand,M. and Speed,T. (2003) A comparison of normalization methods for high density oligonucleotide array data based on variance and bias. *Bioinformatics*, in press.