RMA normalization is a technique for microarrays that corrects, summarizes, and normalizes probe level information from CEL files using the Affymetrix platform. RMA stands for robust multiarray averaging. It has an accuracy that is comparable to MAS 5.0 software, but a greater precision. Normalization is the process of correcting two or more datasets before comparing their gene expression values. RMA normalization has steps for background correction, quantile normalization across arrays, a probe-level model for each probeset across multiple arrays and quality assessment.

MAS5 normalization is a method introduced by Affymetrix. It normalizes each array independently. MAS5 determines the difference in perfect match and mismatch oligonucleotides to gather a robust average. This summarizes the signal from a particular set of probesets across a certain gene. It has a lower precision than RMA normalization.