# Author: Sanders, Date: 02/15/2022, Purpose: Defining RMA and Mas5.0 normalization

RMA is an acronym which stands for Robust Multiarray Averaging. RMA normalization is a method of microarray normalization and summarization found in the Affymetrix Microarray Suite (MAS). RMA uses a model-based background correction, quantile normalization and a robust to complete its tasks. Normalization is used to remove non-biological variations measured in microarrays so that biological differences in gene expression can be detected accurately. RMA takes information from microarrays and background corrects, normalizes, and summarizes the probe level information without the use of the information obtain in the Mis-Match probe.

Mas5.0 is used to provide an algorithm that combines the signals from multiple Perfect-Match (PM) and MM probes. MAS5.0 does this by normalizing the arrays being analyzed independently and sequentially. It calculates the robust average of the PM-MM values unlike other models which normally ignore the MM values. MAS5.0 can return two values to generate the p-score. The p-score is a value that assesses the reliability of each expression level. MAS5.0 finds this value but taking an estimate of transcript concentration and a measure of how much the software actually believes creating a margin within the data.