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RMA normalization

Mas5.0 normalization

What is it, what it does, how does it work?

A microarray is a grid of DNA segments of known sequences that is used to test and map DNA fragments, antibodies, or proteins. To interpret the data generated on these microarrays, microarray analysis techniques are needed. These techniques make it easier to analyze larger outputs of data that could be generated during microarray experiments. Robust Multi-array Average normalization is an algorithm used for preprocessing. There are three steps in preprocessing: background correction that removes local artifacts and noise, normalization that removes array effects, and summarization that combines probe intensities across arrays.

Mas5.0 normalization is described as a sensitive and selective algorithm used to identify differentially expressed genes. This algorithm was developed to combine signals from the multiple Perfect-Match (PM) and Mismatch (MM) probes into a single value that sensitively and accurately represents its concentration. Mas5.0 does this by calculating a robust average of the PM-MM values. It was important to develop this algorithm because RMA normalization overlooks the mismatch probes. This algorithm is often criticized for its high false positive rates.