Functional Genomics
Department of Computer Science and Mathematics
Lebanese American University

Robust Multichip Average Algorithm

Mohamed Mehdi MERBAH

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RMA Summary

We are often required to use a normalization technique to account for differences in gene expression that are due to defects in the experimental equipment, procedure or very large outliers that might eventually affect out final analysis.
RMA is a method for background correction and normalization, the algorithm creates an expression matrix from Affymetrix data. The general approach to RMA works such that all raw probe intensities are background corrected, log2 transformed and normalized with quantile normalization. Once we have normalized data we calculate probe intensity levels and summarize the data.
And so we could summarize the algorithm in the following steps:

- **Background Correction:** an initial-step where the probeset data are corrected to remove all local noise, this is done so that any probe intensity measurement is not affected by adjacent probe measurement. This discrepancy in measurement is referred to as the *probe-effect*.
- **Quantile Normalization:** we can now use the background-corrected probe data. The latter are normalized so that the measurements across all arrays are comparable. We are essentially making all the probeset distributions the same.
- **Probe Level Intensity Calculation:** This uses the backgournd-corrected, normalized and log-transformed probe intensities within a linear model. We use a technique called median-polish to estimate the model's paramters.
- **Summarization:** Now that we have calculated the adjusted intensity values for all probes, we can combine those that refer to the same gene so as to get a final intensity value for each gene.

References

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