An Exploration of Extensions to the RMA Algorithm

張凱明
AstraZeneca (AZ) Pharmaceutical, UK

Abstract

There is frequently a requirement to analyze microarray data at one or more interim stages throughout the course of a study. The RMA algorithm for pre-processing Affymetrix microarray data has an undesirable property that the gene expression intensities on a microarray change when re-pre-processing is necessary due to the inclusion of additional microarrays at different stages of the study.

The use of the RMA algorithm can also be limited by available computer memory. We describe and explore the properties of the RMA+ algorithm based on building an RMA model on a reference set of microarrays and storing the parameters of this model fit. The gene expression values for subsequent microarrays are calculated from these parameters without changing the gene expression values of previously calculated microarrays. We also propose an extension of the RMA+ method, RMA++, which gives a better approximation to RMA.