

DNA Microarrays revolutionized the field of genomics, enabling biologists to study thousands of genes simultaneously. In this monograph we address two major problems in this area. First, how to restore the missing data on the DNA Microarrays, which was corrupted due to various factors. Second, how to condense the enormous information obtained. We introduce several tools from linear and multilinear algebra, and other areas as well, to study systematically these problems. We give explicit algorithms and their analysis to solve these problems. We also survey and compare our methods to other existing methods. Although our examples are from bioinformatics, we are confident that the methods of this monograph apply as well to other branches of science, engineering and finance. The monograph is appropriate for readers from bioinformatics, computational biology, or engineers, who are interested in deep theoretical framework motivated by applications.



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