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Clustering, Fixed Rank Approximation Algorithm, and DNA Microarrays.

In this talk we cover the basics of DNA Microarrays technology and dimension reduction techniques for analysis of gene expression data. Also, we discuss how biological information in gene expression matrix could be extracted, using singular value decomposition method. We will use inverse eigenvalue problem framework in order to introduce Fixed Rank Approximation Algorithm (FRAA) for imputing missing genes in DNA Microarrays. We conclude the talk by some simulation using FRAA and K-means clustering and compare our result with most recent imputation algorithms. (Received September 28, 2005)