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Gene microarray chips measure, simultaneously, the expression levels of every gene of an organism. Comprehensive gene data is useful whenever one wishes to find clusters of genes with similar function, or to classify biological objects or events. Microarrays have been used to study the genetic causes of disease and even to classify and diagnose different types of diseases, such as cancerous tumors. Unfortunately, however, microarrays yield very noisy data. Thus, clustering based on microarray data requires an especially robust measure of the similarity between expression patterns of genes. We propose a correlation coefficient based on Tukey's Biweight S-estimate of shape to analyze the data we extract from microarrays. (This research was carried out in the Pitzer College REU program.) (Received August 30, 2005)