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Sanju Vaidya* (svaidya@mercy, edu), 555 Broadway, Dobbs Ferry, NY 10522. *Analysis of Gene Expressions Using Young Tableaux.*

In the last ten years, DNA microarrays (DNA chips) have been used to analyze functions of various genes. They are used to study gene expression patterns in many diseases such as cancer and diabetes. The main goal in analyzing microarray data is to identify genes differentially expressed across groups of samples or experimental conditions. We will use properties of permutations and Young tableaux to identify the pattern in data series of genes generated by microarray measurements. Young tableaux are certain tabular arrangements of integers. In the third volume of his book on the Art of Computer Programming, Knuth has refined a sorting procedure originated by Robinson and Schenstead. Using the Robinson- Schenstead- Knuth procedure, we will associate Young tableaux to permutations corresponding to data series of genes. We will use the concepts of algorithmic compressibility of Ahnert et al, formula of Frame et al for computing the number of tableaux and theorems of C. Schenstead about the length of the longest increasing and decreasing subsequences of a permutation to identify genes that are significantly related to the target disease. The analysis of gene expressions can lead to improved diagnosis and individualized medical treatment as well as earlier detection of diseases. (Received August 23, 2009)