1095-62-31   **Michael Waterman***, msw@usc.edu. *Sequence Comparison Without Alignment.*

Traditionally the comparison of biological sequences has been based on the order of the letters in the sequences. A drawback of this class of methods is the running time of algorithms designed to discover significant similarity between the sequences. In this talk some simple statistics based of counts of k-letter words will be presented along with some of their unusual properties. (Received August 19, 2013)