

1086-05-2681 **Noah Williams*** (williann@uwec.edu), 5520 Woodcrest Highlands Rd., Eau Claire, WI 54701.
The Deletion-Insertion Model Applied to the Genome Rearrangement Problem. Preliminary report.

Many mathematical models have been developed to help solve the genome rearrangement problem, whose goal is to find the optimal sequence of mutations that transforms one genome into another. However, few of these representations isolate situations in which deletions and insertions are the primary mutations that occur. We created the Deletion-Insertion model, which considers genome rearrangement exclusively by deletions and insertions, in order to provide bioinformaticians with a tool for studying diseases, like Neurofibromatosis, that can develop as the result of a single deletion or insertion within a chromosome. In this research, we strive to strengthen our model by developing an algorithm for the rearrangement of one genome into another using the fewest possible number of deletions and insertions. Additionally, we analyze the efficiency of several algorithms that compute an upper bound for this optimized distance. Our results contribute to the understanding of mutation-based diseases and of the evolutionary relationships that exist between organisms and their biological ancestors. (Received September 25, 2012)