DNA and Traveling Salesmen: Using *Mathematica* as an Aid in Algorithmic Graph Theory

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Abstract

DNA Sequence Alignment and the Traveling Salesman Problem (TSP) are important problems in algorithmic graph theory. The Sequence Alignment Problem takes two incomplete strands of DNA and attempts to match them by inserting, deleting, or changing bases, then giving a score in the end. The solution can be reduced to finding the minimum weight path between two specified points on a directed graph known as the Alignment Graph. This is done by using a dynamic programming algorithm called the Needleman-Wunch Algorithm. The TSP is the classic problem of finding a shortest tour visiting each city once and only once in some geographic region. TSP is NP-hard, but a polynomial-time algorithm by Arora[1996] finds good approximate solutions. I will describe both algorithms and present *Mathematica* implementations.