**Limit:**

At array sizes higher than 22000 x 22000 the algorithm becomes impractical.

**Observations:**

The algorithm drastically improved in performance when I used an array to calculate the alignment score of two characters, instead of using a function.

The DP/traceback algorithm takes about 7 secs to run on the given mitochondrial DNA. The recursive algorithm takes MUCH longer.

**Scientific Impact:**

The algorithm can be used to match any DNA sequence to find out the degree of similarity between them based on the score. This can be useful in finding if two species share any ancestors or close in the evolution timeline they might be, as seen in the case of human vs ape studies.