To test the limits of this algorithm I had it try to compute the differences of increasingly large sequences randomly adding a, c, g, or t as it went. I found that the only real limit on this algorithm was memory when it came to the recursive traceback method. I ran out of memory if my algorithm ran 50 times after to sequence was 100 characters or more. I also reached the limit if I tried to run with a sequence larger than 900 characters. I also found that even after the size of the sequences got past 100 the runtime never went past 10 seconds even when I got to size 900.

The scientific impact of this efficient algorithm is that it allows us to analyze entire DNA sequences in a relatively short amount of time which would be impossible for a recursive method of analysis. The only limitation is memory which is not a problem when passing small sections of the sequence at a time.