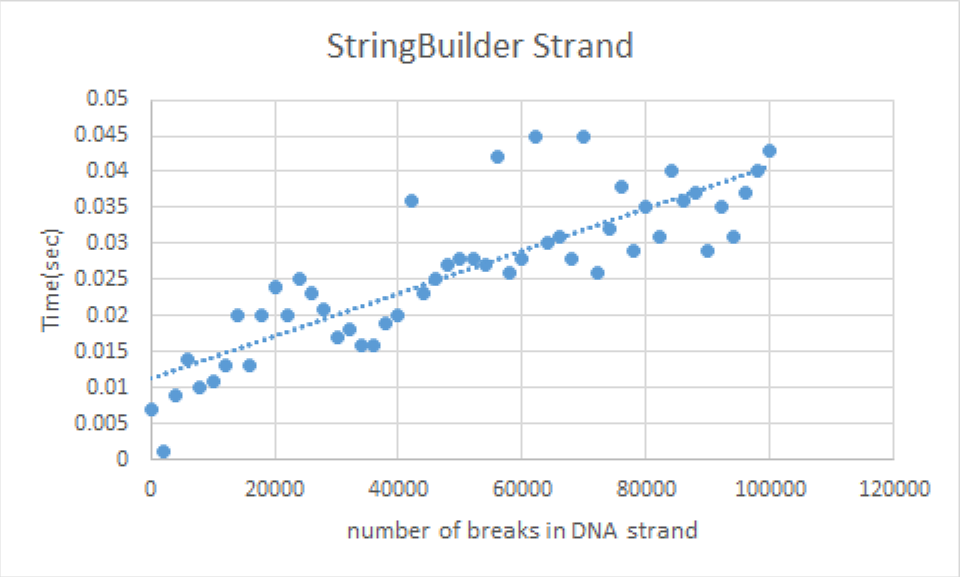
Amber Strange

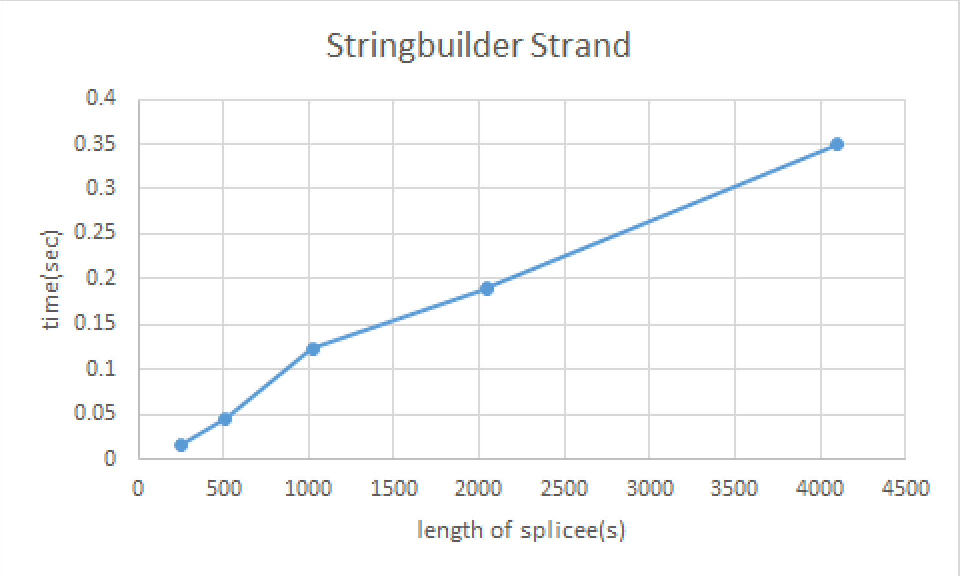
CS201 DNA ANALYSIS

To test these hypotheses, (to change the number of breaks) I created a DNA Strand using a stringbuilder and appending different numbers of the splicee in NewBenchmark.java. Otherwise I created the strand and used the DNA Benchmark code to change splicee length.

NONLINKED HYPOTHESIS:

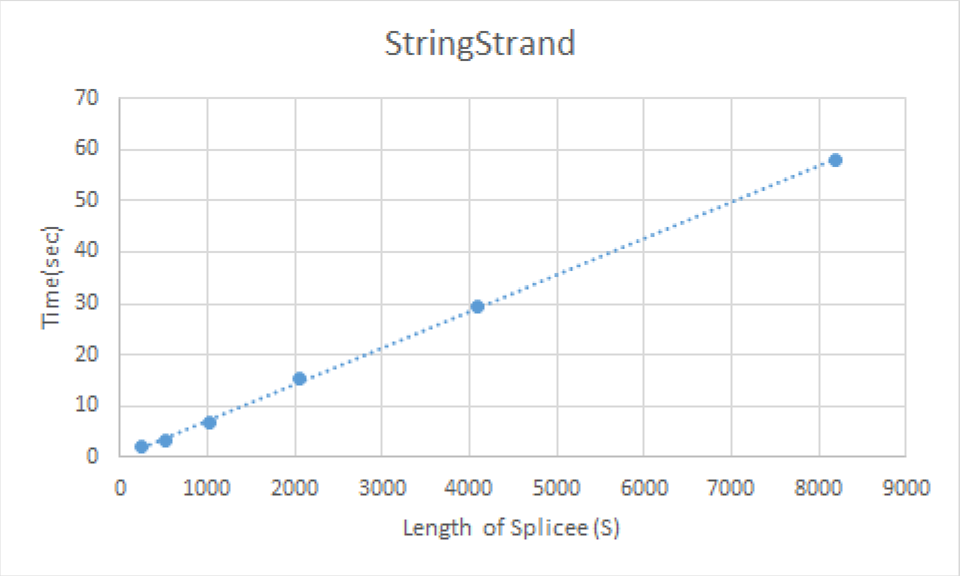


Graph showing a nearly linear relationship between number of breaks and time(O(b) when splicee length(155) and length of strand(5,000,000) is constant).

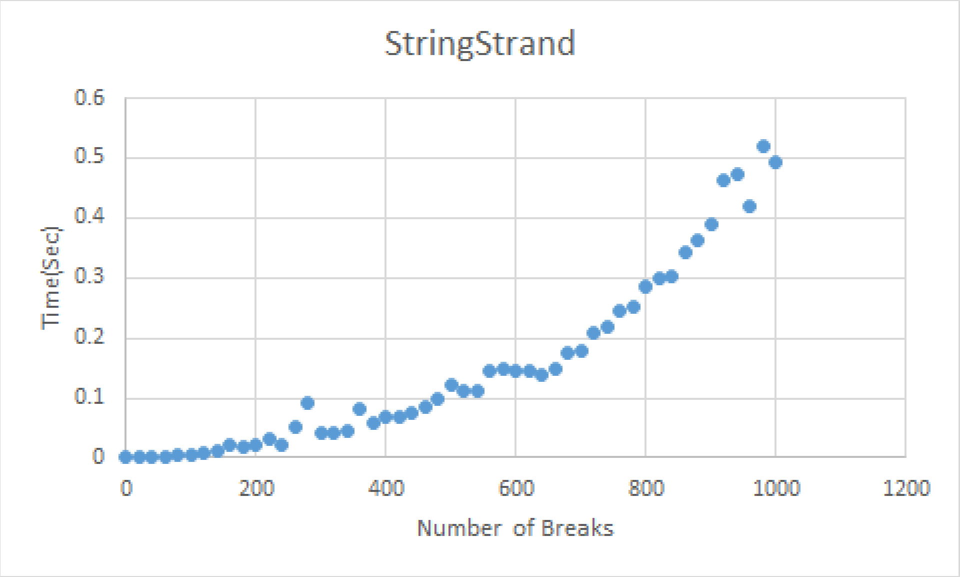


B = 20000 n = 5,000,000

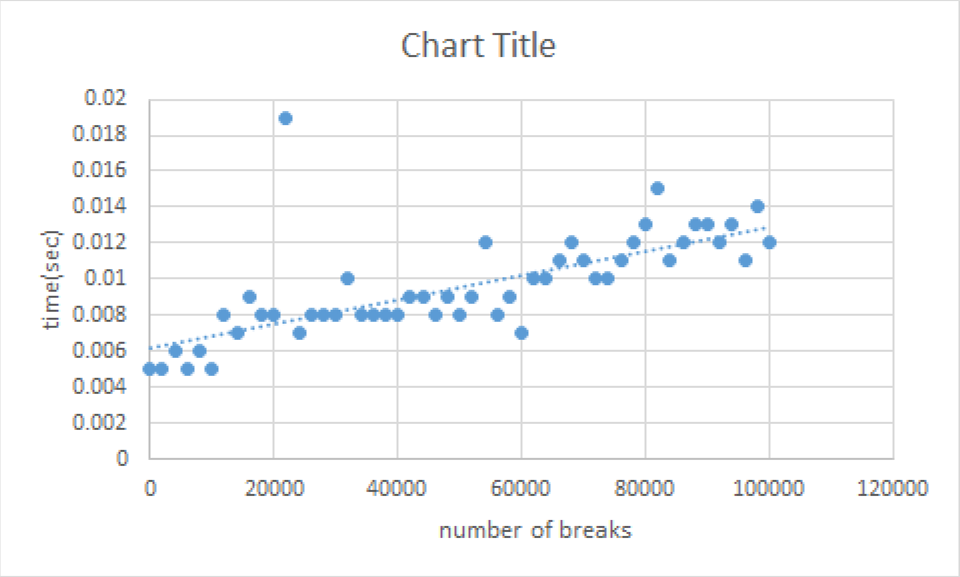
Since when all variables are held constant the runtime is linear with respect to splicee length and number of breaks, although much more affected by splicee length, the runtime for StringBuilder Strand is O(bs) where b is the number of breaks and s is the length of the appended splicee.

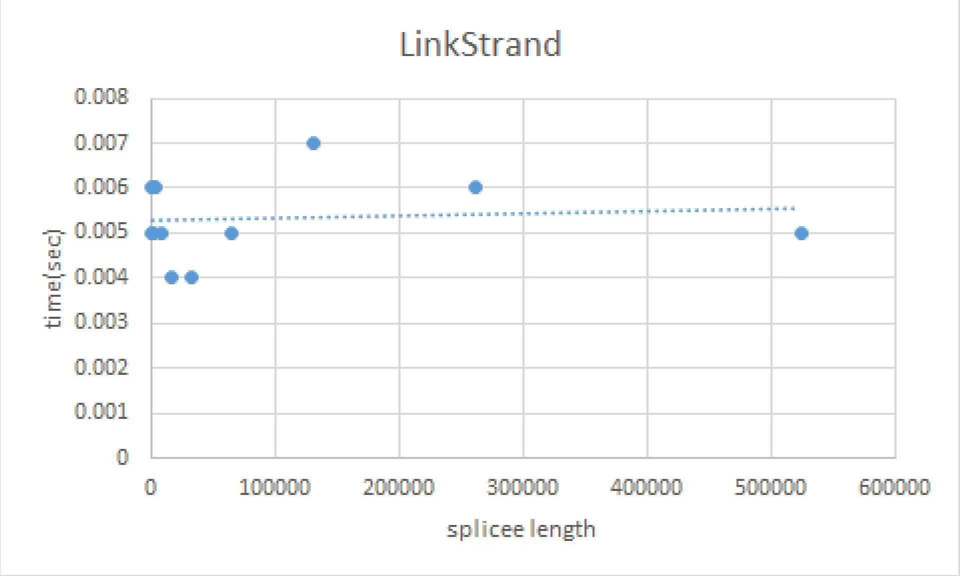


The relationship between runtime and the length of the splicee(or s) is linear when the number of appends was constant (2000), and the strand length(N) was constant at 50,000.



With a string strand, where Dna Strand length is constant(N= 50000), and splicee length is constant (155), the relationship between the runtime and number of breaks is quadratic. When the b=500, t = .124 and when b=100, t = .491; thus, when the number of breaks doubles, the runtime quadruples.





The length of the splicee when N=2500000, and breaks are held constant at (40000) doesn't affect runtime.

This means when the DNA strand length is constant, the run time is only dependent on the number of breaks, and the runtime is O(b)