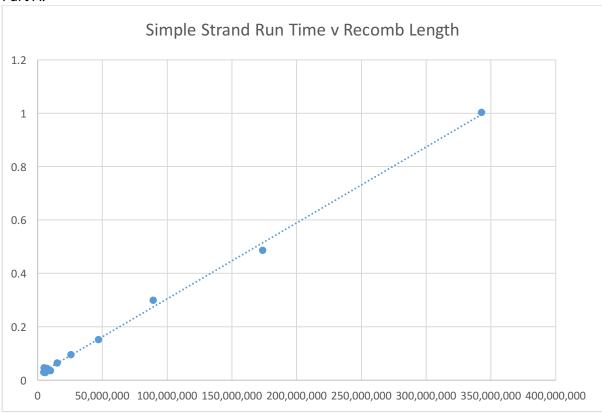
Chetan Reddy Assignment #3 – DNA CS 201 Analysis

Benchmarking Part 1.

Part A.



This process is linear with O(n) notation. We concluded this is the case by looking at the data points and trend line with an R^2 value of 0.99786 and seeing that the trend line is a relatively straight line. We were able to generate this data by running DNABenchmark within Eclipse and then plotting out the Recomb Length on the X axis with the Simple Strand run time on the Y axis.

Part B.

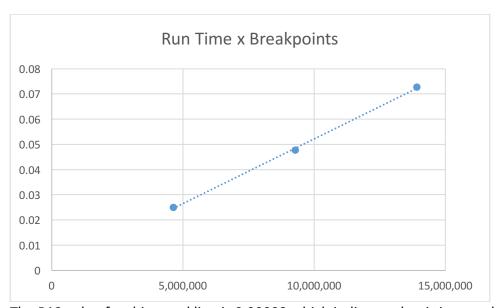
Splicee Size	Heap Size	Time
65,536	46,906,071	0.125
131,072	89,176,791	0.28

We determined the power of two string by looking at the last splice before out of memory error and the associated run time. Please see the table above for more information that is asked for in the analysis.

Benchmarking Part 2.

My LinkStrand code is O(B). The way that I determined this was that I first made three text files, ecoli, ecoli2, and ecoli3. Ecoli2 is two times bigger than ecoli and Ecoli3 is three times bigger than ecoli. Once these were created, I ran the DNA benchmark for these three different text files and averaged the run time for each of the three. My data shows that for the first, ecoli, that had a length of 4,639,221, and a run time average of 0.025. Ecoli2 has a length of 9,278,442 and an average run time of 0.0477. Ecoli3 has a length of 13,917,663 and an average run time of 0.0727. As you can see, the run time is increasing by 2x and 3x as the length of the DNA increases by 2x and 3x. Thus, as the breakpoints increase, the run time increases linearly at O(B). I have included a graph of what this looks like and a table.

ECOLI				
dna length = 4,639,221				
LinkStrand:	256	4,800,471	0.022	# append calls = 1290
LinkStrand:	512	4,965,591	0.021	# append calls = 1290
LinkStrand:	1,024	5,295,831	0.028	# append calls = 1290
LinkStrand:	2,048	5,956,311	0.022	# append calls = 1290
LinkStrand:	4,096	7,277,271	0.023	# append calls = 1290
LinkStrand:	8,192	9,919,191	0.024	# append calls = 1290
LinkStrand:	16,384	15,203,031	0.027	# append calls = 1290
LinkStrand:	32,768	25,770,711	0.027	# append calls = 1290
LinkStrand:	65,536	46,906,071	0.026	# append calls = 1290
LinkStrand:	131,072	89,176,791	0.03	# append calls = 1290
			0.025	
ECOLI2				
dna length = 9,278,442				
LinkStrand:	256	9,600,942	0.047	# append calls = 2580
LinkStrand:	512	9,931,182	0.049	# append calls = 2580
LinkStrand:	1,024	10,591,662	0.047	# append calls = 2580
LinkStrand:	2,048	11,912,622	0.043	# append calls = 2580
LinkStrand:	4,096	14,554,542	0.043	# append calls = 2580
LinkStrand:	8,192	19,838,382	0.047	# append calls = 2580
LinkStrand:	16,384	30,406,062	0.05	# append calls = 2580
LinkStrand:	32,768	51,541,422	0.05	# append calls = 2580
LinkStrand:	65,536	93,812,142	0.053	# append calls = 2580
ECOLI3			0.047666667	
dna length = 13,917,663				
LinkStrand:	256	14,401,413	0.07	# append calls = 3870
LinkStrand:	512	14,896,773	0.07	# append calls = 3870
LinkStrand:	1,024	15,887,493		# append calls = 3870
LinkStrand:	2,048	17,868,933	0.071	# append calls = 3870
LinkStrand:	4,096	21,831,813		# append calls = 3870
LinkStrand:	8,192	29,757,573		# append calls = 3870
LinkStrand:	16,384	45,609,093		# append calls = 3870
LinkStrand:	32,768	77,312,133		# append calls = 3870
LinkStrand:	65,536	140,718,213		# append calls = 3870
			0.072666667	



The R^2 value for this trend line is 0.99923 which indicates that is is very close to being perfectly linear and O(B).