

1)**Benchmark**

The code in SimpleStrand.cutAndSplice is shown below:

```

34 public IDnaStrand cutAndSplice(String enzyme, String splicee) {
35     int pos = 0;
36     int start = 0;
37     StringBuilder search = myInfo;
38     boolean first = true;
39     SimpleStrand ret = null;
40
41     while ((pos = search.indexOf(enzyme, pos)) >= 0) {
42
43         if (first){
44             ret = new SimpleStrand(search.substring(start, pos));
45             first = false;
46         }
47         else {
48             ret.append(search.substring(start, pos));
49
50         }
51         start = pos + enzyme.length();
52         ret.append(splicee);
53         pos++;
54     }
55
56
57
58     if (start < search.length()) {
59         // NOTE: This is an important special case! If the enzyme
60         // is never found, return an empty String.
61         if (ret == null){
62             ret = new SimpleStrand("");
63         }
64         else {
65             ret.append(search.substring(start));
66         }
67     }
68     return ret;
69

```

O(N) Hypothesis

When calling the cutAndSplice in the SimpleStrand class, a splicee is appended to ret. Because ret is of type StringBuilder, whenever a splicee of size S is appended, each operation will be at least $O(S)$. Since ret is built from null, this implies that at the end of n operations using splices of size S, it will take $O(Sn)$ time, where Sn is the total length of the final recombinant strand (ret).

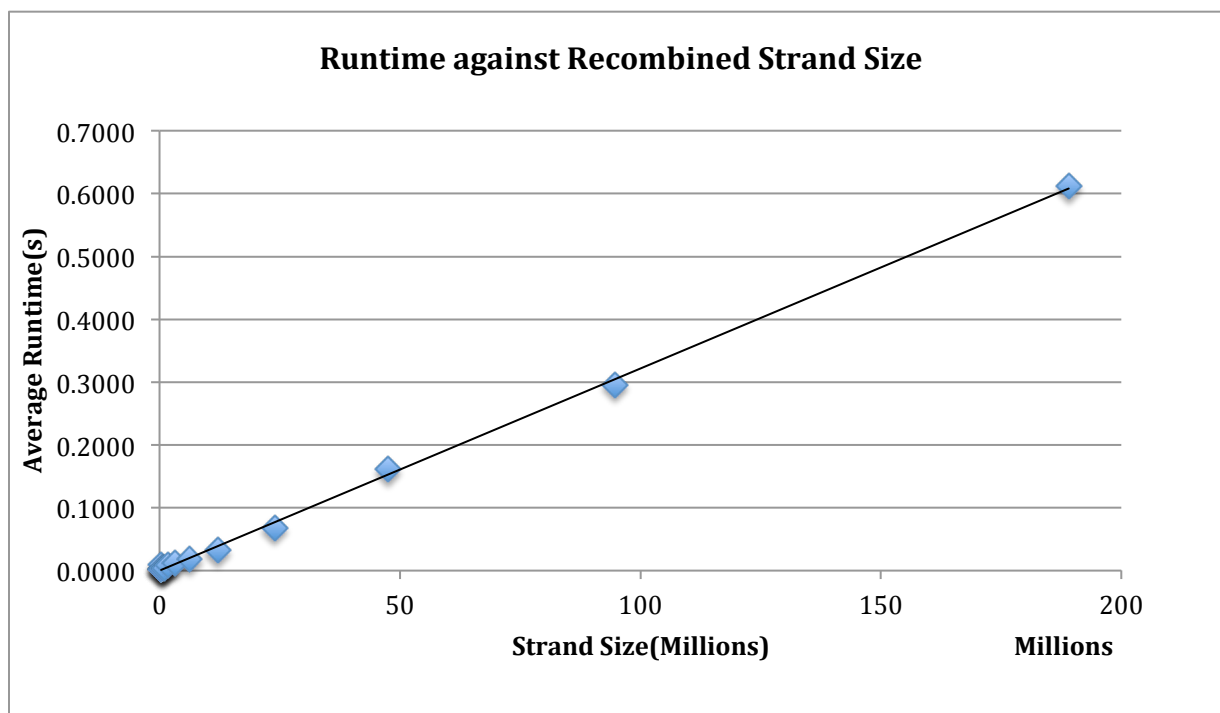
The SimpleStrand.cutAndSplice code was BenchMaked using the class DNABenchMark, and run using 3 different files of different strand lengths. These are :

Ecoli Small : DNA length - 320 126
Ecoli: DNA length - 4,639,221
Ecoli + Ecoli small: DNA length - 4,959,381
Double Ecoli: DNA length - 9,278,443
Tripple Ecoli: DNA length - 13,917,663
Ecoli Quad+Small: DNA length - 18,877,044

For each of the files, DNABenchMark was run 3 times, the running times were then averaged to get a more accurate value.

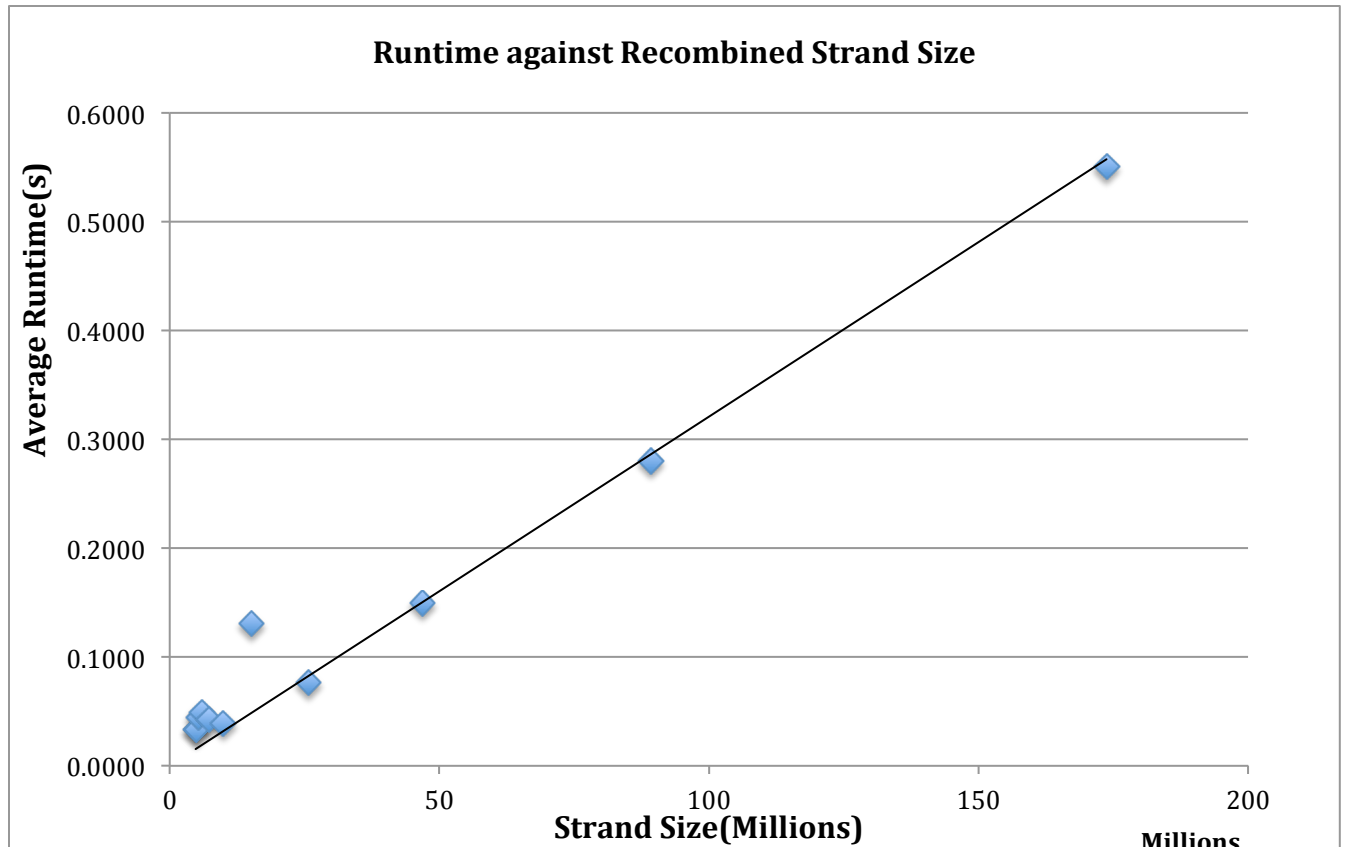
Ecoli Small : DNA length – 320 126

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	Average Runtime(s)
331,410		0.003	0.002	0.002	0.0023
342,930		0.003	0.002	0.002	0.0023
365,970		0.003	0.002	0.003	0.0027
412,050		0.009	0.01	0.009	0.0093
504,210		0.003	0.003	0.003	0.0030
688,530		0.003	0.003	0.003	0.0030
1,057,170		0.003	0.003	0.003	0.0030
1,794,450		0.009	0.01	0.008	0.0090
3,269,010		0.012	0.013	0.013	0.0127
6,218,130		0.018	0.018	0.02	0.0187
12,116,370		0.03	0.033	0.032	0.0317
23,912,850		0.067	0.069	0.068	0.0680
47,505,810		0.159	0.162	0.163	0.1613
94,691,730		0.292	0.301	0.295	0.2960
189,063,570		0.636	0.605	0.595	0.6120



Ecoli: DNA length - 4,639,221

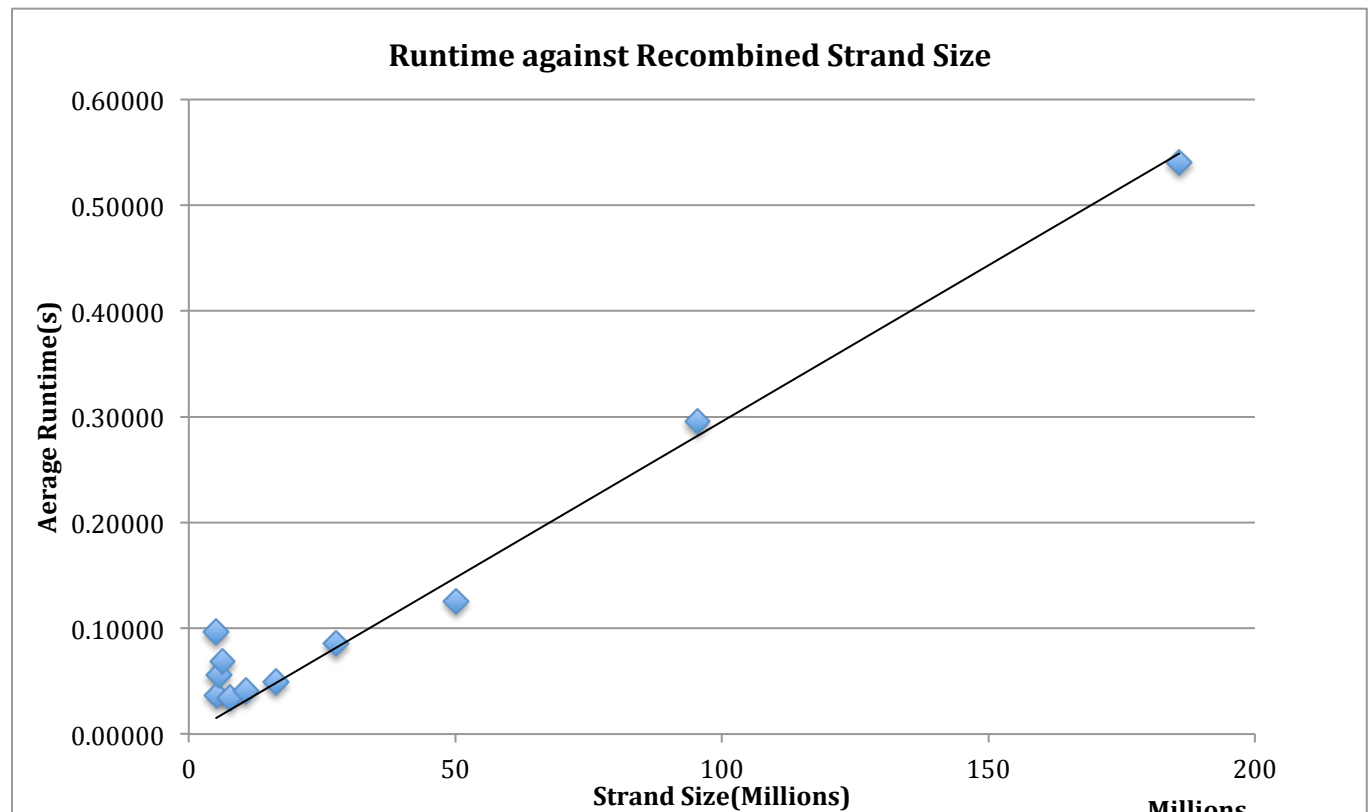
Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	Average Runtime(s)
4,800,471		0.033	0.035	0.032	0.0333
4,965,591		0.034	0.033	0.033	0.0333
5,295,831		0.046	0.044	0.043	0.0443
5,956,311		0.05	0.047	0.049	0.0487
7,277,271		0.043	0.042	0.042	0.0423
9,919,191		0.04	0.039	0.037	0.0387
15,203,031		0.168	0.109	0.115	0.1307
25,770,711		0.089	0.07	0.07	0.0763
46,906,071		0.15	0.149	0.15	0.1497
89,176,791		0.278	0.288	0.275	0.2803
173,718,231		0.531	0.437	0.683	0.5503



Ecoli + Ecoli small: DNA length - 4,959,381

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	AvgRuntime(s)
5,131,881		0.1	0.101	0.088	0.09633
5,308,521		0.036	0.035	0.039	0.03667
5,661,801		0.055	0.059	0.054	0.05600
6,368,361		0.071	0.067	0.067	0.06833
7,781,481		0.034	0.035	0.034	0.03433
10,607,721		0.041	0.041	0.04	0.04067
16,260,201		0.051	0.053	0.043	0.04900
27,565,161		0.0811	0.091	0.0843	0.08547

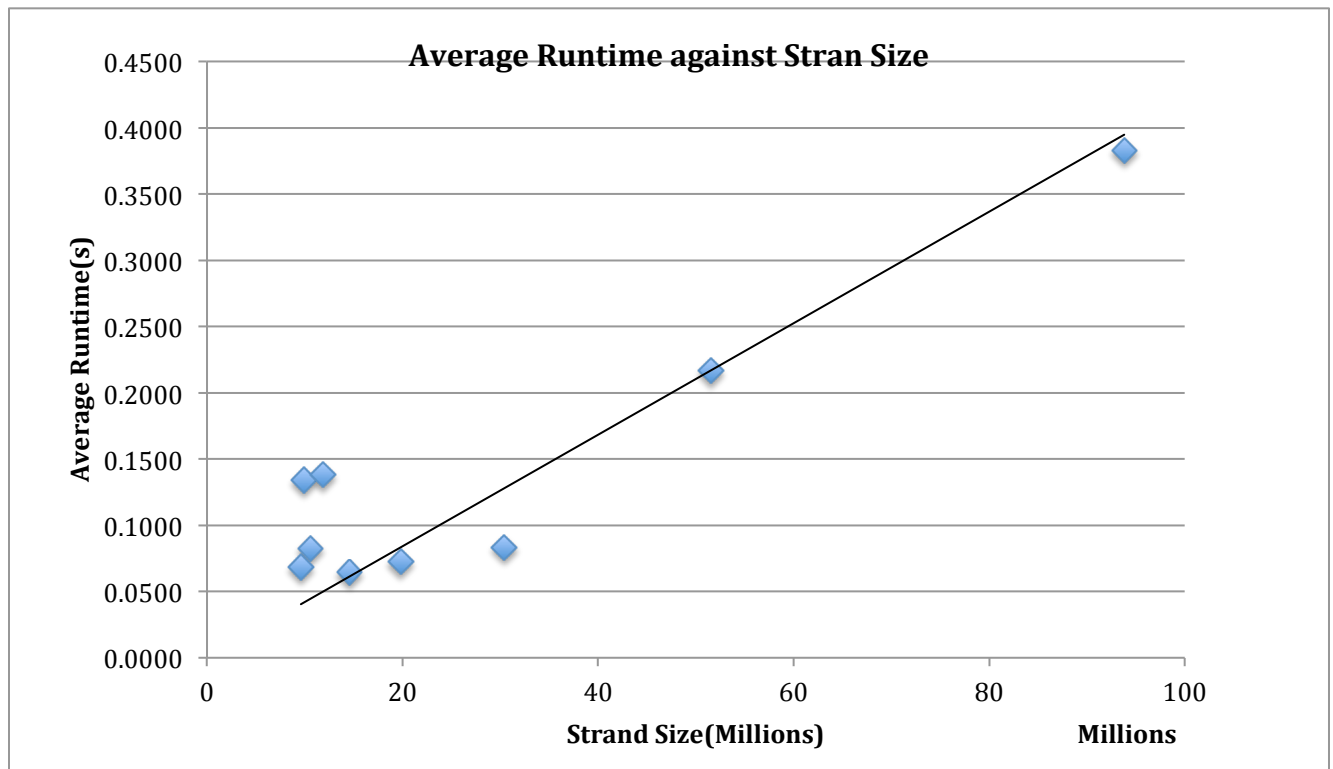
50,175,081		0.138	0.131	0.1066	0.12520
95,394,921		0.307	0.286	0.293	0.29533
185,834,601		0.61	0.582	0.430	0.54067



Double Ecoli: DNA length - 9,278,443

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	AvgRuntime(s)
9,600,943		0.065	0.069	0.071	0.0683
9,931,183		0.178	0.122	0.102	0.1340
10,591,663		0.089	0.079	0.079	0.0823
11,912,623		0.152	0.13	0.132	0.1380
14,554,543		0.064	0.066	0.064	0.0647
19,838,383		0.072	0.073	0.0723	0.0724

30,406,063		0.085	0.083	0.083	0.0837
51,541,423		0.233	0.207	0.211	0.2170
93,812,143		0.38	0.392	0.377	0.3830



For all 3 files used for benchmarking, a graph of running time against combinant strand return size shows a linear relationship. This supports my Big(O) hypothesis - $O(N)$ time, which is linear time.

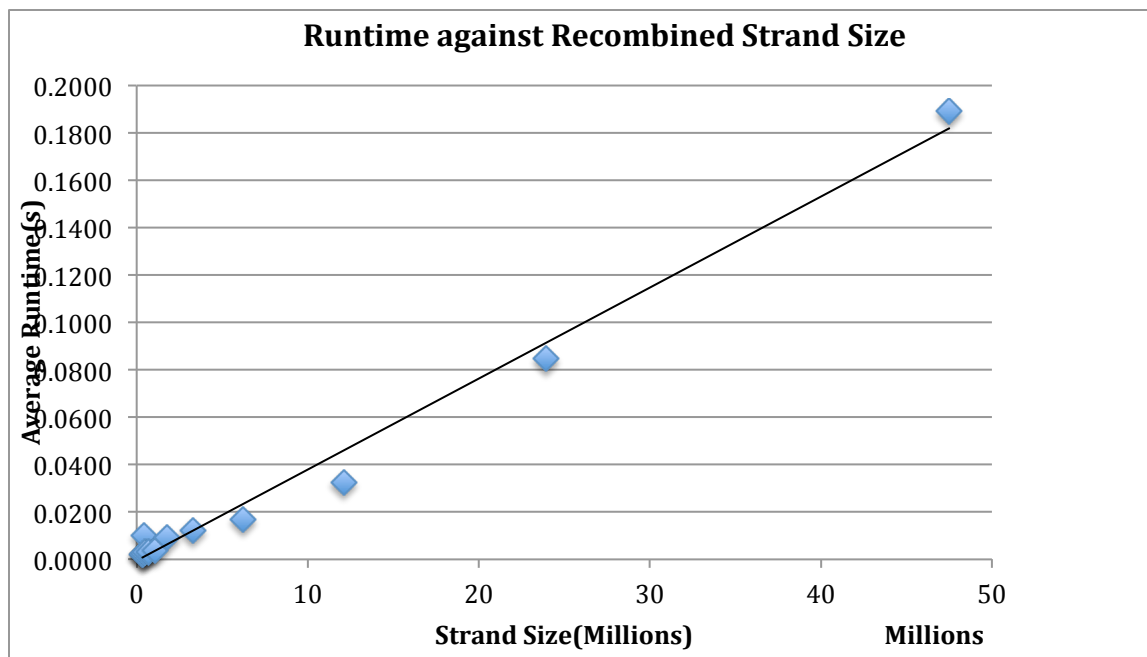
2)

Ecoli Small : DNA length – 320 126

Heap Size -Xmx512M

Table Of Results

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	Average Runtime(s)
331,410		0.002	0.002	0.002	0.0020
342,930		0.002	0.002	0.002	0.0020
365,970		0.003	0.003	0.002	0.0027
412,050		0.01	0.011	0.009	0.0100
504,210		0.003	0.003	0.003	0.0030
688,530		0.003	0.003	0.003	0.0030
1,057,170		0.004	0.004	0.004	0.0040
1,794,450		0.01	0.009	0.009	0.0093
3,269,010		0.012	0.013	0.012	0.0123
6,218,130		0.017	0.017	0.017	0.0170
12,116,370		0.033	0.032	0.033	0.0327
23,912,850		0.097	0.079	0.078	0.0847
47,505,810		0.197	0.189	0.182	0.1893

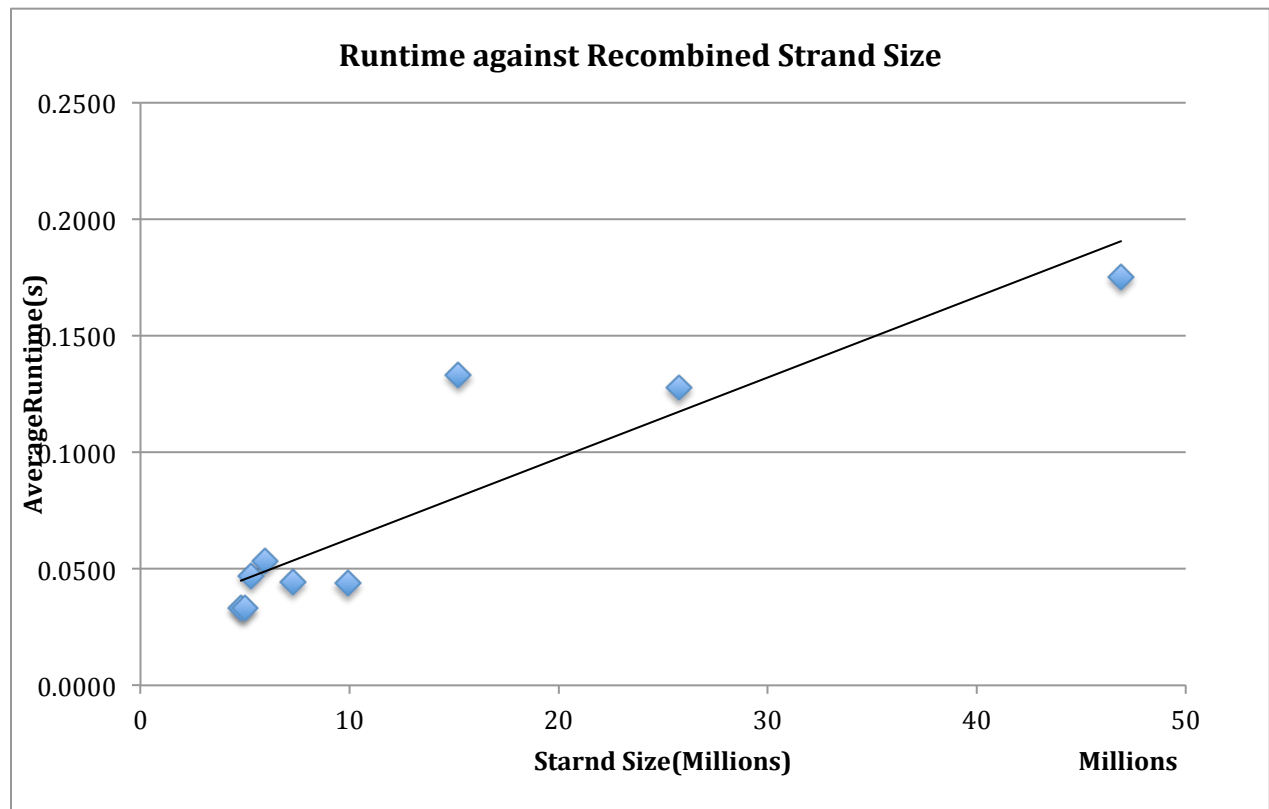


For Ecoli small, the largest splicee that worked without exhausting memory for a heap-size of Xmx512M is of size **1,048,576**.

Ecoli: DNA length - 4,639,221

Heap Size -Xmx512M

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	AvgRuntime(s)
4,800,471		0.034	0.033	0.033	0.0333
4,965,591		0.033	0.032	0.034	0.0330
5,295,831		0.049	0.044	0.048	0.0470
5,956,311		0.055	0.058	0.047	0.0533
7,277,271		0.051	0.038	0.044	0.0443
9,919,191		0.047	0.045	0.039	0.0437
15,203,031		0.12	0.17	0.11	0.1333
25,770,711		0.139	0.126	0.118	0.1277
46,906,071		0.178	0.178	0.17	0.1753



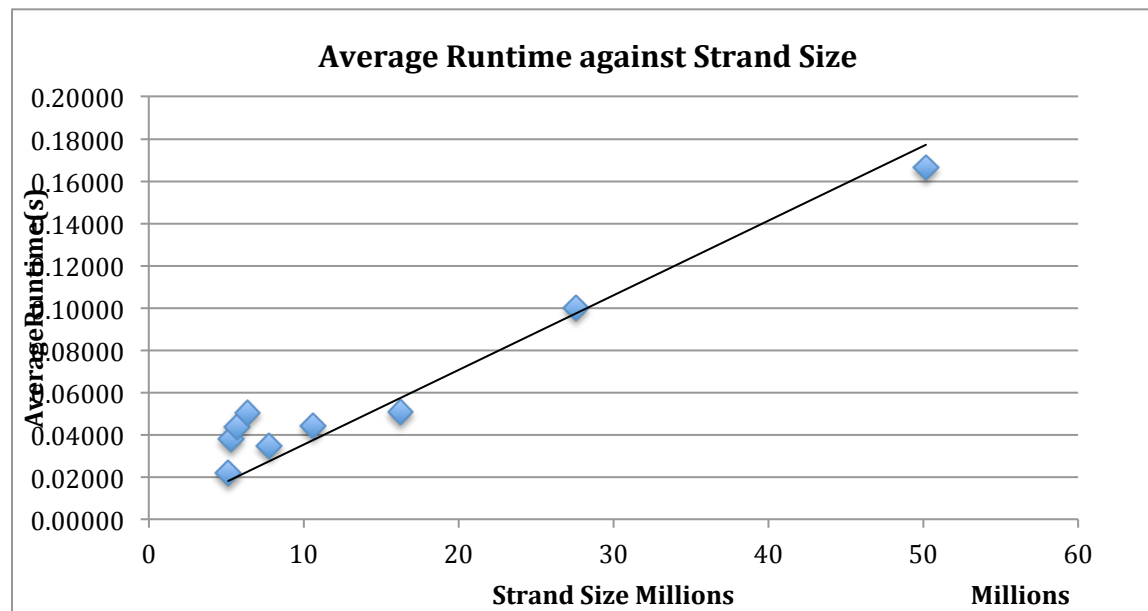
For Ecoli, the largest splicee that worked without exhausting memory for a heap-size of Xmx512M is of size **65,536**

Ecoli + Ecoli small: DNA length - 4,959,381

Heap Size -Xmx512M

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	Average Runtime(s)
5,131,881		0.032	0.021	0.012	0.02167
5,308,521		0.042	0.035	0.037	0.03800
5,661,801		0.052	0.0478	0.0321	0.04397

6,368,361		0.0521	0.0556	0.0438	0.05050
7,781,481		0.035	0.034	0.035	0.03467
10,607,721		0.047	0.042	0.043	0.04400
16,260,201		0.05	0.05	0.052	0.05067
27,565,161		0.106	0.098	0.097	0.10033
50,175,081		0.16	0.171	0.169	0.16667

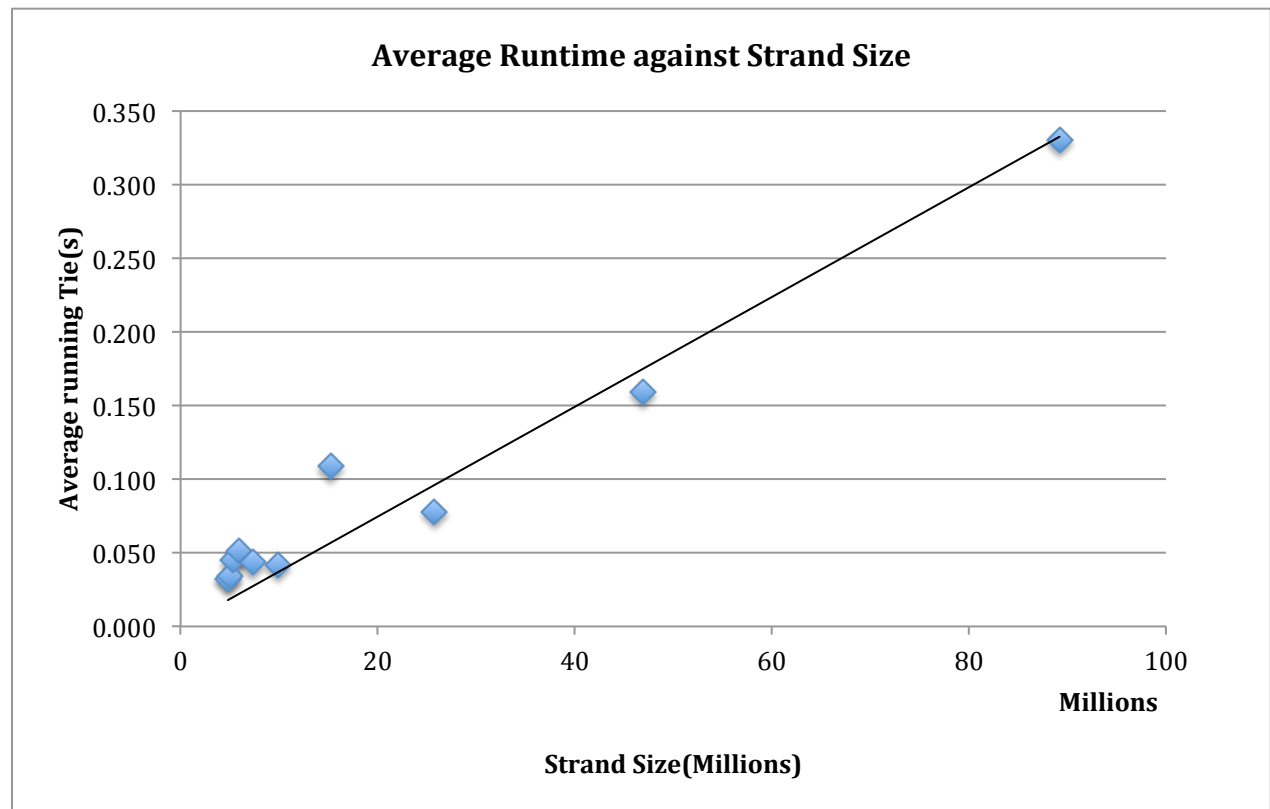


For Ecoli + EcoliSmall, the largest splicee that worked without exhausting memory for a heap-size of Xmx512M is of size **65,536**.

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Ecoli: DNA length - 4,639,221
Heap Size - -Xmx1024M

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	Average Runtime(s)
4,800,471		0.032	0.033	0.032	0.032
4,965,591		0.033	0.036	0.033	0.034
5,295,831		0.044	0.043	0.048	0.045
5,956,311		0.052	0.054	0.047	0.051
7,277,271		0.048	0.041	0.042	0.044
9,919,191		0.045	0.04	0.041	0.042
15,203,031		0.113	0.101	0.112	0.109
25,770,711		0.084	0.074	0.076	0.078
46,906,071		0.174	0.148	0.155	0.159
89,176,791		0.423	0.293	0.275	0.330

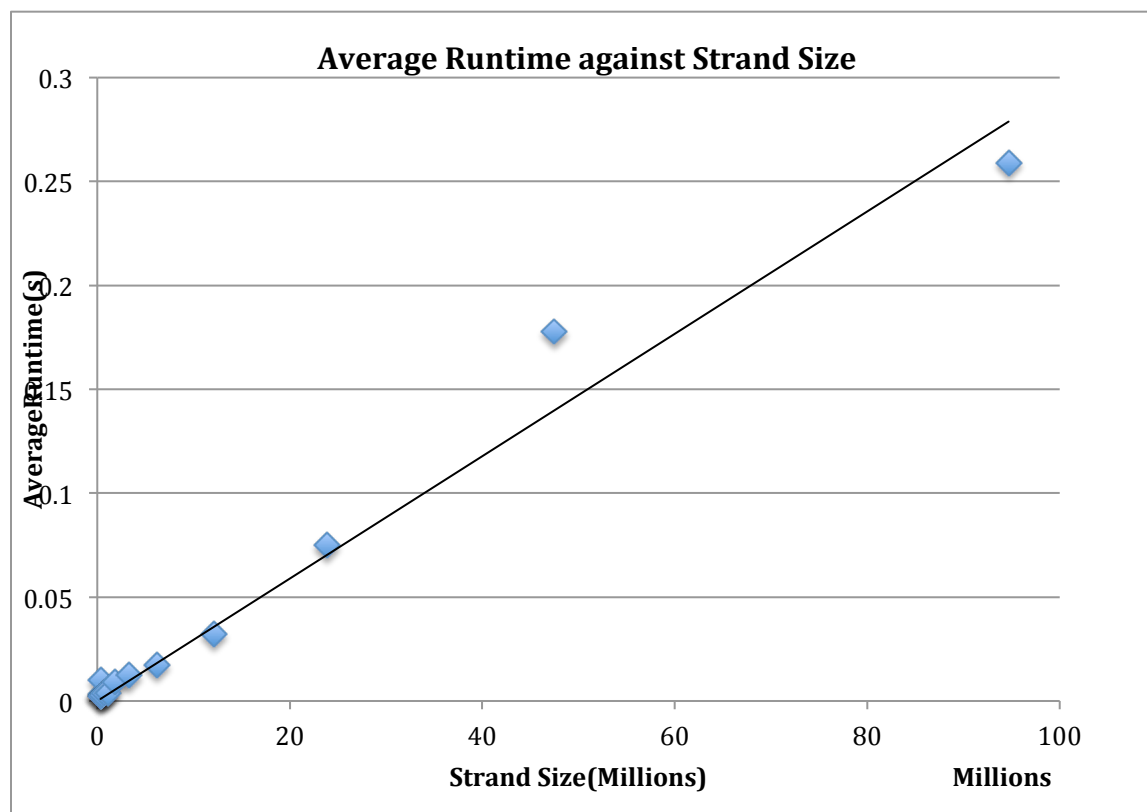


For Ecoli, the largest splicee that worked without exhausting memory for a heap-size of Xmx1024M is of size **131,072**.

Ecoli Small : DNA length – 320 126

Heap Size –Xmx1024M

Recombined Strand Size		Runtime 1(s)	Runtime 2(s)	Runtime 3(s)	AvgRuntime(s)
331,410		0.004	0.003	0.002	0.0030
342,930		0.003	0.002	0.002	0.0023
365,970		0.002	0.003	0.002	0.0023
412,050		0.011	0.01	0.01	0.0103
504,210		0.002	0.003	0.003	0.0027
688,530		0.003	0.004	0.004	0.0037
1,057,170		0.004	0.003	0.004	0.0037
1,794,450		0.009	0.009	0.009	0.0090
3,269,010		0.012	0.012	0.013	0.0123
6,218,130		0.018	0.017	0.017	0.0173
12,116,370		0.033	0.032	0.032	0.0323
23,912,850		0.077	0.079	0.069	0.0750
47,505,810		0.186	0.186	0.161	0.1777
94,691,730		0.257	0.212	0.308	0.2590



For Ecoli_Small, the largest splicee that worked without exhausting memory for a heap-size of Xmx1024M is of size **2,097,152**

Longest Splicee size for Ecoli and Ecoli small relative to memory

	ecoli	ecoli_small
Heap Size -Xmx512M	65,536	1,048,576
Heap Size -Xmx1024M	131,072	2,097,152

From the table above, the longest splice that worked before memory was exhausted, doubled in both cases(ecoli and ecoli_small) when heap size memory allocation was doubled from Xmx512M to Xmx1024M.

This shows that in SimpleStrand, the length of the Splicee influences overall performance and efficiency of the program. This supports the hypothesis

that due to the cutAndSplice method which appends splicee, the size of the splicee results in n operations where n is the size of the splicee, hence as the splicee gets bigger, the operation becomes more inefficient and requires more memory.

4)

.LinkStrand Hypothesis

When implementing LinkStrand, the complexity of splicing is independent of the size of the strand being spliced in. In this implementation, the complexity of creating the recombinant strand is dependent on the number of breaks caused by the restriction enzyme in the original DNA strand.

This is because when calling cutAndSplice in LinkStrand, each splice will cost $O(1)$ time due to fact that at each break, appending is done by simply setting the pointer to the splicee, which is simply $O(1)$ and more efficient than the SimpleStrand append method. Therefore since each break costs $O(1)$, the runtime for cutAndSplice in LinkStrand should be $O(1*B) = O(B)$ where B is the number of breaks caused by the restriction enzyme.

It is for this reason that LinkStrand is more efficient than SimpleStrand in terms of both memory, and time. This can be seen in the results below.

The LinkStrand.cutAndSplice code was BenchMarked using the class DNABenchMark, and run using six different files of different strand lengths. These are :

Ecoli Small : DNA length – 320 126

Ecoli: DNA length - 4,639,221

Ecoli + Ecoli small: DNA length - 4,959,381

Double Ecoli: DNA length - 9,278,443

Tripple Ecoli: DNA length - 13,917,663

Ecoli Quad+Small: DNA length - 18,877,044

The results are shown below

ecoli_small 1024M

dna length = 320,160
cutting at enzyme gaattc

Class	splicee	recomb	time	
LinkStrand:	256	331,410	0.004	# append calls =90
LinkStrand:	512	342,930	0.003	# append calls =90
LinkStrand:	1,024	365,970	0.002	# append calls =90
LinkStrand:	2,048	412,050	0.003	# append calls =90
LinkStrand:	4,096	504,210	0.002	# append calls =90
LinkStrand:	8,192	688,530	0.003	# append calls =90
LinkStrand:	16,384	1,057,170	0.002	# append calls =90
LinkStrand:	32,768	1,794,450	0.003	# append calls =90
LinkStrand:	65,536	3,269,010	0.002	# append calls =90
LinkStrand:	131,072	6,218,130	0.002	# append calls =90
LinkStrand:	262,144	12,116,370	0.002	# append calls =90
LinkStrand:	524,288	23,912,850	0.001	# append calls =90
LinkStrand:	1,048,576	47,505,810	0.002	# append calls =90
LinkStrand:	2,097,152	94,691,730	0.002	# append calls =90
LinkStrand:	4,194,304	189,063,570	0.002	# append calls =90
LinkStrand:	8,388,608	377,807,250	0.002	# append calls =90
LinkStrand:	16,777,216	755,294,610	0.002	# append calls =90
LinkStrand:	33,554,432	1,510,269,330	0.002	# append calls =90
LinkStrand:	67,108,864	3,020,218,770	0.001	# append calls =90

Ecoli

dna length = 4,639,221
cutting at enzyme gaattc

Class	splicee	recomb	time	
LinkStrand:	256	4,800,471	0.025	# append calls = 1290
LinkStrand:	512	4,965,591	0.026	# append calls = 1290
LinkStrand:	1,024	5,295,831	0.026	# append calls = 1290
LinkStrand:	2,048	5,956,311	0.025	# append calls = 1290
LinkStrand:	4,096	7,277,271	0.028	# append calls = 1290
LinkStrand:	8,192	9,919,191	0.032	# append calls = 1290
LinkStrand:	16,384	15,203,031	0.036	# append calls = 1290
LinkStrand:	32,768	25,770,711	0.029	# append calls = 1290
LinkStrand:	65,536	46,906,071	0.025	# append calls = 1290
LinkStrand:	131,072	89,176,791	0.025	# append calls = 1290
LinkStrand:	262,144	173,718,231	0.026	# append calls = 1290
LinkStrand:	524,288	342,801,111	0.028	# append calls = 1290
LinkStrand:	1,048,576	680,966,871	0.026	# append calls = 1290
LinkStrand:	2,097,152	1,357,298,391	0.028	# append calls = 1290
LinkStrand:	4,194,304	2,709,961,431	0.03	# append calls = 1290
LinkStrand:	8,388,608	5,415,287,511	0.025	# append calls = 1290

LinkStrand:	16,777,216	10,825,939,671	0.032	# append calls = 1290
LinkStrand:	33,554,432	21,647,243,991	0.028	# append calls = 1290
LinkStrand:	67,108,864	43,289,852,631	0.153	# append calls = 1290
LinkStrand:	134,217,728	86,575,069,911	0.025	# append calls = 1290

Ecoli+small

dna length = 4,959,381
cutting at enzyme gaattc

Class	splicee	recomb	time	

LinkStrand:	256	5,131,881	0.028	# append calls = 1380
LinkStrand:	512	5,308,521	0.028	# append calls = 1380
LinkStrand:	1,024	5,661,801	0.097	# append calls = 1380
LinkStrand:	2,048	6,368,361	0.027	# append calls = 1380
LinkStrand:	4,096	7,781,481	0.03	# append calls = 1380
LinkStrand:	8,192	10,607,721	0.029	# append calls = 1380
LinkStrand:	16,384	16,260,201	0.027	# append calls = 1380
LinkStrand:	32,768	27,565,161	0.029	# append calls = 1380
LinkStrand:	65,536	50,175,081	0.027	# append calls =

LinkStrand:	131,072	95,394,921	0.028	1380 # append calls = 1380
LinkStrand:	262,144	185,834,601	0.029	1380 # append calls = 1380
LinkStrand:	524,288	366,713,961	0.031	1380 # append calls = 1380
LinkStrand:	1,048,576	728,472,681	0.031	1380 # append calls = 1380
LinkStrand:	2,097,152	1,451,990,121	0.035	1380 # append calls = 1380
LinkStrand:	4,194,304	2,899,025,001	0.027	1380 # append calls = 1380
LinkStrand:	8,388,608	5,793,094,761	0.027	1380 # append calls = 1380
LinkStrand:	16,777,216	11,581,234,281	0.029	1380 # append calls = 1380
LinkStrand:	33,554,432	23,157,513,321	0.027	1380 # append calls = 1380
LinkStrand:	67,108,864	46,310,071,401	0.031	1380 # append calls = 1380
LinkStrand:	134,217,728	92,615,187,561	0.434	1380 # append calls = 1380

double ecoli

dna length = 9,278,443
cutting at enzyme gaattc

Class	splicee	recombtime	
LinkStrand:	256	9,600,943	0.052 # append calls = 2580
LinkStrand:	512	9,931,183	0.056 # append calls = 2580
LinkStrand:	1,024	10,591,663	0.055 # append calls = 2580
LinkStrand:	2,048	11,912,623	0.052 # append calls = 2580

LinkStrand:	4,096	14,554,543	0.052 # append calls = 2580
LinkStrand:	8,192	19,838,383	0.053 # append calls = 2580
LinkStrand:	16,384	30,406,063	0.122 # append calls = 2580
LinkStrand:	32,768	51,541,423	0.056 # append calls = 2580
LinkStrand:	65,536	93,812,143	0.053 # append calls = 2580
LinkStrand:	131,072	178,353,583	0.051 # append calls = 2580
LinkStrand:	262,144	347,436,463	0.053 # append calls = 2580
LinkStrand:	524,288	685,602,223	0.051 # append calls = 2580
LinkStrand:	1,048,576	1,361,933,743	0.051 # append calls = 2580
LinkStrand:	2,097,152	2,714,596,783	0.054 # append calls = 2580
LinkStrand:	4,194,304	5,419,922,863	0.062 # append calls = 2580
LinkStrand:	8,388,608	10,830,575,023	0.051 # append calls = 2580
LinkStrand:	16,777,216	21,651,879,343	0.050 # append calls = 2580
LinkStrand:	33,554,432	43,294,487,983	0.051 # append calls = 2580
LinkStrand:	67,108,864	86,579,705,263	0.051 # append calls = 2580
LinkStrand:	134,217,728	173,150,139,823	0.051 # append calls = 2580

Tripple Ecoli

ecoli_tripple

dna length = 13,917,663

cutting at enzyme gaattc

Class	splicee	recomb	time	

LinkStrand				# append calls =
:	256	14,401,413	0.086	3870
LinkStrand				# append calls =
:	512	14,896,773	0.092	3870
LinkStrand				# append calls =
:	1,024	15,887,493	0.096	3870
LinkStrand	2,048	17,868,933	0.137	# append calls =

:				3870
LinkStrand				# append calls =
:	4,096	21,831,813	0.077	3870
LinkStrand				# append calls =
:	8,192	29,757,573	0.08	3870
LinkStrand				# append calls =
:	16,384	45,609,093	0.078	3870
LinkStrand				# append calls =
:	32,768	77,312,133	0.079	3870
LinkStrand				# append calls =
:	65,536	140,718,213	0.079	3870
LinkStrand				# append calls =
:	131,072	267,530,373	0.077	3870
LinkStrand				# append calls =
:	262,144	521,154,693	0.077	3870
LinkStrand				# append calls =
:	524,288	1,028,403,333	0.082	3870
LinkStrand				# append calls =
:	1,048,576	2,042,900,613	0.089	3870
LinkStrand				# append calls =
:	2,097,152	4,071,895,173	0.076	3870
LinkStrand				# append calls =
:	4,194,304	8,129,884,293	0.079	3870
LinkStrand				# append calls =
:	8,388,608	16,245,862,533	0.076	3870
LinkStrand				# append calls =
:	16,777,216	32,477,819,013	0.091	3870
LinkStrand				# append calls =
:	33,554,432	64,941,731,973	0.147	3870
LinkStrand		129,869,557,89		# append calls =
:	67,108,864	3	0.076	3870
LinkStrand	134,217,72	259,725,209,73		# append calls =
:	8	3	4.916	3870

Quad Ecoli

ecoli_quad+small

dna length =

18,877,044

cutting at enzyme gaattc

Class	splicee	recomb	time	

LinkStrand:	256	19,533,294	0.213	# append calls = 5250
LinkStrand:	512	20,205,294	0.106	# append calls = 5250
LinkStrand:	1,024	21,549,294	0.111	# append calls = 5250
LinkStrand:	2,048	24,237,294	0.11	# append calls = 5250
LinkStrand:	4,096	29,613,294	0.105	# append calls = 5250
LinkStrand:	8,192	40,365,294	0.107	# append calls = 5250
LinkStrand:	16,384	61,869,294	0.11	# append calls = 5250
LinkStrand:	32,768	104,877,294	0.105	# append calls = 5250
LinkStrand:	65,536	190,893,294	0.103	# append calls = 5250
LinkStrand:	131,072	362,925,294	0.104	# append calls = 5250
LinkStrand:	262,144	706,989,294	0.105	# append calls = 5250
LinkStrand:	524,288	1,395,117,294	0.122	# append calls = 5250

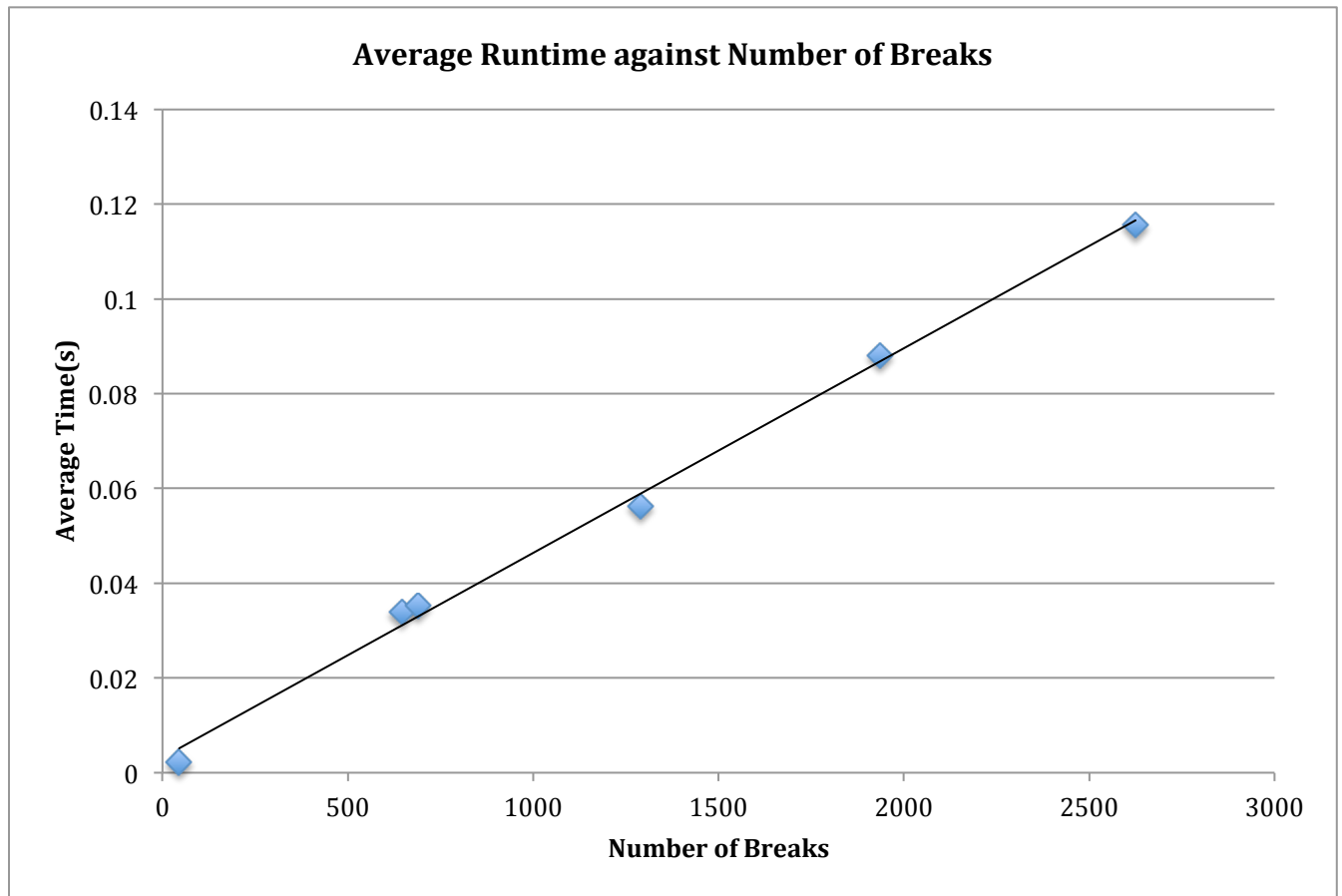
LinkStrand:	1,048,576	2,771,373,294	0.106	# append calls = 5250
LinkStrand:	2,097,152	5,523,885,294	0.103	# append calls = 5250
LinkStrand:	4,194,304	11,028,909,294	0.107	# append calls = 5250
LinkStrand:	8,388,608	22,038,957,294	0.103	# append calls = 5250
LinkStrand:	16,777,216	44,059,053,294	0.103	# append calls = 5250
LinkStrand:	33,554,432	88,099,245,294	0.167	# append calls = 5250
LinkStrand:	67,108,864	176,179,629,294	0.107	# append calls = 5250

The running time for each text file was averaged for the different splice sizes. As can be seen from the tables above, the runtime is independent of the splice size.

The number of breaks in the DNA strand were found by dividing the number of append calls by 2, since at each break, the append method was called twice. (For joining the front and back of the splicee node to DNA strand).

The results are in the table below:

Number of Append Calls	Number of Breaks	Avearge Runtime(s)
90	45	0.00221
1290	645	0.0339
1380	690	0.03532
2580	1290	0.05635
3870	1935	0.08810526
5250	2625	0.11563158



The graph of Average runtime against the number of breaks in a DNA strand shows a linear time relationship. This supports the hypothesis from Big(O) that the runtime is $O(B)$ where B is the number of breaks in the DNA strand.

The runtime for LinkStrand was more efficient than that of SimpleStrand, and it was independent of the length of the splicee itself, but only depended on the number of breaks. Which is shown in the results above.

LinkStrand also performed better than SimpleStrand in terms of the lengths of the recombinant strand it could return before running out of memory. This was due to the efficiency of the cutAndSplice method in LinkStrand which was discussed earlier.

