Compsci 201 P4 Analysis Annie Lin and Eden Deng

(Please see runtime results for DNABenchmark and AnalysisDNA at the bottom)

Question 1: are the benchmark timings for StringStrand consistent with the explanation below that the time to execute cutAndSplice is $O(b^2S)$?

Note that the value of \mathbf{b} is half the number of calls to append since each cut (except the first) is modeled by two calls of append in the method **cutAndSplice** -- see the code. This means that \mathbf{b}^2 will be constant in the benchmark, but S will vary.

Answer:

The benchmark timings for StringStrand are consistent with O(b²S) cutAndSplice runtime efficiency.

b is the occurrences of the enzyme, and S is the length of the splicee. In each run, b remains constant, and as S doubles, runtime also nearly doubles. The trend is increasingly obvious as S becomes larger. For example, when S increases from 131,072 to 262,144, time increases from 11.154 to 23.884; when S increases from 262,144 to 524,288, time increases from 23.884 to 47.238.

As seen in the results from AnalysisDNA, where the number of occurrences of restriction enzyme sites is increasing linearly with each trial holding splice size constant, the runtime for StringStrand is consistent with O(b^2S). When b doubles from the first to second trial, the runtime increases by close to a factor of four (4.810 to 11.206). Similarly, when b doubles again from the second trial to the fourth trial, the runtime increases by approximately a factor of four (11.206 to 42.432).

Question 2: are the benchmark timings for **StringBuilderStrand** consistent with the explanation below that the time to execute cutAndSplice is **O(bS)**?

Note that the value of **b** is half the number of calls to append since each cut (except the first) is modeled by two calls of append in the method **cutAndSplice** -- see the code.

Answer:

The benchmark timings for StringBuilderStrand are consistent with O(bS) cutAndSplice runtime efficiency.

In each run, b remains constant, and as S doubles, runtime also nearly doubles. For example, when S increases from 131,072 to 262,144, time increases from 0.252 to 0.417. (The trend only becomes obvious when S becomes larger. When S is small, time is always less than 0.05 seconds, so the inconsistency is negligible.

In AnalysisDNA where b is increasing linearly with each trial, the results are consistent with O(bS) runtime complexity. For instance, when b doubles from the fourth trial to the eighth trial, the runtime also roughly doubles from 0.071 to 0.191, as expected.

Question 3: Explain why the time for LinkStrand does not change much at all over all the runs in the benchmark program. Explain why you think memory is exhausted at the specific strand size you see in your timings -- as compared to exhaustion for String and StringBuilder.

Answer:

In LinkStrand, each time when cutAndSplice is implemented, no new string is generated; instead, the nodes undergoing change point to the same splice using pointers (which is constant efficiency).

Memory is exhausted at strand size 536,870,912, which is 1,000 times larger than that of StringStrand 524,288, and 2,000 times larger than that of StringBuilderStrand 262,144. LinkStrand implementations use a lot less memory because pointers are used in cutAndSplice and no new string is generated; on the other hand, StringStrand and StringBuilderStrand do generate new strings, which causes memory to be exhausted a lot earlier.

Running DNA Benchmark

StringStrand

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

Class	splicee	recomb time appends
StringStrand:	256	4,800,471 0.446 1290
StringStrand:	512	4,965,591 0.457 1290
StringStrand:	1,024	5,295,831 0.523 1290
StringStrand:	2,048	5,956,311 0.544 1290
StringStrand:	4,096	7,277,271 0.671 1290
StringStrand:	8,192	9,919,191 0.924 1290
StringStrand:	16,384	15,203,031 1.462 1290
StringStrand:	32,768	25,770,711 2.580 1290
StringStrand:	65,536	46,906,071 5.924 1290
StringStrand:	131,072	89,176,791 11.154 1290
StringStrand:	262,144	173,718,231 23.884 1290
StringStrand:	524,288	342,801,111 47.238 1290

StringBuilderStrand

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

Class	splicee	recon	nb time	append	ls	
StringBuilderStr	rand:	256	4,800,471	0.041	1290	
StringBuilderStr	rand:	512	4,965,591	0.031	1290	
StringBuilderStr	rand:	1,024	5,295,831	0.027	1290	
StringBuilderStr	rand:	2,048	5,956,311	0.030	1290	
StringBuilderStr	rand:	4,096	7,277,271	0.024	1290	
StringBuilderStr	rand:	8,192	9,919,191	0.007	1290	
StringBuilderStr	rand:	16,384	15,203,031	0.012	1290	
StringBuilderStr	rand:	32,768	25,770,711	0.036	1290	
StringBuilderStr	rand:	65,536	46,906,071	0.033	1290	
StringBuilderStr	rand:	131,072	89,176,791	0.252	1290	
StringBuilderStr	rand:	262,144	173,718,23	1	0.417	1290

LinkStrand

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

cutting at onzyme gaatte						
splicee	recomb	time	append	ls		
1			11			
256	4,800,471	0.027	1290			
512	4,965,591	0.021	1290			
1,024	5,295,831	0.004	1290			
2,048	5,956,311	0.006	1290			
4,096	7,277,271	0.006	1290			
8,192	9,919,191	0.004	1290			
16,384	15,203,031	0.004	1290			
32,768	25,770,711	0.003	1290			
65,536	46,906,071	0.004	1290			
131,072	89,176,791	0.004	1290			
262,144	173,718,231		0.004	1290		
524,288	342,801,111		0.010	1290		
1,048,576	680,966,871		0.004	1290		
2,097,152	1,357,298,39	1	0.004	1290		
4,194,304	2,709,961,43	1	0.006	1290		
8,388,608	5,415,287,51	1	0.007	1290		
16,777,216	10,825,939,67	11	0.005	1290		
33,554,432	21,647,243,99	1	0.007	1290		
67,108,864	43,289,852,63	31	0.005	1290		
134,217,728	86,575	,069,9	11	0.009	1290	
268,435,456	173,14	5,504,4	71	0.006	1290	
536,870,912	346,28	6,373,5	91	0.083	1290	
	splicee 256 512 1,024 2,048 4,096 8,192 16,384 32,768 65,536 131,072 262,144 524,288 1,048,576 2,097,152 4,194,304 8,388,608 16,777,216 33,554,432 67,108,864 134,217,728 268,435,456	splicee recomb 256	splicee recomb time 256	splicee recomb time appendent of the splice recomb time appendent of the split of t	splicee recomb time appends 256 4,800,471 0.027 1290 512 4,965,591 0.021 1290 1,024 5,295,831 0.004 1290 2,048 5,956,311 0.006 1290 4,096 7,277,271 0.006 1290 8,192 9,919,191 0.004 1290 16,384 15,203,031 0.004 1290 32,768 25,770,711 0.003 1290 65,536 46,906,071 0.004 1290 131,072 89,176,791 0.004 1290 262,144 173,718,231 0.004 1290 524,288 342,801,111 0.010 1290 1,048,576 680,966,871 0.004 1290 2,097,152 1,357,298,391 0.004 1290 4,194,304 2,709,961,431 0.006 1290 8,388,608 5,415,287,511 0.007 1290 16,777,216 10,825,939,67	

Running AnalysisDNA

StringStrand

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

Class	splicee	recomb	time	append	S
StringStrand:	4,096	14,554,542	4.810	2580	
StringStrand:	4,096	21,831,813	11.206	3870	
StringStrand:	4,096	29,109,084	24.138	5160	
StringStrand:	4,096	36,386,355	42.432	6450	
StringStrand:	4,096	43,663,626	57.036	7740	
StringStrand:	4,096	50,940,897	68.456	9030	
StringStrand:	4,096	58,218,168	91.178	10320	
StringStrand:	4,096	65,495,439	120.57	4	11610
StringStrand:	4,096	72,772,710	159.55	8	12900
StringStrand:	4,096	80,049,981	207.12	9	14190

StringBuilderStrand

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

Class	splicee	recon	ıb	time	append	ls
StringBuilderStr	and:	4,096	7,2	77,271	0.079	1290
StringBuilderStr	and:	4,096	14,	554,542	0.124	2580
StringBuilderStr	and:	4,096	21,	831,813	0.198	3870
StringBuilderStr	and:	4,096	29,	109,084	0.071	5160
StringBuilderStr	and:	4,096	36,	386,355	0.140	6450
StringBuilderStr	and:	4,096	43,	663,626	0.246	7740
StringBuilderStr	and:	4,096	50,9	940,897	0.212	9030
StringBuilderStr	and:	4,096	58,2	218,168	0.191	10320
StringBuilderStr	and:	4,096	65,4	495,439	0.102	11610
StringBuilderStr	and:	4,096	72,	772,710	0.457	12900

LinkStrand

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

Class	splicee	recomb	time	appends
LinkStrand:	4,096	7,277,271	0.070	1290
LinkStrand:	4,096	14,554,542	0.069	2580
LinkStrand:	4,096	21,831,813	3 0.017	3870
LinkStrand:	4,096	29,109,084	0.048	5160
LinkStrand:	4,096	36,386,355	0.034	6450
LinkStrand:	4,096	43,663,626	0.049	7740
LinkStrand:	4,096	50,940,897	0.039	9030
LinkStrand:	4,096	58,218,168	3 0.079	10320
LinkStrand:	4,096	65,495,439	0.143	11610
LinkStrand:	4,096	72,772,710	0.073	12900