SimpleStrand DNABenchmark results versus different heap sizes

| Length of DNA splicee / Heap size (MB) | 256MB | 512MB | 1024MB |
|---:|:---:|:---:|:---:|
| 256 | 0.002 | 0.002 | 0.002 |
| 512 | 0.002 | 0.002 | 0.002 |
| 1,024 | 0.014 | 0.014 | 0.010 |
| 2,048 | 0.002 | 0.002 | 0.002 |
| 4,096 | 0.002 | 0.002 | 0.002 |
| 8,192 | 0.002 | 0.002 | 0.002 |
| 16,384 | 0.004 | 0.003 | 0.006 |
| 32,768 | 0.004 | 0.004 | 0.004 |
| 65,536 | 0.007 | 0.008 | 0.008 |
| 131,072 | 0.035 | 0.037 | 0.038 |
| 262,144 | 0.088 | 0.090 | 0.093 |
| 525,288 | 0.151 | 0.140 | 0.146 |
| 1,048,576 | 0.255 | 0.246 | 0.247 |
| 2,097,152 | | 0.436 | 0.430 |
| 4,194,304 | | | 0.818 |
| 8,388,608 | | | |

DNABenchmark results versus different heap sizes
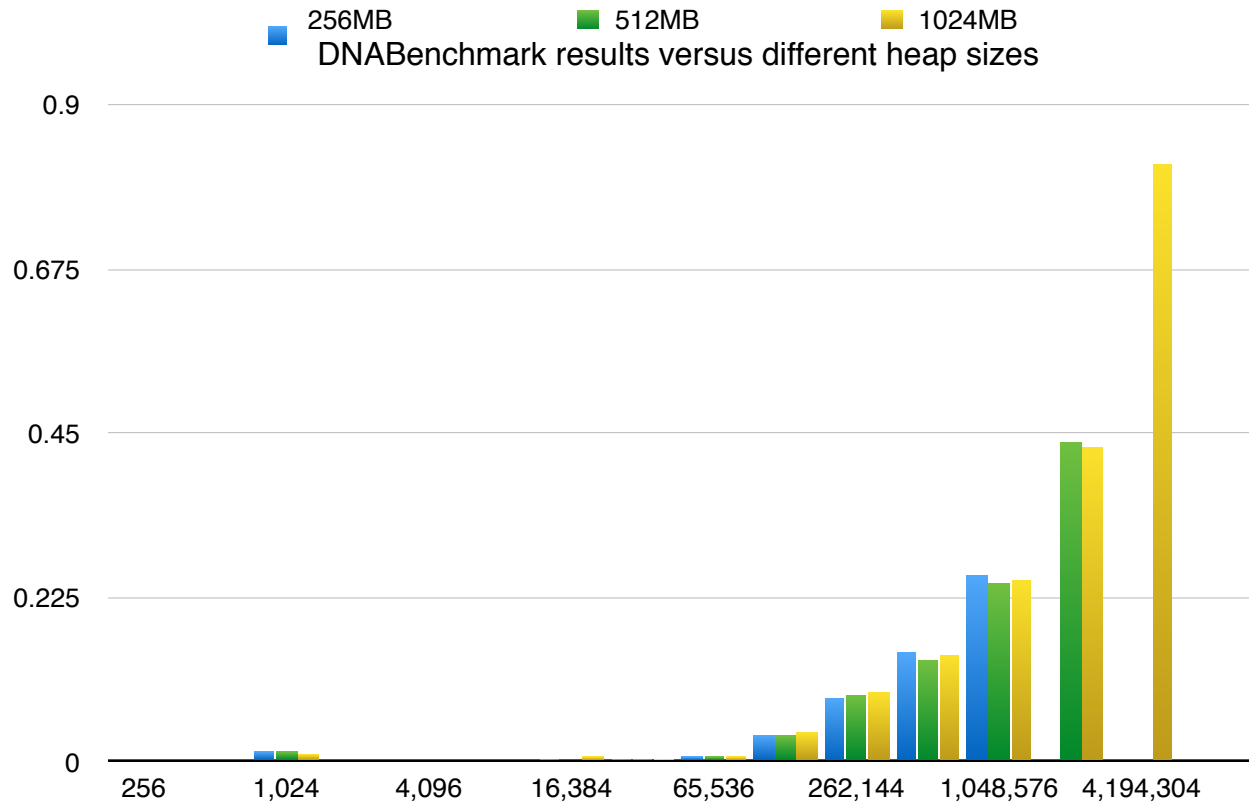
- We observe that the maximum splicee length increases linearly with the maximum heap size allocated.

- With a linearly increasing heap size (as powers of 2) from 256MB to 512MB, we see that the maximum length of splicee length is raised by one interval, from 1,048,576 to 2,097,152. Similarly, from 512MB to 1024MB, splicee length increases from 2,097,152 to 4,194,304.

- This shows that the operation is limited linearly by the amount of available memory and doubling of the splicee length is accomplished by doubling the amount of memory, which indicates that the operation is O(N).

SimpleStrand DNABenchmark results versus different DNA lengths

| Length of DNA splicee / DNA length | 320,160 | 4,639,221 |
|---|---|---|
| 256 | 0.002 | 0.064 |
| 512 | 0.002 | 0.053 |
| 1,024 | 0.014 | 0.078 |
| 2,048 | 0.002 | 0.045 |
| 4,096 | 0.002 | 0.044 |
| 8,192 | 0.002 | 0.076 |
| 16,384 | 0.004 | 0.085 |
| 32,768 | 0.004 | |
| 65,536 | 0.007 | |
| 131,072 | 0.035 | |
| 262,144 | 0.088 | |
| 525,288 | 0.151 | |
| 1,048,576 | 0.255 | |
| 2,097,152 | | |
| 4,194,304 | | |
| 8,388,608 | | |

DNABenchmark results versus different DNA lengths
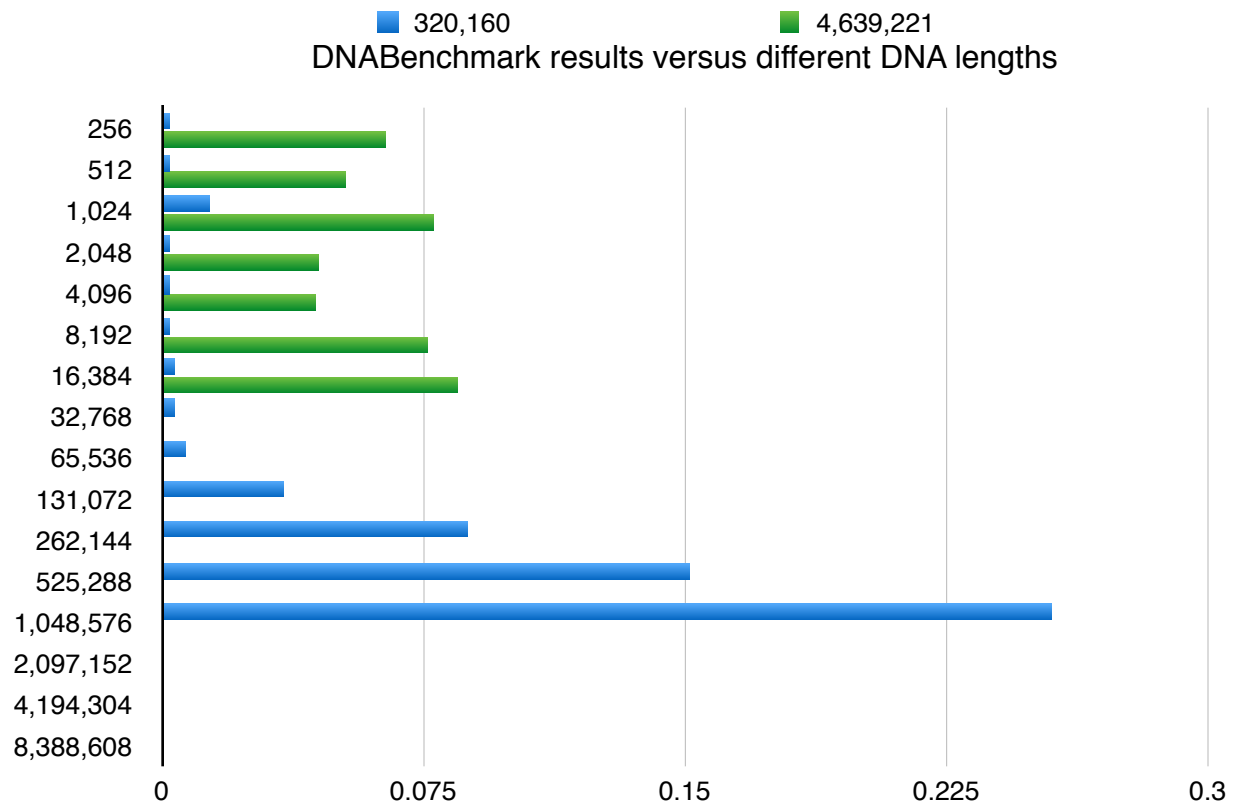
- 320,160
- 4,639,221



- The longer DNA strand has 4,639,221 bases while the shorter DNA strand has 320,160 bases; the longer DNA strand is roughly 14.5x the length of the strand.

- Given that relative size of both strands, the timings of DNABenchmark behave similarly with the timings of the longer strand almost always at least 14.5x longer.

- For a heap size of 256MB, the shorter DNA strand could run up to a splicee length of 1,048,576, in contrast to the longer DNA strand which runs up to 16,384.

- Note also that the longer DNA strand is around $2^4$ times the length of the shorter DNA strand. Now consider that the splicee lengths are increasing exponents of 2 (i.e., from 256 to 512), we observe that the shorter DNA strand is $2^4$ times shorter than the DNA strand and is able to run at least 4 (or 6 in this case) more splicee lengths.

- These indicate that the operations is related linearly with the length of the DNA strand and splicee, or otherwise O(N).

LinkStrand DNABenchmark results versus different DNA lengths

| Length of DNA splicee / DNA length | 320,160 | 4,639,221 |
|---:|:---:|:---:|
| 256 | 0.002 | 0.043 |
| 512 | 0.002 | 0.031 |
| 1,024 | 0.002 | 0.036 |
| 2,048 | 0.002 | 0.045 |
| 4,096 | 0.002 | 0.030 |
| 8,192 | 0.002 | 0.033 |
| 16,384 | 0.009 | 0.031 |
| 32,768 | 0.002 | 0.031 |
| 65,536 | 0.002 | 0.030 |
| 131,072 | 0.002 | 0.033 |
| 262,144 | 0.002 | 0.031 |
| 525,288 | 0.002 | 0.031 |
| 1,048,576 | 0.002 | 0.033 |
| 2,097,152 | 0.002 | 0.035 |
| 4,194,304 | 0.002 | 0.042 |
| 8,388,608 | 0.015 | 0.043 |
| 16,777,216 | 0.002 | 0.037 |
| 33,554.432 | 0.002 | 0.034 |

- For DNA length with 4,639,221 bases and enzyme gaattc, there are 645 breaks.

- For DNA length with 320,160 bases and enzyme gaattc, there are 45 breaks.

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LinkStrand DNABenchmark results versus different DNA lengths
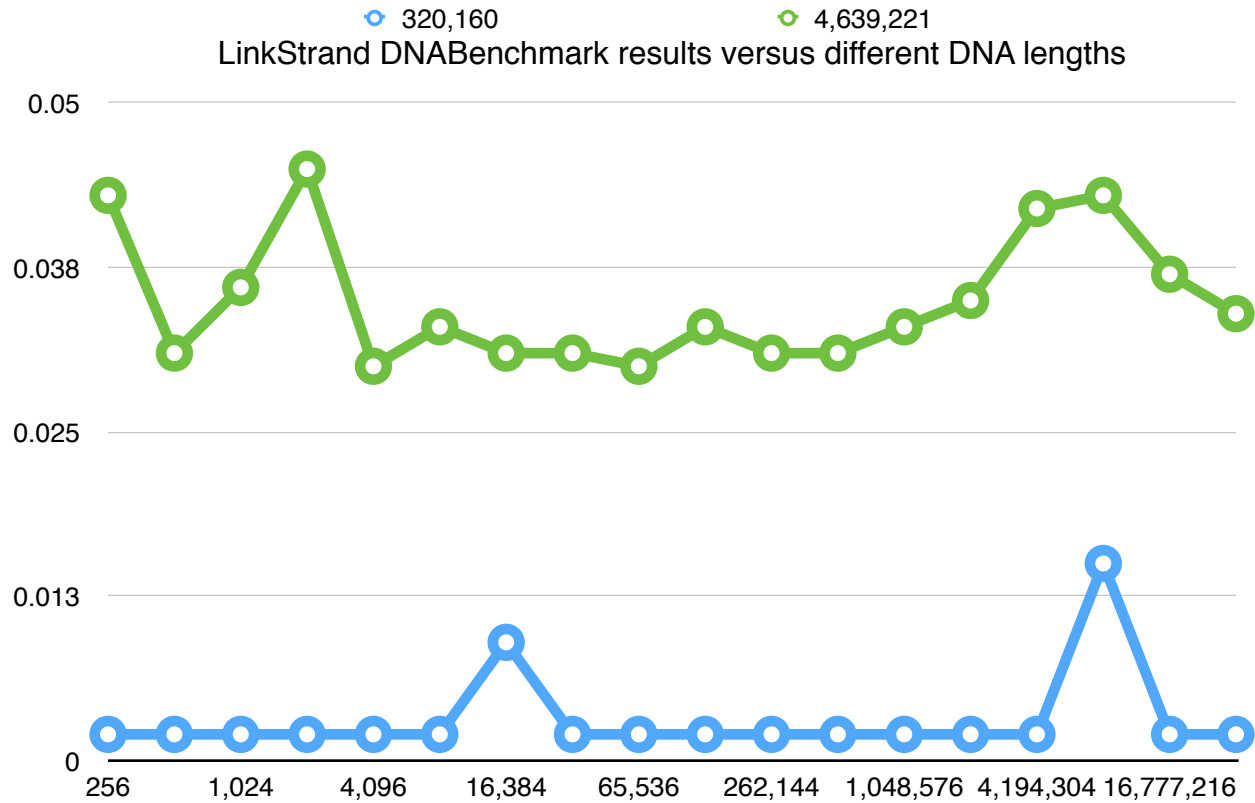
- For both DNA strands of different lengths, we observe that the time to run operations are independent of the splicee length and the timings for each DNA strand are almost the same.

- Given that the longer DNA strand has 645 breaks in contrast to the shorter DNA strand's 45 breaks — which is similarly 14.5x as many breaks — we observe that the timings are correspondingly about 14.5x times as large.

- As such, we see a linear relationship between operation time and the number of breaks there are in the DNA strand. This indicates that for B breaks, the program is O(B).