String Strand Timing Data

dna length = 320,160

cutting at enzyme gaattc

----------------------------------------------------------------------

Class dna,N splicee,S recomb time(ms) breaks,b

----------------------------------------------------------------------

StringStra: 320,160 10,000 769,890 14 44

StringStra: 320,160 20,000 1,219,890 12 44

StringStra: 320,160 40,000 2,119,890 73 44

StringStra: 320,160 80,000 3,919,890 36 44

StringStra: 320,160 160,000 7,519,890 69 44

StringStra: 320,160 320,000 14,719,890 69 44

StringStra: 320,160 640,000 29,119,890 157 44

StringStra: 320,160 1,280,000 57,919,890 185 44

StringStra: 320,160 10,000 769,890 9 44

StringStra: 640,320 10,000 1,539,780 16 89

StringStra: 1,280,640 10,000 3,079,560 34 179

StringStra: 2,561,280 10,000 6,159,120 120 359

StringStra: 5,122,560 10,000 12,318,240 496 719

--------------- Memory Exhaustion Benchmark ---------------

DNABenchmark

dna length = 320,160

cutting at enzyme gaattc

----------------------------------------------------------------------

Class dna,N splicee,S recomb time(ms) breaks,b

----------------------------------------------------------------------

StringStra: 320,160 10,000 769,890 6 44

StringStra: 320,160 20,000 1,219,890 17 44

StringStra: 320,160 40,000 2,119,890 10 44

StringStra: 320,160 80,000 3,919,890 13 44

StringStra: 320,160 160,000 7,519,890 19 44

StringStra: 320,160 320,000 14,719,890 36 44

StringStra: 320,160 640,000 29,119,890 67 44

StringStra: 320,160 1,280,000 57,919,890 139 44

StringStra: 320,160 10,000 769,890 6 44

StringStra: 640,320 10,000 1,539,780 11 89

StringStra: 1,280,640 10,000 3,079,560 33 179

StringStra: 2,561,280 10,000 6,159,120 115 359

StringStra: 5,122,560 10,000 12,318,240 442 719

--------------- Memory Exhaustion Benchmark ---------------

Class splicee recomb time appends

StringStra: 256 4,800,471 0.042 1290

StringStra: 512 4,965,591 0.044 1290

StringStra: 1,024 5,295,831 0.037 1290

StringStra: 2,048 5,956,311 0.041 1290

StringStra: 4,096 7,277,271 0.051 1290

StringStra: 8,192 9,919,191 0.069 1290

StringStra: 16,384 15,203,031 0.100 1290

StringStra: 32,768 25,770,711 0.178 1290

StringStra: 65,536 46,906,071 0.313 1290

StringStra: 131,072 89,176,791 0.691 1290

StringStra: 262,144 173,718,231 1.289 1290

StringStra: 524,288 342,801,111 2.418 1290

StringBuilder timing Data

dna length = 320,160

cutting at enzyme gaattc

----------------------------------------------------------------------

Class dna,N splicee,S recomb time(ms) breaks,b

----------------------------------------------------------------------

StringBuil: 320,160 10,000 769,890 3 44

StringBuil: 320,160 20,000 1,219,890 3 44

StringBuil: 320,160 40,000 2,119,890 3 44

StringBuil: 320,160 80,000 3,919,890 3 44

StringBuil: 320,160 160,000 7,519,890 3 44

StringBuil: 320,160 320,000 14,719,890 7 44

StringBuil: 320,160 640,000 29,119,890 9 44

StringBuil: 320,160 1,280,000 57,919,890 21 44

StringBuil: 320,160 10,000 769,890 1 44

StringBuil: 640,320 10,000 1,539,780 3 89

StringBuil: 1,280,640 10,000 3,079,560 6 179

StringBuil: 2,561,280 10,000 6,159,120 10 359

StringBuil: 5,122,560 10,000 12,318,240 18 719

--------------- Memory Exhaustion Benchmark ---------------

dna length = 320,160

cutting at enzyme gaattc

----------------------------------------------------------------------

Class dna,N splicee,S recomb time(ms) breaks,b

----------------------------------------------------------------------

StringBuil: 320,160 10,000 769,890 2 44

StringBuil: 320,160 20,000 1,219,890 2 44

StringBuil: 320,160 40,000 2,119,890 3 44

StringBuil: 320,160 80,000 3,919,890 3 44

StringBuil: 320,160 160,000 7,519,890 5 44

StringBuil: 320,160 320,000 14,719,890 8 44

StringBuil: 320,160 640,000 29,119,890 10 44

StringBuil: 320,160 1,280,000 57,919,890 11 44

StringBuil: 320,160 10,000 769,890 2 44

StringBuil: 640,320 10,000 1,539,780 3 89

StringBuil: 1,280,640 10,000 3,079,560 7 179

StringBuil: 2,561,280 10,000 6,159,120 9 359

StringBuil: 5,122,560 10,000 12,318,240 18 719

--------------- Memory Exhaustion Benchmark ---------------

LinkStrand timing Data

dna length = 320,160

cutting at enzyme gaattc

----------------------------------------------------------------------

Class dna,N splicee,S recomb time(ms) breaks,b

----------------------------------------------------------------------

LinkStrand: 320,160 10,000 769,890 2 44

LinkStrand: 320,160 20,000 1,219,890 3 44

LinkStrand: 320,160 40,000 2,119,890 2 44

LinkStrand: 320,160 80,000 3,919,890 2 44

LinkStrand: 320,160 160,000 7,519,890 2 44

LinkStrand: 320,160 320,000 14,719,890 2 44

LinkStrand: 320,160 640,000 29,119,890 1 44

LinkStrand: 320,160 1,280,000 57,919,890 1 44

LinkStrand: 320,160 10,000 769,890 1 44

LinkStrand: 640,320 10,000 1,539,780 3 89

LinkStrand: 1,280,640 10,000 3,079,560 6 179

LinkStrand: 2,561,280 10,000 6,159,120 9 359

LinkStrand: 5,122,560 10,000 12,318,240 17 719

--------------- Memory Exhaustion Benchmark ---------------

dna length = 320,160

cutting at enzyme gaattc

----------------------------------------------------------------------

Class dna,N splicee,S recomb time(ms) breaks,b

----------------------------------------------------------------------

LinkStrand: 320,160 10,000 769,890 2 44

LinkStrand: 320,160 20,000 1,219,890 2 44

LinkStrand: 320,160 40,000 2,119,890 2 44

LinkStrand: 320,160 80,000 3,919,890 2 44

LinkStrand: 320,160 160,000 7,519,890 2 44

LinkStrand: 320,160 320,000 14,719,890 2 44

LinkStrand: 320,160 640,000 29,119,890 2 44

LinkStrand: 320,160 1,280,000 57,919,890 1 44

LinkStrand: 320,160 10,000 769,890 1 44

LinkStrand: 640,320 10,000 1,539,780 2 89

LinkStrand: 1,280,640 10,000 3,079,560 5 179

LinkStrand: 2,561,280 10,000 6,159,120 10 359

LinkStrand: 5,122,560 10,000 12,318,240 17 719

--------------- Memory Exhaustion Benchmark ---------------

dna length = 4,639,221

cutting at enzyme gaattc

----------------------------------------------------------------------

Class dna,N splicee,S recomb time(ms) breaks,b

----------------------------------------------------------------------

LinkStrand: 4,639,221 10,000 11,085,351 20 644

LinkStrand: 4,639,221 20,000 17,535,351 16 644

LinkStrand: 4,639,221 40,000 30,435,351 15 644

LinkStrand: 4,639,221 80,000 56,235,351 15 644

LinkStrand: 4,639,221 160,000 107,835,351 14 644

LinkStrand: 4,639,221 320,000 211,035,351 14 644

LinkStrand: 4,639,221 640,000 417,435,351 15 644

LinkStrand: 4,639,221 1,280,000 830,235,351 15 644

LinkStrand: 4,639,221 10,000 11,085,351 14 644

LinkStrand: 9,278,442 10,000 22,170,702 32 1,289

LinkStrand: 18,556,884 10,000 44,341,404 59 2,579

LinkStrand: 37,113,768 10,000 88,682,808 127 5,159

LinkStrand: 74,227,536 10,000 177,365,616 256 10,319

--------------- Memory Exhaustion Benchmark ---------------

Question 1 .

The time complexity of the cutAndSplice function in StringStrand should be expressed as O(Nb + b^2S). This is due to the quadratic runtime (b^2S) involved in appending the new string intended for replacement, where b represents the number of strings to be created. Additionally, the time required for adding the non-replaced string is proportional to N/b, and since this operation is performed b times, it contributes Nb to the overall complexity which is addes tp b^2S. The observed empirical results align with the anticipated theoretical expectations, demonstrating a quadratic increase in time with each execution.

Question 2.

The time complexity of the cutAndSplice function in StringStrand is O(N + bS). This is derived from the bS component, representing the runtime for appending a string of size S to a StringBuilder, repeated b times. The N component accounts for appending N/b-sized strings b times, resulting in a total of N. These two components are added together since they are not nested but occur in the same run. Empirical results confirm the theoretical expectations, showcasing a runtime that appears to follow a linear time complexity.

Question 3

A StringStrand object would consume N + bS bytes of memory. This is determined by the total length of the resulting String in the StringStrand, with N representing the length of the appended strings and bS accounting for the size of each appended string, multiplied by the number of times the operation is performed. This memory usage is more efficient compared to StringBuilder, as the latter essentially operates as an array and needs to double in size when its limit is exceeded. This doubling process may result in unused memory spaces in the array, contributing to a higher overall memory footprint.

Question 4

The asymptotic runtime complexity of using the LinkStrand in the cutAndSplice method is O(N). This is because the method iterates through the DNA Strand b times, creating a LinkStrand object and appending a substring of length S to each of these strands. Although the operation involves appending substrings of length S b times, the time complexity simplifies down to being dependent only on the size of the original LinkStrand, which is represented as N. Consequently, the overall time complexity of the method is O(N).

Empirical results from DNABenchmark support this analysis, demonstrating a linear increase in runtime with the size of the original DNA Strand (N) and no discernible pattern beyond that. This empirical evidence reinforces the conclusion that the time complexity of the cutAndSplice method, when using LinkStrand, is empirically observed to be O(N).

Question 5

In summary, the total memory required to store the result of a cutAndSplice operation on a LinkStrand object is approximately (8\*2B) + N + S bytes. The initial DNA strand is composed of a series of linked lists, with each node (totaling 2B nodes) containing strings of length S, resulting in a memory requirement of N bytes. The spliced DNA strand is stored as a string of length S. During the cutAndSplice operation, as B nodes are removed and replaced with the splice, each node will then occupy 8 bytes of memory storage. The overall memory needed for the new DNA strand after the cutAndSplice operation is given by (2B) \* 8 bytes.

Additionally, considering the total number of characters needed to store the strands from the cutAndSplice operation within LinkStrand, which includes N (number of strands) and S (final strand), the overall memory requirement for the LinkStrand object with the operation is calculated as (8\*2B) + N + S bytes.