CS201 DNA Project Analysis*

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1 Benchmarking Method

I use the JMH framework for benchmarking. Please refer to my Markov Project Analysis for detailed explanation.

I generate the testing data with the simplest method. The enzyme is always a single character "B". The splice is a sequence of character "S" with length S. The source is the concatenation of b "B"s and (N-b) "x"s.

For example, with $N=10,\ b=2,\ S=3,$ the cutAndSplice() method (for StringStrand) would be:

```
String source = "BBxxxxxxxxx";

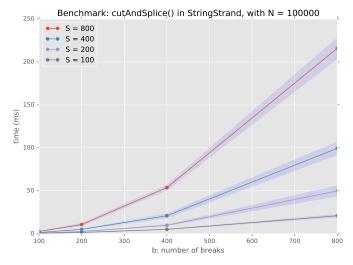
String enzyme = "B";

String splicee= "SSS";

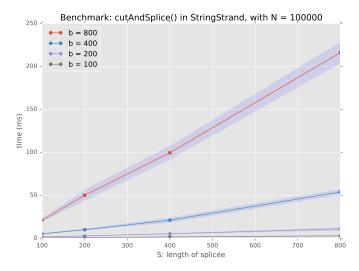
(new StringStrand(source)).cutAndSplice(enzyme, splicee);
```

2 Non Linked List Hypotheses

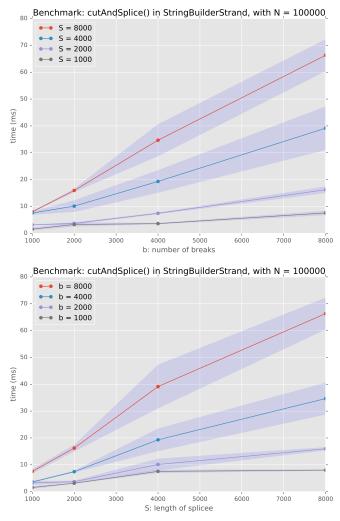
From the following two figures, we know that the cutAndSplice () method of StringStrand is $O(b^2S)$.



^{*}See https://github.com/kepingwang/JavaBenchmark for the full benchmarking project.

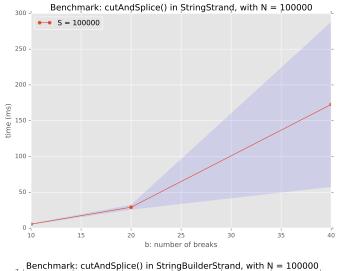


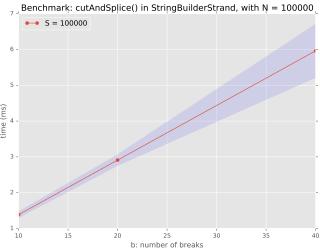
From the following two figures, we know that the cutAndSplice() method of StringBuilderStrand is O(bS).



From the following two figures, we confirm that b and S are multiplied in the run time of non linked list strands because the run time is quadratic/linear in b even when b is very

small relative to S.

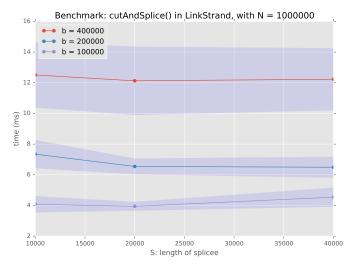




Finally the running time of cutAndSplice() for both StringStrand and StringBuilderStrand have to be at least O(n), since the method has to go through the whole strand to find pieces that matches the enzyme.

3 LinkStrand Hypothesis

From the following figure, we can see that the run time of cutAndSplice() int LinkStrand is irrelevant to S (of course when S is much smaller than N).



From the two following figures, we notice that the run time of cutAndSplice() int LinkStrand is linear in both N and b. Besides, when b becomes very small relative to N, the run time is dominated by N, so we know that the run time is O(b+N) (instead of O(bN)).

