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COMP3506

Assignment2

Report



Evaluation of Branch Order Heuristics

Although I did not have the opportunity to implement heuristics in my own implementation, I can discuss the implications that such an implementation would have had upon performance.

The implementation of branch order heuristics in this implementation would allow the application to be 'selective' when finding alignments. The `findAlignment` method implements a process that finds the required alignment of the dna sequence. By comparing the first element of each sequence with a matching element in the current consensus first (accounting for the dna offset in the process and then checking each subsequent element for a match), we can find an optimal match sooner. The `Alignment` function would therefore run in $O(n \log n)$ rather than $O(n*m)$ time. If we take into consideration the datasets provided in the test case then this could cut as much as 50% off of the running time.

Evaluation of Re-Use Calculations Trick

The re-use of previous calculations would allow the program to record the profile that has been provided by previous calls of the `findAlignment` method. This would avoid repeating the same operation more than once. This would alter the running time significantly, as there would be fewer operations to be performed by the method. The average time complexity would be $O(n \log n)$.