Assembling genome of bacterium from de novo transcriptome

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PROBLEM

We are facing a problem about DNA assembling, with some DNA segments the genome all the sequence represent must be reconstructed to be related with a specie. It must be developed an on-line algorithm that will constantly reading DNA sequences and it should determine if it belong or no to a bacterium, this process must be done efficiently in terms of memory and time with the less possible mistakes generated in the final complete sequence.

RELATED WORK

[1] A de novo Genome Assembler based on MapReduce and Bi-directed de Bruijn Graph

This paper talk about the development of an algorithm that uses MapReduce and Bi-directed Bruijn Graph for efficient dna assembly, MapReduce is used in the process to parallelize and optimize the construction, compaction and cleaning of the graph.

First the algorithm read the sequences from the de novo, and while reading, it creates an undirected de Bruijn Graph, this kind of graph in its classical way is a directed graph, because of this, creating a Bi-directed form require some specials changes during the construction, after that it must be cleaned, because during the reading it may happen some errors, so the algorithm eliminated duplicated, and unnecessary nodes, and repeated or useless paths between the nodes. The pros of this implementation are that the traversal of the graph once it's already cleaned (fixed all the bubbles and gaps) it's very easy to reconstruct the genome, giving more consistent results with less errors.

[2] HipMer: An Extreme-Scale De Novo Genome Assembler

In this article the authors explore efficient ways of: generating the k-mers of the gnome, traverse the de Bruijn graph and solve the errors occurred during the DNA reading.

For the first step while reading the sequence they categorize the k-mers according of its occurrence in the sequence, that way the ones with less recurrence can be determined as an error, as this algorithm is applied the memory used is reduced by 85%. Another improvement is in the traversal of the de Bruijn graph where the algorithm divide the graph into different contigs, so each of the contigs can be traversed by a different processor dividing the amount of time required for reconstructing the genome. The last step of the algorithm is to identify and solve the problems caused by the bad reading, things like overlapped contigs, gaps between contigs, and ambiguous contigs of the graph called bubbles, this is solved by parallelizing the process and generating different states of the genomes with different possibilities of reconstructing it.

[3] Using Matching DNA sequences Algorithms: Aho-Corasick (AC) and Boyer Moore (BM)

Is usual to see these two algorithms to make high-efficiency comparison between two or more completes DNA. In our actual application, we search two equal n-sequence (Prefix and Suffix) present in two segments of DNA, because those algorithms were made for exact string matching and multi pattern finding, and we are looking for a not exactly length string, however, it can be very useful to search the longest n-substring common in all sequences, something that we need to construct K-Overlap graph or Bruijn Graph. For this reason, is important to consider in our solutions this kind of Algorithms.

The Aho-Corasick algorithm use two main stages: A Finite state machine construction stage and a matching stage. The finite state machine construct a suffix-tree, and the matching stage makes find out the pattern set within the given string. This make a "graph" that can contain cycles, and make possible find all the paths given the suffix of the sequences and patterns.

The Boyer Moore algorithm is an efficient string searching algorithm that is consider
the most efficient string-matching algorithm in usual applications, for example, in text editors and commands substitutions. The reason is that it works the fastest when the alphabet is moderately sized (in this case 4) and the pattern is relatively long.

[4] K-Overlap Graph with TSP

A K-overlap graph is a di-graph in which each string in a collection is represented by a node and node *s* is connected to *t* with a directed edge if and only if some suffix of *s* equals a prefix of *t.* We say that *k* is the length of the suffix and prefix present in both strings, the weight of every edge is the k for those nodes connected by this edge. For our application, we assume that the length of the string is more

than *k* and less than 100, also the nodes are the n-segments of DNA. To see the final and complete DNA sequence we find the shortest path which visits every node exactly once, this is the TSP (Traveling Salesman Problem).

The problem with this solution is that we are using NP-complete problems to find the complete DNA sequence, more exactly the TSP and get the common k-substrings between all the n-segments, so its complexity is not really good, but always give a correct solution. Another important characteristic of this solution is that it can't consider the possible ambiguity between the overlap of two or more segments, in that case we need to make a check to verify if every three nucleobases of the ARNm exist, in that case, the DNA sequence is correct.

REFERENCES

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