SyntenyFinder: A Synteny Blocks Generation and Genome Comparison Tool

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Introduction

Recent advances in sequencing and genome assembling technologies are resulting in many finished genomes. The comparison of these genomes has been emerging as a powerful tool for genome interpretations and has led to many important scientific discoveries. The genome comparison tasks often require genomes to be decomposed to a collection of synteny blocks – long regions of conserved DNA.

[Here we insert a colorful picture about synteny blocks]

Currently existing tools can reconstruct synteny blocks from genomes represented as sequences of enumerated local alignments, or *anchors*. We propose *SyntenyFinder* – a tool for finding synteny blocks in genomes represented as nucleotide sequences. Our approach is based on de Bruijn graph and can be applied to closely related genomes.

De Bruijn graphs

K-dimensional de Bruijn graph $G(k)$ is a graph which vertex set consists of all possible k-length strings over the alphabet $\{A, C, G, T\}$. For each $(k+1)$ - substring w in the given string S we add to $G(k)$ an edge that connects k-prefix of w with k-suffix of w and label the edge with index of the first character of w.

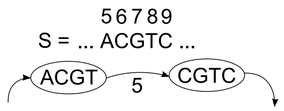


Figure 1: Forming edge set of a **4**-dimensional de Bruijn graph

In this graph we allow only paths that have consecutive labels on edges, so each valid path spells a substring from S. Non-branching paths in the graph $G(k)$ indicate repeats in the string S, i.e. synteny blocks. But in real genomes synteny blocks contain variations that disrupt non-branching paths. These variations create so called *bulges* in the graph. In order to reconstruct synteny blocks we must *simplify* the graph.

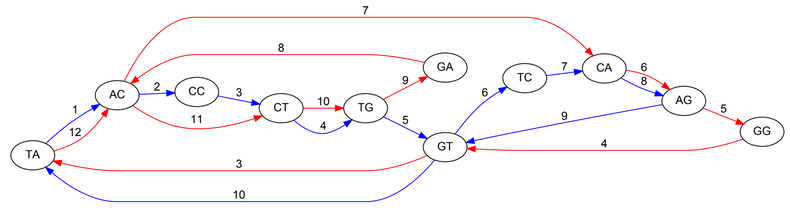
SyntenyFinder algorithm

Given two numbers k and δ and a set $S = \{S_1, S_2, \ldots, S_n\}$ of chromosomes represented as nucleotide strings, our algorithm works as follows:

- Concatenate all string in S into the supergenome $\hat{S}$
- Construct graph $G_+(k)$ from $\hat{S}$ and color all it's edges *blue*
- Construct graph $G_-(k)$ from reverse-complementary of $\hat{S}$ and color all it's edges *red*
- Obtain $G(k) = G_+(k) \cup G_-(k)$ and change $\hat{S}$ so that $G(k)$ doesn't contain bulges with both branches having size $< \delta$
- Output non-branching paths

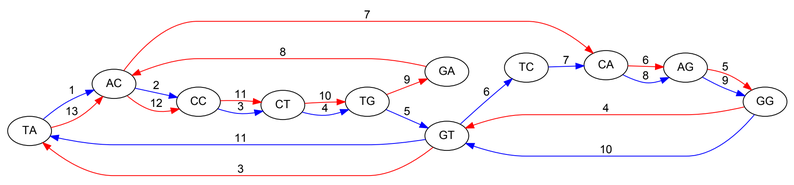
At any moment during simplification there is one-to-one correspondence between the string $\hat{S}$ and the graph – any changes in $\hat{S}$ are immediately reflected in $G(k)$.

5' TACCTGTCAGTA 3'
3' ATGGACAGTCAT 5'



(a) De Bruijn graph $G(k)$ built from $\hat{S} =$ "*TACCTGTCAGTA*". Two paths ("*AC*", "*CC*", "*CT*") and ("*AC*", "*CT*") form a *bulge* that indicate an indel in the substrings "*ACCT*" and "*ACT*".

5' TACCTGTCAGGTA 3'
3' ATGGACAGTCCAT 5'



(b) The same graph after collapsing the bulge. Now long non-branching path spells synteny block "*TACCTG*".

Figure 2: Illustration of *de Bruijn* graphs and simplification process

Results

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Discussion

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References

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