Universität Bielefeld
Technische Fakultät

AG Genominformatik
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Algorithms in Genome Research

Winter 2021/2022

Exercises

Number 11, Discussion: 2022 February 04

1. What is an *open* pangenome and what is a *closed* pangenome?

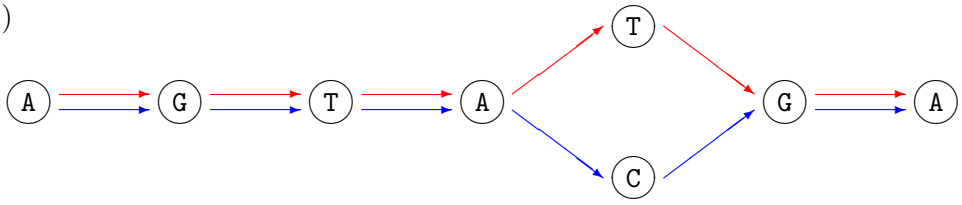
   Schematically, how do an open and a closed pangenome look like

   - as a Venn diagram in gene-based pangenomics?
   - as a pangenome graph in genome-based pangenomics?

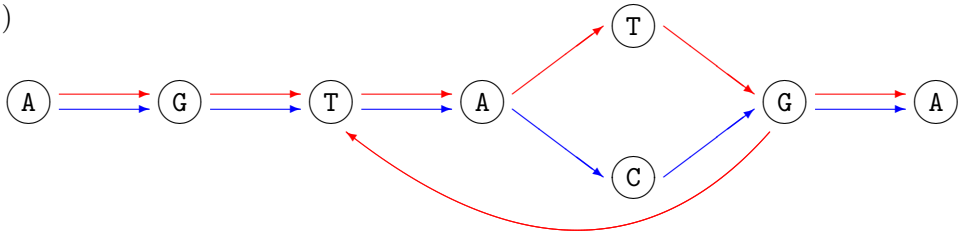
2. Two popular data structures to represent a genome-based pangenome are the variation graph and the colored de Bruijn graph.

   (a) Given the following two variation graphs, find colored de Bruijn graphs of dimension $k = 3$ that contain the same sets of strings.

   (a.1)

   (a.2)

   (b) Given the following three "genome" sequences. Construct their compacted colored de Bruijn graph of dimension $k = 4$.

   CAGGATCAGAACGGC
   GGACCCAGGATAGA
   AGGACCCATAGAACGGC

   Find a variation graph that represents the same set of strings.

3. Develop the details of an algorithm that takes as input a variation graph G and a query sequence S, and finds a position in G where an optimal (unit-cost) semi-global alignment of S and any (sub)string represented in G ends.

   Note: First consider that G is a directed acyclic graph (DAG). Then generalize your algorithm to the case where G may contain cycles.