

Algorithms in Genome Research
Winter 2025/2026

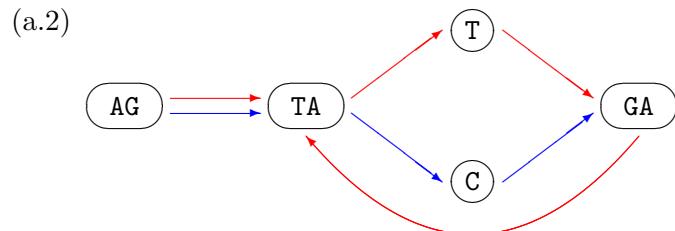
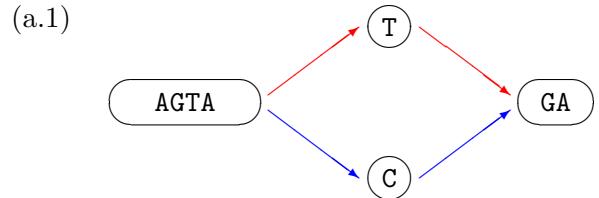
Exercises

Number 9, Discussion: 2026-January-16

1. Pangenome openness.
 - (a) What is an *open* pangenome and what is a *closed* pangenome?
 - (b) Schematically, how do an open and a closed pangenome look like
 - as a Venn diagram in gene-based pangenomics?
 - as a pangenome graph (e.g. variation graph or colored de Bruijn graph) in genome-based pangenomics?
 - (c) Why is it better to speak only of the *openness* of a pangenome?
2. Construct the positional Burrows Wheeler Transformation (pBWT) after processing the following six binary strings (representing genomic haplotypes):

$$\begin{aligned}s_1 &= 10101010000101011 \\s_2 &= 01101101000110001 \\s_3 &= 01001101000101011 \\s_4 &= 10101111000111001 \\s_5 &= 01101001000101011 \\s_6 &= 10001010000101011\end{aligned}$$

- (a) Is there a pronounced recombination site visible?
- (b) What is the largest haplotype block ending at the end of this genomic region?
3. 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 compacted colored de Bruijn graphs of dimension $k = 3$ that contain the same sets of strings.



(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.

4. 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.