

## Algorithms in Genome Research

Winter 2025/2026

### Exercises

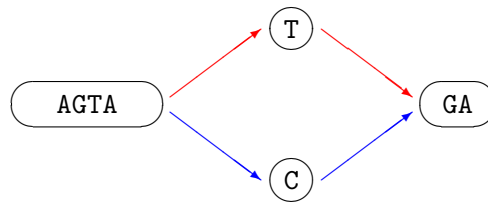
#### Number 9, Discussion: 2026-January-16

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):

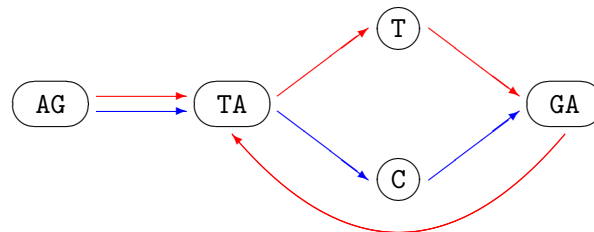
```
s1  =  10101010000101011
s2  =  01101101000110001
s3  =  01001101000101011
s4  =  10101111000111001
s5  =  01101001000101011
s6  =  10001010000101011
```

- (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.

(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.

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.*