

# Overlap Graph for Assembling and Scaffolding Algorithms: Paradigm Review and Implementation Proposals

Victor Epain

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# Overlap Graph for Assembling and Scaffolding Algorithms: Paradigm Review and Implementation Proposals

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26th October 2022

# Abstract

Assembling Deoxyribonucleic Acid (DNA) *fragments* based on their *overlaps* remains the main *assembly* paradigm with long DNA fragments sequencing technologies, independently of the aim to resolve only one or several haplotypes. Since an overlap can be seen as a *succession relationship* between two oriented fragments, the *directed graph* structure has emerged as the more appropriate data structure for handling overlaps. However, this *graph* paradigm did not appear to take benefit of the *reverse* symmetry of the orientated fragments and their overlaps, which is a result of blind DNA doublestrand sequencing. Thus, the *bi-directed graph* paradigm was introduced to be the one that reduces the graph size by handling the reverse symmetry, and since becomes the mainly used graph paradigm. Nevertheless, graph paradigms have never been contrasted before, and no implementations were described. Here we make a complete review on the existing overlap graph paradigms. Furthermore, we present different implementations that are theoretically compared in terms of memory, and their impact on the design and on the time of some basic graph algorithms. We also show that by adapting close logic implementations, a graph paradigm can be switched to another.

## Keywords

Directed graph · Overlaps

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# 1 Introduction

#### What is complementary strands?

Double-stranded Deoxyribonucleic Acid (DNA) molecules still cannot be entirely sequenced. In fact, every *sequencing* technology (*sequencer*) generates numerous overlapping genomic *fragments*.

# 1.1 Reads

A DNA fragment obtained from a sequencing stage is denoted by *read*.

# ► Definition 1.1: Raw reads

Let  $\mathcal{R}_{aw}$  be the set of raw reads.  $\forall r \in \mathcal{R}_{aw}$ , let define the following attributes:

- $-r_{rid} \in \mathbb{N}$ , the read's integer identifier (index)
- $r_{seq} \in \Sigma^+$  the read's sequence, where  $\Sigma = \{A, T, G, C\}$  is *nucleotide* alphabet

A read can be sequenced from one *strand* or from its complement.

## ► Axiom 1.1: Double-stranded DNA sequencing

- i. The two DNA strands are both sequenced.
- ii. A strand is read in reverse order to the order of its complementary strand.
- iii. Given two reads, it is not possible to know *a priori* it they have been sequenced from the same strand.

The Definition 1.2 formalises Axiom 1.1 point iii.:

## ► Definition 1.2: Strand identifier

Let strand\_iid:  $\mathcal{R}_{aw} \to \{0,1\}$  be the function which returns the DNA strand identifier for a read.

Then Axiom 1.1 point iii. can be mathematically formalised:

 $\exists (q,r) \in \mathcal{R}_{aw}^{2}, q \neq r \mid \texttt{strand\_iid}(q) \neq \texttt{strand\_iid}(r)$ 

Axiom 1.1 suggests that combining two reads may result in a chimaera mix of the two strands because all the reads have not been sequenced from the same strand. Furthermore, only keeping the original sequence of the reads can result in the loss of strand parts during the *assembly* stage that aims to reconstruct the longest true parts of one strand. To solve these issues, it is sometimes necessary to consider the complementary sequence of some reads (i.e. the sequences on the complementary strand). For this, the sequence of the concerned reads are reversed (the end becomes the beginning, and vice versa) and each of its nucleotides is complemented ( $A \rightleftharpoons T, G \rightleftharpoons C$ ). Arbitrarily, the original sequence of a read is denoted as the *forward*, while the *reverse* denotes the reverse-complement. In the following, determining what sequence is taken for a read is defined as *orienting* it. Finally, it is necessary to consider both the forward and the reverse orientation for all the reads. Figure 1 explains the meaning of forward and reverse orientations in the context of sequencing technology.

#### Definition 1.3: Reversed reads

Let  $\mathcal{R}_{ev} = \{u_r \mid u_f \in \mathcal{R}_{aw}\}$  denote the set of reversed reads. Thus  $\mathcal{R} = \mathcal{R}_{aw} \cup \mathcal{R}_{ev}$ . Let  $u \in \mathcal{R}_{aw}$  be a read. Subscript is added to u to precise its orientation:

- $u_f$  means that u is read in forward orientation (i.e. the original sequence of u, hence  $u_f \in \mathcal{R}_{aw}$ )
- $u_r$  means that u is read in reverse orientation (i.e. the reversecomplemented sequence of u, hence  $u_r \in \mathcal{R}_{ev}$ )

Now the set of all oriented reads  $\mathcal{R}$  was built, the reverse operation can be defined:

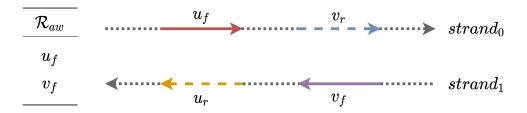
#### Definition 1.4: The reverse operation for reads

For a given read  $u \in \mathcal{R}$ ,  $\overline{u}$  denotes its reverse, where:

- $\overline{u}_{rid} = u_{rid}$  (i.e. a read u and its reverse  $\overline{u}$  have the same identifier)
- $\overline{u}_{seq} = \overline{u_{seq}} = \overline{b_1 b_2 \cdots b_n} = \overline{b_{n-1}} \cdots \overline{b_1} \text{ where } n \in \mathbb{N} \text{ is the length of the nucleotides sequence, and } \forall i \in [\![1;n]\!], b_i \text{ is the } i^{th} \text{ nucleotide base and}$

 $\overline{b_i}$  its complementary nucleotide base.

Note that  $\overline{u_f} = u_r$  and  $\overline{u_r} = u_f$ .



# Figure 1 – Double-stranded DNA sequencing.

 $u_f, v_f$  are two reads from the raw reads set  $\mathcal{R}_{aw}$  obtained from a double-stranded DNA sequencing stage. By default, f (forward) denotes the reading orientation of the raw reads' sequence that gives their sequence, while r (reverse) denotes the reading orientation of the raw reads' sequence that gives their reversed complemented sequence. In this illustration case,  $u_f$  was sequenced from strand  $strand_0$  (strand\_iid( $u_f$ ) = 0) while  $v_f$  was sequenced from strand  $strand_1$  (strand\_iid( $v_f$ ) = 1).

# ► Axiom 1.2: Belonging to one strand

The definition of  $\mathcal{R}$  set and Axiom 1.1 point ii. give the following statement:

 $\forall r \in \mathcal{R}, \text{strand\_iid}(r) = 1 - \text{strand\_iid}(\overline{r})$ 

# 1.2 Overlaps

Reads must be assembled to reconstruct the entire *genome* since they are shorter than the length of the strand from which they have been sequenced (see Axiom 1.1). To assemble the reads means to find the original order of the (oriented) reads. Thus, the assembly stage is at least based on oriented reads *alignments* that define a *succession relationship* between them. One alignment type that answers this issue is *overlap*.

# ► Definition 1.5: Overlap

— An overlap between two nucleotides sequences (u, v) is a semi-global alignment or a close mapping between the end of sequence  $u_{seq}$  and the beginning of sequence  $v_{seq}$ .

— Let define  ${\mathcal O}$  the set of overlaps.

All four scenarios for sequence overlap are depicted in Figure 2.

### ▶ Property 1.1: Overlap reverse symmetry

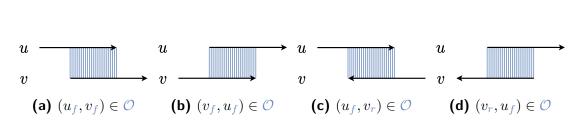
One overlap between two sequences always implies one overlap between the reversed sequences:

$$\forall (q,r) \in \mathcal{R}^2, \ (q,r) \in \mathcal{O} \iff (\overline{r},\overline{q}) \in \mathcal{O}$$

 $\triangleright$  Proof

From Definition 1.3, it is sufficient to take one alignment between two sequences u and v, evaluated by an alignment score, that represents an overlap (hence succession relationship), and remark that:

- i. the alignment score remains the same if the alignment is (reversely) read from v to u,
- *ii.* the score remains the same if each nucleotide is transformed to its complement,
- iii. combining points *i*. and *ii*. results in an alignment between  $\overline{v}$  and  $\overline{u}$  with the same alignment score as alignment u v





u and v are two sequences, represented by an arrow that shows the forward orientation. Each subfigure illustrates one overlap case: (a)  $u_f$  overlaps  $v_f$  (hence  $v_r$  overlaps  $u_r$ ) (b)  $v_f$  overlaps  $u_f$  (hence  $u_r$  overlaps  $v_r$ ) (c)  $u_f$  overlaps  $v_r$  (hence  $v_f$  overlaps  $u_r$ ) (d)  $v_r$  overlaps  $u_f$  (hence  $u_r$  overlaps  $v_f$ ).

Analogously with Definition 1.4, Definition 1.6 extends the reverse operation to overlaps:

#### ► Definition 1.6: The reverse operation for overlaps

For a given overlap  $(q,r) \in \mathcal{O}$ ,  $\overline{(q,r)}$  denotes its reverse i.e.  $(\overline{r}, \overline{q})$ .

# 2 Storing Overlaps in a Graph Structure

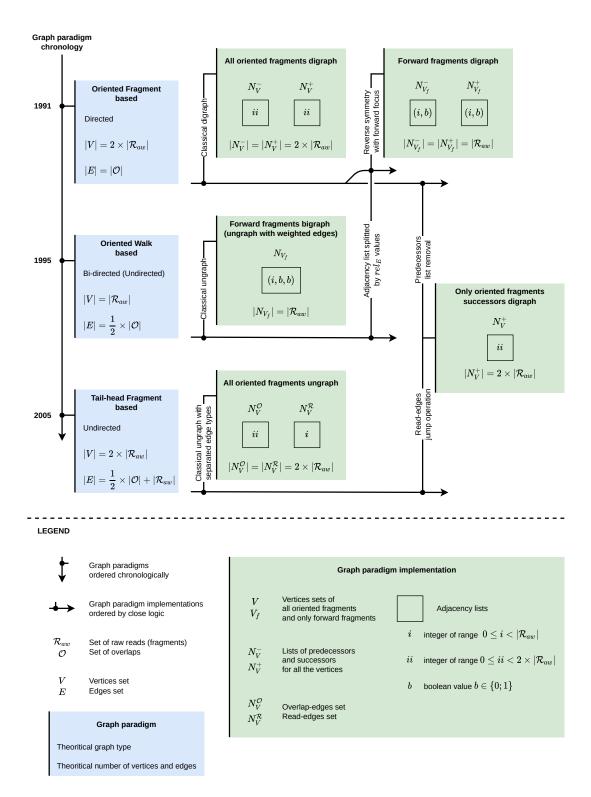
Overlaps between the reads can be represented in a *graph* structure. A graph is a mathematical object composed of *vertices* connected by *edges*. This graph structure would respect the following requirements:

- 1. Querying requirements
  - given an oriented read, getting every overlapping oriented reads
  - given two oriented reads, answering true if and only if they overlap
- 2. Dynamic requirements
  - adding a read/overlap
  - removing a read/overlap

Given all reads, the overlaps between them could be represented in a squared sparse matrix (of size  $\mathcal{R}^2$ ). Sparse matrix compression as Compressed Sparse Row (CSR) or Compressed Sparse Column (CSC) are known for efficiently storing the matrix and enable fast overlap existence querying. Finally, they enable fast edges iteration, but suffer from requirements 2 and can not be immediately adapted for handling overlaps reverse symmetry.

Thus, adjacency list structure seems to be adapted to dynamically add vertices and edges.

Sections 2.1 to 2.3 below offer a complete review of graph paradigms, while Sections 3.1 to 3.3 propose graph implementations for each graph paradigm in the way of its philosophy. Figure 3 summarises the different graph paradigms and their implementations.



# **Figure 3 – Graph paradigms and their implementations respectively ordered chronologically and by logical adaptation.**

**Blue boxes:** they correspond to graph paradigms. They are described by the type of graph they represent, the number of vertices and edges if they have to be drawn. **Green boxes:** they correspond to discussed graph implementations. After their name, the second line gives the adjacency list(s) definition set(s), following by the description of the type it (they) contain(s), finally the last line give the length of the adjacency list(s) (i.e. the number of vertices for which the *neighbours* are given). *Ungraph*, *digraph*, and *bigraph* respectively stand for *undirected graph*, *directed graph* and *bi-directed graph*.

Fix Oriented FragmentS Based and Tail-head FragmentS based

# 2.1 Directed Graph: Oriented Fragments Based

The directed graph structure was the first idea to represent oriented reads and their overlaps, as overlaps are succession relationships. As far as we know, this structure was first mentioned in 1991 by Kececioglu [1]. Later, it was also described by Chin et al. [2], Kamath et al. [3], Andonov et al. [4], Shafin et al. [5] and Cheng et al. [6] in their respective assembly method.

# ► Definition 2.1: Oriented fragment based directed graph

Let G = (V, E) a directed graph such that:

- V is the set of vertices, where each  $v \in V$  represents an oriented read. For each read, there are two vertices (one for the forward orientation, and one for the reverse orientation). Thus, each  $v \in V$  has the following attributes:
  - $-v_{rid} \in \mathbb{N}$  the identifier of the read it represents
  - $-v_{or} \in \{0,1\}$  the orientation of the read it represents (equals to 0 if forward, else equals to 1 if reverse)
- E is the set of edges, where each  $(u, v) \in E$  represents oriented read u overlapping oriented read v.

Figure 4 shows how each overlap case is represented in the directed graph.

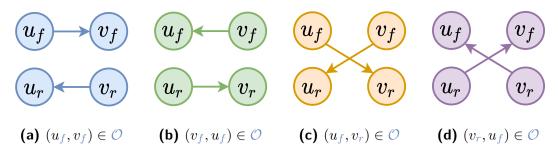


Figure 4 – Overlap cases in the directed graph.

u and v are two sequences represented by two vertices each  $(u_f, u_r \text{ and } v_f, v_r)$ . Each subfigure illustrates one overlap impact on the directed graph: (a)  $(u_f, v_f) \in E$  (hence  $(v_r, u_r) \in E$ ) (b)  $(v_f, u_f) \in E$  (hence  $(u_r, v_r) \in E$ ) (c)  $(u_f, v_r) \in E$  (hence  $(v_f, u_r) \in E$ ) (d)  $(v_r, u_f) \in E$  (hence  $(u_r, v_f) \in E$ ).

▶ Property 2.1: Sizes of the oriented fragment based directed graph
Let G = (V, E) be an oriented fragment based directed graph:
- |V| = 2 × |R<sub>aw</sub>| = |R|
- |E| = |O|

Because there are two vertices for each read, such that one of them represents the reverse of the other one, it is possible to define a reverse operation for this graph. Definition 2.2 extends Definitions 1.4 and 1.6:

## Definition 2.2: The reverse operation for vertices and edges in the oriented fragment based directed graph

**Vertices** For a given vertex  $v \in V$ ,  $\overline{v}$  denotes its reverse, where:

$$\begin{split} & - \ \overline{v}_{rid} = v_{rid} \\ & - \ \overline{v}_{or} = 1 - v_{or} \end{split}$$

**Edges** For a given edge  $e = (u, v) \in E$ ,  $\overline{e} = (\overline{v}, \overline{u})$  denotes its reverse.

Definition 2.3 specifies what a valid walk (and a valid path) is in this graph:

#### ▶ Definition 2.3: Walking in oriented fragment based directed graph

A valid walk results in a valid path  $p = v_0 v_1 \cdots v_{n-1} \in V^n \mid n \in \mathbb{N}$  in the graph G = (V, E) that respects the following criteria:

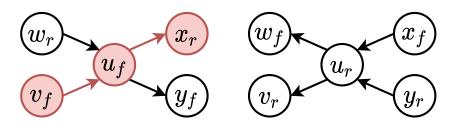
**Contiguity** Two consecutive vertices in the path must be connected by an edge in the graph:

$$\forall i \mid 0 \leq i < n - 1, (v_i, v_{i+1}) \in E$$

**Exclusive orientation** There is at most one orientation for each vertex in path p:

$$\forall v \in p, \overline{v} \notin p$$

Note that walking in this graph is quite similar that walking in a classic directed graph, except that it is not possible to walk through a vertex and its reverse. Figure 5 gives an example of a valid walk in the directed graph.



■ Figure 5 – Valid walk example in the oriented fragment based directed graph.

A valid walk that begins from vertex  $v_f$  is coloured in red. This walk results in a path  $p = v_f u_f x_r$ .

Finally, Property 2.2 suggests that this directed graph inherits a reverse symmetry property analogous to Property 1.1:

# Property 2.2: Reverse symmetry for the vertices and the edges

$$\begin{split} & - \quad \forall v \in V, \overline{v} \in V. \\ & - \quad \forall (u,v) \in E, \overline{(u,v)} = \left(\overline{v}, \overline{u}\right) \in E. \end{split}$$

#### $\triangleright$ Proof

By construction (see Definition 2.1), the first point is immediate. Concerning the second point, it is sufficient to note that if  $(r,q) \in \mathcal{O}$  (hence  $(u,v) \in E$ ), then  $(\overline{q},\overline{r}) \in \mathcal{O}$  (hence  $(\overline{v},\overline{u}) \in E$ ), where r and q are two oriented reads in  $\mathcal{R}$ , respectively represented by vertices u and v in V.

Figure 4 also illustrates Property 2.2.

# 2.2 Bi-directed Graph: Oriented Walk Based

In order to avoid creating two vertices for each read (and thus creating two edges for each overlap), the bi-directed graph structure to store overlaps was introduced by E. W. Myers in 1995 [7]. The key idea is to represent each read with only one vertex and keep the strict necessary overlap information between two reads on the edge connecting two vertices. Definition 2.4 provides a formal description. It was also described by Sommer et al. [8], Hernandez et al. [9] and Salmela et al. [10] in their respective assembly method.

#### Definition 2.4: Oriented walk based bi-directed graph

Let  $G = (V, E, or_E, rel_E)$  a bi-directed graph such that:

- V is the set of vertices, where each  $v \in V$  represents a non-oriented read. For each read, there are only one vertex. Thus, each vertex  $v \in V$  has an identifier of the read it represents  $v_{rid} \in \mathbb{N}$ .
- E is the set of edges, where each  $(u, v) \in E$  represents an overlap between oriented read u and oriented read v. The overlap information are given by  $or_{uv}$  and  $rel_{uv}$ :
  - the orientation of u relatively to this of v is given by edge attribute  $or_E$ : if the orientations are the same, then  $or_{uv} = 0$ , else  $or_{uv} = 1$
  - given that u identifier is lexicographically less that this of v,  $rel_{uv} = 0$  if u in forward orientation overlaps v (in orientation given by  $or_{uv}$ ), else,  $rel_{uv} = 1$  if v (in orientation given by  $or_{uv}$ ) overlaps u in forward orientation

While visually each edge has two extremities in the bi-directed graph, in memory the graph is undirected. Figure 6 shows how visually and how internally each overlap is stored in the bi-directed graph.

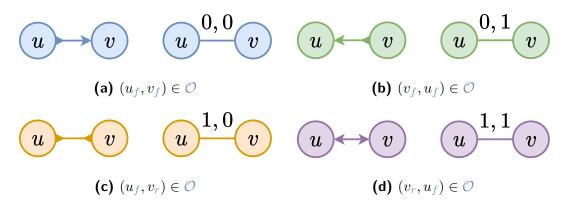


Figure 6 – Overlap cases in the bi-directed graph.

u and v are two unoriented sequences. Each subfigure illustrates one overlap impact on the bi-directed graph. For each, the first subfigure corresponds to the visualisation of a bi-directed edge, and the second shows the same information but with an undirected edge with  $or_{uv}$  and  $rel_{uv}$  attributes. (a) u and v have the same orientation in the overlap hence  $or_{uv} = 0$ , u in forward orientation overlaps v hence  $rel_{uv} = 0$  (b) u and v have the same orientation in the overlap hence  $or_{uv} = 0$ , u in forward orientation is overlapped by v hence  $rel_{uv} = 1$  (c) u and v do not have the same orientation in the overlap hence  $or_{uv} = 1$ , u in forward orientation overlaps v hence  $rel_{uv} = 0$  (d) u and v do not have the same orientation in the overlap hence  $or_{uv} = 1$ , u in forward orientation is overlapped by v hence  $rel_{uv} = 1$ 

#### ▶ Property 2.3: Sizes of the oriented walks based bi-directed graph

Let G = (V, E) be an oriented walks based bi-directed graph:

 $- |V| = |\mathcal{R}_{aw}| = \frac{1}{2} \times |\mathcal{R}|$  $- |E| = \frac{1}{2} \times |\mathcal{O}|$ 

As the vertices represent unoriented reads and the overlaps are succession relationships between two oriented reads, it is necessary to define a variable for each vertex that gives its orientation:

## ► Definition 2.5: Vertex orientation variable

At each vertex  $v \in V$  is associated a variable  $v_{or}$  that gives its orientation.

Given an overlap between two oriented reads, the variables of the two vertices that correspond to them (but unoriented) must respect their orientation. Definition 2.6 formalises this constraint that named co-validity constraint:

## Definition 2.6: Co-validity for the orientation variables of the edge' extremities

Let  $(u, v) \in E$  be an edge. The orientation variables  $u_{or}$  and  $v_{or}$  are co-valid according the edge's attributes when:

— they are co-valid for  $or_{uv}$  attribute:

$$|u_{or} - v_{or}| = or_{uv}$$

- they are co-valid for  $rel_{uv}$  attribute:

$$u_{or} = \begin{cases} rel_{uv} & \text{if } u_{rid} < v_{rid} \\ |(1 - or_{uv}) - rel_{uv}| & \text{if } u_{rid} > v_{rid} \end{cases}$$

To know if the orientation variables are co-valid, the identifiers of the two consecutive vertices have to be compared. To avoid this verification, one may remark that the attribute  $rel_{uv}$  equals to  $1 - rel_{vu}$ , and can suggest a change in the attribute value, depending on the vertex u or v from which the edge (u, v) is considered. But this would contradict the bi-directed graph paradigm philosophy (which is a undirected graph paradigm) since having two different edge attributes  $rel_{uv}$  and  $rel_{vu}$  implies that the graph is directed.

As the graph is bi-directed, it is possible to define a reverse operation. Analogously to Definition 2.2, Definition 2.7 formalises the reverse operation in the bi-directed graph.

# Definition 2.7: The reverse operation for vertices and edges in the oriented walk based bi-directed graph

**Vertices** For a given vertex  $v \in V$  and a fixed orientation variable  $v_{or}$ ,  $\overline{v}$  denotes its reverse, where:

 $- \overline{v}_{rid} = v_{rid}$  $- \overline{v}_{or} = 1 - v_{or}$ 

**Edges** For a given edge  $e = (u, v) \in E$  and fix co-valid orientation variables  $u_{or}$  and  $v_{or}$ ,  $\overline{e} = (\overline{v}, \overline{u})$  denotes its reverse.

According to Definition 2.4, given  $(u, v) \in E$  and one orientation for u or for v, it is necessary to check  $rel_{uv}$  value to determine the succession relationship between oriented u and oriented v. This particularity makes the bi-directed graph *oriented*  walk dependent. Definition 2.8 specifies what a valid walk is in this graph.

## ► Definition 2.8: Walking in oriented walk based bi-directed graph

A valid walk results in a path  $p = v_0 v_1 \cdots v_{n-1} \in V^n \mid n \in \mathbb{N}$  in the graph  $G = (V, E, or_E, rel_E)$  that respects the following criteria:

#### Contiguity

— Two consecutive vertices in the path must be connected by an edge in the graph:

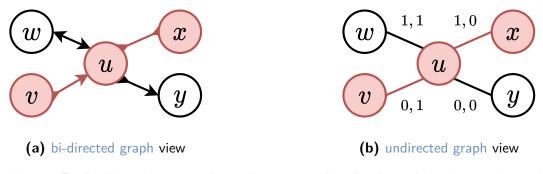
$$\forall i \mid 0 \le i < n - 1, (v_i, v_{i+1}) \in E$$

— Given the vertices' orientation  $v_{i_{or}}$  and  $v_{i+1_{or}}$ , they must be co-valid.

Exclusive orientation At most one orientation is chosen for each vertex:

$$\forall v_i, v_j \in p, v_i = v_j \implies i = j$$

Figure 7 gives an example of a valid walk in the bi-directed graph. Note that walking in this graph is not similar to walking in a classical undirected graph because the orientation variables must be co-valid.



**Figure 7** – Valid walk example in the oriented walks based bi-directed graph. A valid walk is coloured in red. As the graph is undirected, the resulting path can be read in two possible ways: from vertex v or from vertex x. Let  $p_v = vux$  the one that begins from v such that  $v_{or} = 0, u_{or} = 0, x_{or} = 1$ . Thus,  $p_x = xuv$  is the one that begins from x such that  $x_{or} = 0, u_{or} = 1, v_{or} = 1$ . Note that  $p_x = \overline{p_v}$ . In (a) edges are drawn bidirected while in (b) they are drawn undirected.

Thanks to edges attributes  $or_E$  and  $rel_E$ , the bi-directed graph inherits a reverse symmetry property analogous to Property 1.1:

# ▶ Property 2.4: Reverse symmetry for the edges

Given an edge  $(u, v) \in E$  and its attributes  $or_{uv}$  and  $rel_{uv}$ , an overlap and its reverse are encoded in the graph.

#### ⊳ Proof

Without any loss of generality, let suppose that u identifier is lexicographically less that this of v.

- If  $or_{uv} = 0$ :

- if  $rel_{uv} = 0$ , then: if u orientation is fixed forward, then overlap  $(u_f, v_f)$  is obtained; while if u orientation is fixed reverse, then  $(v_r, u_r)$  is obtained (because  $rel_{uv}$  determines if oriented v is after or before u in forward orientation)
- else: if u orientation is fixed forward, then overlap  $(v_f, u_f)$  is obtained; while if u orientation is fixed reverse, then  $(u_r, v_r)$  is obtained.

- Else:

- if  $rel_{uv} = 0$ , then: if u orientation is fixed forward, then overlap  $(u_f, v_r)$  is obtained; while if u orientation is fixed reverse, then  $(v_f, u_r)$  is obtained.
- else: if u orientation is fixed forward, then overlap  $(v_r, u_f)$  is obtained; while if u orientation is fixed reverse, then  $(u_r, v_f)$  is obtained.

# 2.3 Undirected Graph: Tail-Head Fragments Based

A new undirected graph structure was presented by E. W. Myers in 2005 [11]: one read is represented by its tail and its head. Both the tail and the head are vertices, and there is one edge from the tail to the head. Passing through first the tail and then the head corresponds to choose the read in forward orientation, while passing through first the head and then the tail corresponds to choose it in reverse orientation. This new type of edges are called read-edges, at the opposite of overlap-edges that correspond to overlaps. A walk in the graph must alternate between read-edges and overlap-edges. This representation was also described in the Mäkinen et al.'s book [12] and by Li [13] for its assembly method.

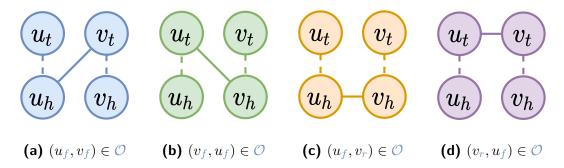
#### ► Definition 2.9: Tail-head Fragments Based undirected graph

Let G = (V, E) a undirected graph such that:

- V is the set of vertices, where each  $v \in V$  represents one of the extremity of one read. For each read, there are two vertices  $v_t, v_h$  (respectively for the tail of the read, and for its head). Thus, each  $v \in V$  has the following attributes:
  - $-v_{rid} \in \mathbb{N}$  the identifier of the read it represents
  - $-v_{ext} \in \{0,1\}$  the extremity of the read it represents (equals to 0 if it is the head, else equals to 1 if it is the tail<sup>a</sup>)
- $E = E^{\mathcal{R}} \cup E^{\mathcal{O}}$  is the set of edges, such that:
  - each undirected read-edge  $(v_t, v_h) \in E^{\mathcal{R}}$  encodes the two possible read orientations (forward if from  $v_t$  to  $v_h$ , else reverse)
  - each undirected overlap-edge  $(u, v) \in E^{\mathcal{O}}$  represents which extremity of read u is overlapping which extremity of read v

 $^{a}$ The values for the extremities are arbitrary: while selecting 0 for the tail and 1 for the head appears more natural, switching the values will be interesting later.

Figure 8 shows for all the overlap cases how they are represented in the undirected graph.



#### Figure 8 – Overlap cases in the undirected graph.

 $u_t, u_h$  and  $v_t, v_h$  are respectively the tail and the head of reads u and v. Dashed edges correspond to read-edges while plain edges correspond to overlap-edges. Each subfigure illustrates one overlap impact on the undirected graph: (a)  $(u_h, v_t) \in E$  (b)  $(v_h, u_t) \in E$  (c)  $(u_h, v_h) \in E$  (d)  $(v_t, u_t) \in E$ .

#### ▶ Property 2.5: Sizes of the tail-head fragment based undirected graph

Let G = (V, E) be an oriented walks based bi-directed graph:

 $-|V| = 2 \times |\mathcal{R}_{aw}| = |\mathcal{R}|$  $-|E| = \frac{1}{2} \times |\mathcal{O}| + |\mathcal{R}_{aw}|$ 

As for each read there are two vertices that represent their two extremities, it is possible to define a reverse operation. Analogously to Definitions 2.2 and 2.7, Definition 2.10 formalises the reverse operation in the undirected graph.

# ► Definition 2.10: The reverse operation for vertices and edges in the tail-head fragment based undirected graph

**Vertices** For a given vertex  $v \in V$ ,  $\overline{v}$  denotes its reverse, where:

 $\begin{array}{l} - \ \overline{v}_{rid} = v_{rid} \\ - \ \overline{v}_{or} = 1 - v_{or} \end{array}$ 

**Edges** For a given edge  $e = (u, v) \in E$ ,  $\overline{e} = (v, u)$  denotes its reverse.

Because of the partition of edges set E in two subsets, walking in this graph does not correspond to a traditional undirected graph walk. Definition 2.11 specifies what a valid walk is in this graph.

# Definition 2.11: Walking in tail-head fragments based undirected graph

A valid walk results in a path  $p = v_0 v_1 \cdots v_{2k-1} \in V^{2k} \mid k \in \mathbb{N}$  in the graph  $G = (V, E^{\mathcal{R}} \cup E^{\mathcal{O}})$  that respects the following criteria:

Contiguity Read-edges and overlap-edges alternate in the path:

— odd-numbered edges in the path are read-edges:

 $\forall i \mid 0 \le i \le k, (v_{2i}, v_{2i+1}) \in E^{\mathcal{R}}$ 

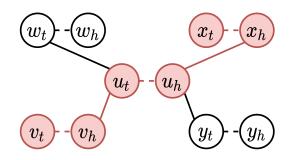
— even-numbered edges in the path are overlap-edges:

 $\forall i \mid 1 \le i < k, (v_{2i-1}, v_{2i}) \in E^{\mathcal{O}}$ 

Exclusive orientation At most one orientation is chosen for each vertex:

 $\forall v_i, v_j \in p, v_i = v_j \implies i = j$ 

Note that walking in this graph is not similar that walking in a classic undirected graph, because a valid walk must alternate between read-edges and overlap-edges. Figure 5 gives an example of a valid walk in the undirected graph.



# Figure 9 – Valid walk example in the tail-head fragment based undirected graph.

A valid walk is coloured in red. As the graph is undirected, the resulting path can be read in two possible ways: from vertex  $v_t$  or from vertex  $x_t$ . Let  $p_v = v_t v_h u_t u_h x_h x_t$  the one that begins from  $v_t$ , thus  $p_x = x_t x_h u_h u_t v_h v_t$  is the one that begins from  $x_t$ . Note that  $p_x = \overline{p_v}$ .

Because the set of vertices contains the two extremities of each read, the undirected graph inherits a reverse symmetry property analogous to Property 1.1:

# Property 2.6: Reverse symmetry for the read-edges and the overlap-edges

Given one overlap-edge  $(u, v) \in E^{\mathcal{O}}$  and the two read-edges  $(u_t, u_h) \in E^{\mathcal{R}}$ and  $(v_t, v_h) \in E^{\mathcal{R}}$ , one overlap and its reverse are encoded in the graph.

 $= \forall (v_t, v_h) \in E, (v_h, v_t) \in E, \text{ where } v_t \text{ corresponds to the tail of read } v \text{ and } v_h \text{ corresponds to its head.}$ 

$$- \forall (u,v) \in \underline{E}, (v,u) \in \underline{E}.$$

#### $\triangleright$ Proof

- Read-edge  $(v_t, v_h)$  corresponds to reading read v in forward orientation, hence  $(v_h, v_t)$  correspond to reading it in reverse orientation.
- Let  $(u, v) \in E^{\mathcal{O}}$  be an overlap-edge, hence read-edges  $(\overline{u}, u)$  and  $(v, \overline{v})$ are considered. Moreover, overlap-edge (v, u) is also in  $E^{\mathcal{O}}$ , hence read-edges  $(u, \overline{u})$  and  $(\overline{v}, v)$  are considered, and they correspond to the

reverse of the previous read-edges.

Figure 8 also illustrates Property 2.6.

#### 3 **Overlap Graph Implementations**

For each graph paradigm in Section 2 at least one implementation is proposed in Sections 3.1 to 3.3. A map of all implementations and the graph paradigms they follow is illustrated in Figure 3.

In the following, let consider that all the overlaps in overlaps set  $\mathcal{O}$  are kept, and reads in reads set  $\mathcal{R}_{aw}$  participate in at least one overlap. Also let suppose that  $min_{r \in \mathcal{R}_{aw}} r_{rid} = 0$  and  $max_{r \in \mathcal{R}_{aw}} r_{rid} = |\mathcal{R}_{aw}| - 1$ . The previous assertions permit to easily build an index on read identifiers *rid*. Also, mathematical terms as G = (V, E) remain the same as in Section 2.

#### 3.1Directed Graph: Oriented Fragments Based

Section 3.1.1 describes the first implementation idea for the oriented fragment based directed graph, while Sections 3.1.2 and 3.1.3 takes the benefits of reverse symmetry to build a more clever implementation.

#### 3.1.1All Oriented Fragments Directed Graph (DGA)

For each read, there are two vertices in the directed graph. Remind that each read identifier  $r_{rid}$  corresponds to a unique integer identifier (it is an index, see Definition 1.1).

The All Oriented Fragments Directed Graph (DGA) implementation is the first and the simplest idea that follows a classical directed graph implementation. Thus, for each read  $r \in \mathcal{R}_{aw}$  there are two vertices  $v_f, v_r \in V$  such that the index of  $v_f$  is equal to  $2 \times r_{rid}$  and the index of  $v_r$  is equal to  $2 \times r_{rid} + 1$ . Definition 3.1 formalises indices sets.

# ► Definition 3.1: Graph indices set for DGA

Let  $Vind = [0; 2 \times |\mathcal{R}_{aw}|]$  be the set of indices for the vertices:  $- |Vind| = 2 \times |\mathcal{R}_{aw}|$ 

 $- \forall v_{ind} \in Vind, v_{ind} = 2 \times v_{rid} + v_{or}$ , where  $v_{rid}$  corresponds to the read's identifier and  $v_{or} \in \{0, 1\}$  its orientation

Let  $Eind = [0; |\mathcal{O}|]$  be the set of indices for the edges:

- $\begin{array}{l} |Eind| = |\mathcal{O}| \\ \forall e_{ind} \in Eind, \ e_{ind} \ \text{corresponds to the index of edge } e, \ \text{such that} \\ \left| e_{ind} \overline{e}_{ind} \right| = 1 \end{array}$

It is possible now to build the two adjacency lists: the first one for the predecessors, the second one for the successors. They both contain respectively the index of each predecessor, resp. of each successor vertices as the same way as a classic directed graph implementation. They also contain the index of the edge. Definition 3.2 details the way the implementation is built.

add edge index

#### Definition 3.2: DGA implementation

DGA graph implementation is built by:

- **Predecessor list**  $N_V^- \forall v \in V, \forall u \in N_v^-, u_{ind}$  is the index of a predecessor of vertex v
- Successor list  $N_V^+ \ \forall v \in V, \forall w \in N_v^+, w_{ind}$  is the index of a successor of vertex v

Figure 10 illustrates the impact of overlap cases on the structure. For clarity's sake, only the indices of the predecessors (successors) are written.

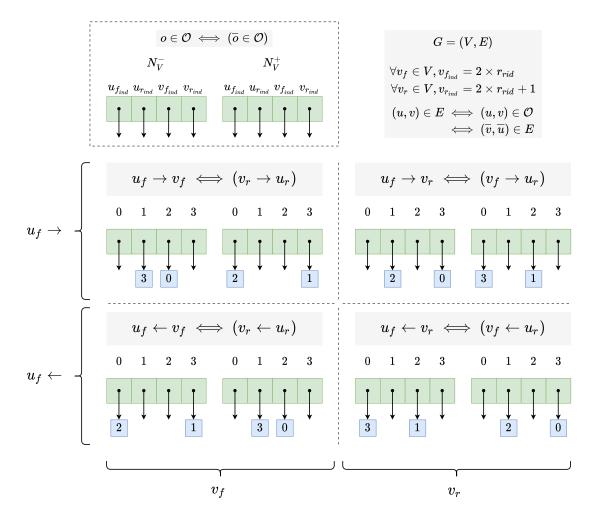
Proposition 3.1 gives the amount of octet DGA implementation consumes.

#### Proposition 3.1: DGA memory consumption

The memory size of the graph Mem(DGA) (in octets) is equals to:

$$Mem(DGA) = 2 \times (2 \times |\mathcal{R}_{aw}| + 1) \times P$$
$$+ 2 \times |\mathcal{O}| \times \left( \left\lceil \frac{1 + \log_2 |\mathcal{R}_{aw}|}{8} \right\rceil + \left\lceil \frac{\log_2 |\mathcal{O}|}{8} \right\rceil \right)$$

where P is the memory size of a memory address.





At the top left, the dot lined box corresponds to the legend for each of the four overlap cases. The grey mathematical formula above provides the overlap and its reverse symmetric overlap, under parenthesis, for the illustrated case. Under, there are the two adjacency lists (the first one contains the predecessors, the second one contains the successors): they both contain the indices of the predecessors/successors. At the top right, the grey box gives some graph properties.

⊳ Proof

proof here

# 3.1.2 Only Oriented Fragments' Successors Directed Graph (DGS)

DGA implementation suffer from redundancies in the data because it does not take benefits from the reverse symmetry. Only Oriented Fragments' Successors Directed Graph (DGS) implementation takes benefits from the symmetry hence while the structure follows the one of DGA, only the successor list is kept. Definition 3.3 details how it is built in memory.

add edge index

## ► Definition 3.3: DGS implementation

DGS graph implementation is built by the successor list  $N_V^+$  such that  $\forall v \in V, \forall w \in N_v^+$ ,  $w_{ind}$  is the index of a successor of vertex v. Also, for each successor w of vertex v

Figure 11 illustrates the impact of each overlap type on DGS implementation. For clarity's sake, only the indices of the successors are written, but not the edge indices.

Proposition 3.2 gives the amount of octet DGS implementation consumes.

#### Proposition 3.2: DGS memory consumption

The memory size of the graph Mem(DGS) (in octets) is equals to:

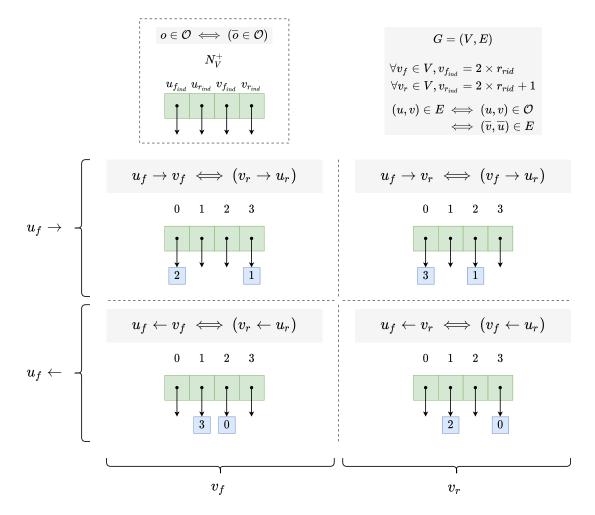
$$Mem(DGS) = (2 \times |\mathcal{R}_{aw}| + 1) \times P$$
$$+ |\mathcal{O}| \times \left( \left\lceil \frac{1 + \log_2 |\mathcal{R}_{aw}|}{8} \right\rceil + \left\lceil \frac{\log_2 |\mathcal{O}|}{8} \right\rceil \right)$$

where P is the memory size of a memory address.

#### $\triangleright$ Proof

For each vertex there is a pointer to its successor list, hence  $2 \times |\mathcal{R}_{aw}|$ pointers, and there is one pointer to the vertices' successor list. Then, for each successor, its index is provided ( $\lceil \log_2 2 \times |\mathcal{R}_{aw}| \rceil$  bits), and the edge index is provided too ( $\lceil \log_2 |\mathcal{O}| \rceil$  bits). These numbers are divided by eight and rounded up to the nearest integer to get the number of octets. Then the sum is multiplied by the number of overlaps ( $|\mathcal{O}|$ ).

### verify if same with commented



## Figure 11 – Only oriented fragments successors directed graph implementation.

At the top left, the dot lined square corresponds to the legend for each of the four overlap cases. The grey mathematical formula above provides the overlap and its reverse symmetric overlap, under parenthesis, for the illustrated case. Under, there is the successor list: it contains the indices of the successors. At the top right, the grey square gives some graph properties.

Proposition 3.3 answer the issue of getting the predecessors.

# ► Proposition 3.3: DGS reverse symmetry to retrieve predecessors

For each vertex  $v \in V$ :

i. its predecessors are the reverse of its reverse' successors

#### 3 GRAPH IMPLEMENTATIONS

ii. the edge index of  $(u, v) \in E$  is the reverse of this of  $(\overline{v}, \overline{u}) \in E$ 

⊳ Proof

Let  $v \in V$  be a vertex. Let  $u \in V$  such that  $(u, v) \in E$ . Thus:

- *i.*  $(\overline{v}, \overline{u}) \in E$ , hence  $\overline{u}$  is the successor of  $\overline{v}$  that is the reverse of v. Finally,  $\overline{\overline{u}} = u$ , that is the predecessor of v.
- ii. If  $\overline{e}_{ind}$  is the edge index of edge  $(\overline{v}, \overline{u})$ , then  $e_{ind} = \overline{e}_{ind} + c$  (where c = 1 if  $\overline{e}_{ind}$  is even, else c = -1) corresponds to the edge index of the reverse of  $(\overline{v}, \overline{u})$  hence the edge index of (u, v).

# 3.1.3 Forward Fragments Directed Graph (DGF)

As for DGS implementation, the last implementation of the directed graph structure, Forward Fragments Directed Graph (DGF), takes benefits from the reverse symmetry. DGF focuses only on the neighbours of the vertices that represent the reads in forward orientation (hence the reads in raw reads set  $\mathcal{R}_{aw}$ ). Therefore, the vertices indices set is not build as previously. Hence for each read  $r \in \mathcal{R}_{aw}$ , let  $v_{ind} = r_{rid}$  be the index of the vertex that represents it. Because an overlap involves two oriented reads, the neighbours' orientation must be included to the adjacency lists. Hence for each neighbour  $v \in V$  in the predecessors/successor lists of a forward vertex, let  $v_{indor} = (v_{ind,v_{or}})$  be its oriented neighbour. Definition 3.4 describes the different sets, and Definition 3.5 details the DGF implementation. For clarity's sake, only the indices of the predecessors/successors are written, but not the edge indices.

#### Definition 3.4: Graph indices set for DGA

Let  $Vind = [0; |\mathcal{R}_{aw}|]$  be the set of indices for the vertices:

$$- |Vind| = |\mathcal{R}_{aw}|$$

 $- \forall v_{ind} \in Vind, v_{ind} = v_{rid}$ , where  $v_{rid}$  corresponds to the read's identifier

Let  $Vindor = [0; |\mathcal{R}_{aw}| [ \times \{0; 1\}$  be the set of indices enriched by a boolean value for the oriented vertices:

 $- |Vindor| = 2 \times |\mathcal{R}_{aw}|$ 

 $- \forall v_{indor} \in Vindor, v_{indor} = (v_{rid}, v_{or}),$  where  $v_{rid}$  corresponds to the read's identifier and  $v_{or}$  to its orientation

Let  $Eind = [0; |\mathcal{O}|]$  be the set of indices for the edges:

 $\begin{array}{l} - |Eind| = |\mathcal{O}| \\ - \forall e_{ind} \in Eind, \ e_{ind} \ \text{corresponds to the index of edge } e, \ \text{such that} \\ \left| e_{ind} - \overline{e}_{ind} \right| = 1 \end{array}$ 

add edge index

#### Definition 3.5: DGF implementation

DGF graph implementation is built by:

- **Predecessor list for the forward**  $N_{V_f}^- \quad \forall v \in V_f, \forall u \in N_v^-, u_{ind}$  is the index of a predecessor of vertex v, and  $u_{or}$  gives its orientation
- Successor list for the forward  $N_{V_f}^+$   $\forall v \in V_f, \forall w \in N_v^+, w_{ind}$  is the index of a successor of vertex v, and  $w_{or}$  gives its orientation

#### Proposition 3.4: DGF memory consumption

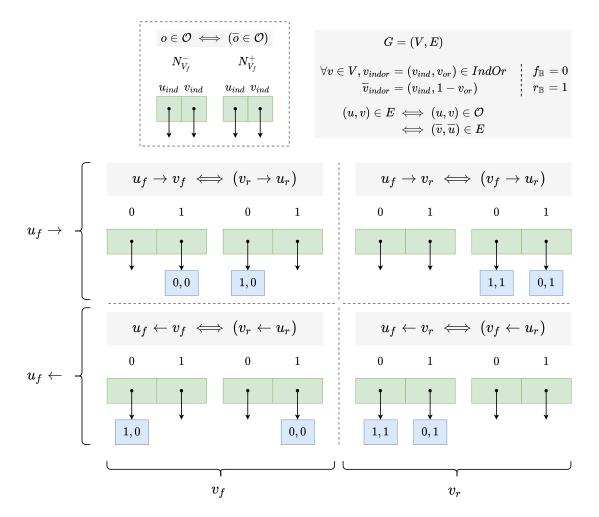
The memory size of the graph Mem(DGF) (in octets) is equals to:

$$Mem(DGF) = 2 \times (|\mathcal{R}_{aw}| + 1) \times P + |\mathcal{O}| \times \left( \left\lceil \frac{1 + \log_2 |\mathcal{R}_{aw}|}{8} \right\rceil + \left\lceil \frac{\log_2 |\mathcal{O}|}{8} \right\rceil \right)$$

where P is the memory size of a memory address.

⊳ Proof

For each (forward) vertex there is a pointer to its predecessor and successor lists, hence  $2 \times |\mathcal{R}_{aw}|$  pointers, and there is one pointer to the vertices' predecessor and successor lists (hence +2). Then, for each predecessor/successor, its index and a boolean orientation value are provided ( $\left[\log_2 2 \times |\mathcal{R}_{aw}|\right]$  bits), and the edge index is provided too ( $\left\lceil \log_2 |\mathcal{O}| \right\rceil$  bits). These numbers are divided by eight and rounded up to the nearest integer to get the number of





At the top left, the dot lined square corresponds to the legend for each of the four overlap cases. The grey mathematical formula above provides the overlap and its reverse symmetric overlap, under parenthesis, for the illustrated case. Under, there are the two adjacency lists for the forward (the first one contains the predecessors, the second one contains the successors): they both contain the couples index-orientation of the predecessors/successors. At the top right, the grey square gives some graph properties.

octets. Then the sum is multiplied by the number of overlaps  $(|\mathcal{O}|)$ .

#### verify if same with commented

Note that in contrast to Proposition 3.2, the memory consumption of adjacency lists pointers is equals to  $2 \times (|\mathcal{R}_{aw}| + 1)$  (versus  $(2 \times |\mathcal{R}_{aw}| + 1)$ ). In fact, the extra P is due to an extra adjacency list.

Proposition 3.5 answer the issue of getting the predecessors/successors of the reverse.

#### ▶ Proposition 3.5: DGF reverse symmetry to retrieve predecessors

For each vertex  $v \in V_r$ :

- i. its predecessors are the reverse of its reverse' successors
- ii. its successors are the reverse of its reverse' predecessors
- iii. the edge index of  $(u, v) \in E$  is the reverse of this of  $(\overline{v}, \overline{u}) \in E$

#### $\triangleright$ Proof

Let  $v \in V[r]$  be a vertex that represents a reverse read.

- Let  $u \in V$  such that  $(u, v) \in E$ . Thus:
  - *i.*  $(\overline{v}, \overline{u}) \in E$ , hence  $\overline{u}$  is the successor of  $\overline{v}$  that is the reverse of v. Finally,  $\overline{\overline{u}} = u$ , that is the predecessor of v.
  - ii. If  $\overline{e}_{ind}$  is the edge index of edge  $(\overline{v}, \overline{u})$ , then  $e_{ind} = \overline{e}_{ind} + c$  (where c = 1 if  $\overline{e}_{ind}$  is even, else c = -1) corresponds to the edge index of the reverse of  $(\overline{v}, \overline{u})$  hence the edge index of (u, v).
- Let  $w \in V$  such that  $(v, w) \in E$ . Thus:
  - *i.*  $(\overline{w}, \overline{v}) \in E$ , hence  $\overline{w}$  is the predecessor of  $\overline{v}$  that is the reverse of v. Finally,  $\overline{\overline{w}} = w$ , that is the successor of v.
  - ii. If  $\overline{e}_{ind}$  is the edge index of edge  $(\overline{w}, \overline{v})$ , then  $e_{ind} = \overline{e}_{ind} + c$  (where c = 1 if  $\overline{e}_{ind}$  is even, else c = -1) corresponds to the edge index of the reverse of  $(\overline{w}, \overline{v})$  hence the edge index of (v, w).

# 3.2 Bi-directed Graph: Oriented Walk Based

# 3.2.1 Forward Fragments Bi-directed Graph (BG)

In the bi-directed graph, there is one vertex for each raw read in  $\mathcal{R}_{aw}$ . Hence for each vertex v is associated an index  $v_{ind} = v_{rid}$ . An overlap and its reverse are represented by only one edge that carries strictly necessary overlap attributes, as described in Definition 2.4. Remind that the bi-directed graph is equivalent to a undirected graph: that's implemented by Unoriented Fragments Bi-directed Graph (BG) implementation. Definition 3.4 describes the different sets, and Definition 3.5 details the DGF implementation. For clarity's sake, only the indices of the predecessors/successors are written, but not the edge indices.

## ► Definition 3.6: Graph indices set for BG

Let  $Vind = [0; |\mathcal{R}_{aw}|]$  be the set of indices for the vertices:

 $- |Vind| = |\mathcal{R}_{aw}|$ 

 $- \forall v_{ind} \in Vind, v_{ind} = v_{rid}$ , where  $v_{rid}$  corresponds to the read's identifier

Let  $Eind = \left[\!\left[0; \frac{1}{2} \times |\mathcal{O}|\right]\!\right]$  be the set of indices for the edges:

 $- |Eind| = \frac{1}{2} \times |\mathcal{O}|$ 

 $- \forall e_{ind} \in Eind, e_{ind} \text{ corresponds to the index of edge } e$ 

#### put paragraph in definition

Concerning the edge indices  $e_{ind}$ , it is possible to use their euclidean quotient by two  $e'_{ind}$  in memory and retrieving them thanks to the orientation of the fewer vertex index (let say u). In fact, if the considered overlap uses  $u_f$ , then  $e_{ind} = 2 \times e'_{ind}$ , else  $e_{ind} = 2 \times e'_{ind} + 1$ 

#### ► Definition 3.7: BG implementation

BG graph implementation is built by:

Neighbours list for the forward  $N_V \ \forall v \in V, \forall w \in N_v, w_{ind}$  is the index of a neighbour of vertex v

**Edges attributes** for each neighbour w of a vertex v two boolean values are provided:  $or_{vw}$  and  $rel_{vw}$  (see Definition 2.4)

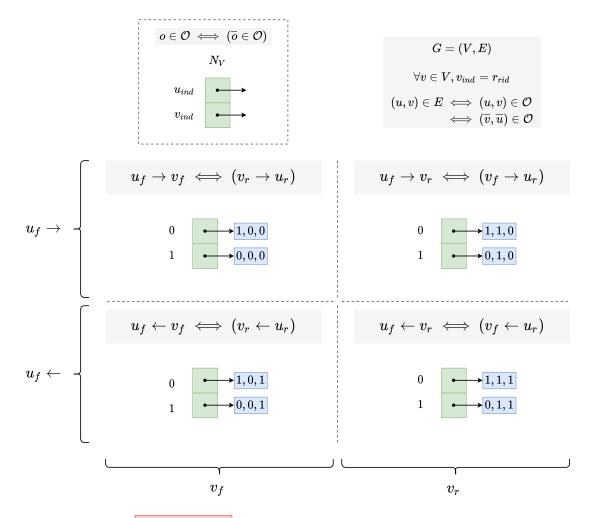


Figure 13 – caption title All four overlap cases structured in the bidirected graph.

At the top, the dot lined square corresponds to the legend for the four overlap cases. The mathematical formula above the line is the overlap such that u is in forward orientation, and the reverse symmetric overlap is under parenthesis. Under the line, there is the one list that contains, in order, the index of the neighbour, the value of  $or_{uv}$  and the value of  $rel_{uv}$ .

# ► Proposition 3.6: BG memory consumption

The memory size of the graph Mem(BG) (in octets) equals:

$$Mem(BG) = (|\mathcal{R}_{aw}| + 2) \times P$$
$$+ |\mathcal{O}| \times \left( \left\lceil \frac{\log_2 |\mathcal{R}_{aw}|}{8} \right\rceil + \left\lceil \frac{\log_2 |\mathcal{O}| - 1}{8} \right\rceil \right)$$
$$32 + \left\lceil \frac{|\mathcal{O}|}{8} \right\rceil \quad V. \text{ Epain}$$

where P is the memory size of a memory address.

#### $\triangleright$ Proof

For each (unoriented) vertex there is a pointer to its neighbour list, hence  $|\mathcal{R}_{aw}|$  pointers, and there is one pointer to the vertices' neighbour list and one to the edges attribute list (hence +2). Then, for each neighbour, its index is provided ( $\lceil \log_2 |\mathcal{R}_{aw}| \rceil$  bits), and the edge index is provided too ( $\lceil \log_2 (\frac{1}{2} \times |\mathcal{O}|) \rceil$  bits). These numbers are divided by eight and rounded up to the nearest integer to get the number of octets. Then the sum is multiplied by the number of overlaps ( $|\mathcal{O}|$ ). Finally, for each edge index  $(\frac{1}{2} \times |\mathcal{O}|)$ , there are two boolean edge attributes.  $\frac{1}{2} \times |\mathcal{O}| \times 2$  is divided by eight and rounded up to get the number of octets.

#### verify if same as comments

The four combinations of edges' attributes or and rel let representing all the overlap cases and their reverse without any redundancy. To verify the reverse symmetry, it is sufficient (and easier) to choose an orientation of u and calculate the overlap case with the edges' attributes.

# 3.2.2 Forward Fragments Directed Graph (DGF)

#### description

ref figure from digraph implementation revsymg

memory

# 3.3 Undirected Graph: Tail-Head Fragments Based

# 3.3.1 All Oriented Fragments Undirected Graph (UGA)

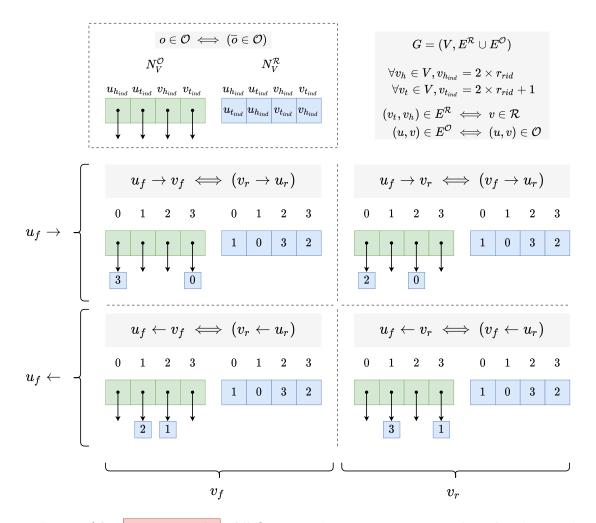
fix for ungraph

For each read, there are two vertices in the directed graph. Remind that each read identifier  $r_{rid}$  correspond to a unique integer identifier (it is an index,

3

see Definition 1.1). Thus, for each read  $r \in \mathcal{R}_{aw}$  there are two vertices  $v_f, v_r \in V$  such that the index of  $v_f$  is equal to  $2 \times r_{rid}$  and the index of  $v_r$  is equal to  $2 \times r_{rid} + 1$ .

It is possible now to build the adjacency lists (one list for the predecessors, and another one for the successors).



**Figure 14 – caption title** All four overlap cases structured in the directed graph.

At the top left, the dot lined square corresponds to the legend for the four overlap cases. The grey mathematical formula above is the overlap such that u is in forward orientation, and the reverse symmetric overlap is under parenthesis. Under, there are the two adjacency lists (the first one contains the neighbours for overlap-edges, the second one contains the neighbours for read-edge): they both contain the indices of the neighbours. Top right grey square gives some graph properties.

memory			
34	V. Epain		

# 3.3.2 Read-edges Jump Directed Graph (DGS)

description

Cref figure only oriented frag succs digraph

memory

remarque que l'on peut arriver visuellement au digraph

# 4 Memory and Time Costs

4.1 Algorithms

4.1.1 Subfunctions

## ► Algorithm 1: Reverse operation on index

Require: Vertex/edge index *ind*.
Ensure: Returns index of the reverse vertex/edge.

function REV(*ind*)
if *ind* | 2 then
return *ind* + 1
return *ind* - 1

For clarity's sake,  $\operatorname{REV}(ind) = \overline{ind}$ .

Require: List of tuple *list*, edge index *e<sub>ind</sub>*, index *t<sub>ind</sub>* of the place of edge index in the tuple contained in *list*. The edge index must be in a tuple.
Ensure: Returns the index of the tuple containing *e<sub>ind</sub>* in *list*.
1: function GET\_INDEX(*list*, *e<sub>ind</sub>*, *t<sub>ind</sub>*)
2: *list<sub>ind</sub>* ← 0

- 3: while  $list[list_{ind}][t_{ind}] \neq e_{ind}$  and  $list_{ind} < |list| 1$  do
- 4:  $list_{ind} \leftarrow list_{ind} + 1$
- 5: **return** *list*<sub>ind</sub>

### 4.1.2 Iterating Over the Predecessors

### ► Algorithm 3: Iterate over the predecessors for DGS

**Require:** Graph G = (V, E), vertex  $v \in V$ , empty list *preds*. **Ensure:** The returned list contains the predecessors of v in graph G and the corresponding edge index. 1: function DGS\_PREDS(G, v, preds)2: for  $(u, e_{ind}) \in N_{\overline{v}}^+$  do 3:  $preds.APPEND(\overline{u}, \overline{e_{ind}})$ 

4: **return** *preds* 

### ► Algorithm 4: Iterate over the predecessors for DGF

**Require:** Graph G = (V, E), vertex  $v \in V$ , orientation of  $v v_{or} \in \{0, 1\}$ , empty list preds. **Ensure:** The returned list contains the predecessors of v in graph G and the corresponding edge index. 1: function DGF\_PREDS $(G, v, v_{or}, preds)$ if  $v_{or} = 0$  then  $\triangleright v$  forward 2: for  $(u, e_{ind}) \in N_v^-$  do 3:  $preds.APPEND(u, e_{ind})$ 4: 5: else for  $(u, u_{or}, e_{ind}) \in N^+_{\overline{u}}$  do 6:  $preds.APPEND(u, 1 - u_{or}, \overline{e_{ind}})$ 7: 8: return preds

#### ► Algorithm 5: Iterate over the predecessors for BGU

**Require:** Graph G = (V, E), vertex  $v \in V$ , orientation of  $v v_{or} \in \{0, 1\}$ , empty list *preds*.

**Ensure:** The returned list contains the predecessors of v in graph G and the corresponding edge index.

```
1: function BGU_PREDS(G, v, v_{or}, preds)
          orientations \leftarrow (0, 1)
                                                                     ▷ forward/reverse orientations
 2:
          for (u, e'_{ind}) \in N_v do
 3:
               if v < u then
 4:
                    if v_{or} = 0 then
 5:
                         if rel_{uv} = 1 then
 6:
                                                                               \triangleright u_f \rightarrow v_f \text{ or } u_r \rightarrow v_f
 7:
                               preds.APPEND(u, orientations[or_{uv}], 2 \times e'_{ind})
                    else if rel_{uv} = 0 then
                                                                                \triangleright u_f \rightarrow v_r \text{ or } u_r \rightarrow v_r
 8:
                         preds.APPEND(u, orientations[1 - or_{uv}], 2 \times e'_{ind} + 1)
 9:
               else if v_{or} = 0 then
10:
                    if or_{uv} = 0 then
11:
                         if rel_{uv} = 0 then
12:
                                                                                                \triangleright u_f \rightarrow v_f
                               preds.APPEND(u, 0, 2 \times e'_{ind})
13:
                    else if rel_{uv} = 1 then
                                                                                                \triangleright u_r \rightarrow v_f
14:
                         preds.APPEND(u, 1, 2 \times e'_{ind} + 1)
15:
               else if or_{uv} = 0 then
16:
                    if rel_{uv} = 1 then
17:
                                                                                                 \triangleright u_r \rightarrow v_r
                         preds.APPEND(u, 1, 2 \times e'_{ind} + 1)
18:
               else if rel_{uv} = 0 then
19:
                                                                                                \triangleright u_f \rightarrow v_r
                    preds.APPEND(u, 0, 2 \times e'_{ind})
20:
          return preds
21:
```

### 4.1.3 Iterating Over the Successors

### ► Algorithm 6: Iterate over the successors for DGS

**Require:** Graph G = (V, E), vertex  $v \in V$ , empty list *succs*. **Ensure:** The returned list contains the successors of v in graph G.

1: function DGS\_SUCCS(G, v, succs)

- 2: for  $(w, e_{ind}) \in N_v^+$  do
- 3:  $succs.APPEND(w, e_{ind})$
- 4: return *succs*

### ► Algorithm 7: Iterate over the successors for DGF

**Require:** Graph G = (V, E), vertex  $v \in V$ , orientation of  $v v_{or} \in \{0, 1\}$ , empty list *succs*.

**Ensure:** The returned list contains the successors of v in graph G.

1: function DGF\_SUCCS( $G, v, v_{or}, succs$ ) if  $v_{or} = 0$  then  $\triangleright v$  forward 2: for  $(w, e_{ind}) \in N_v^+$  do 3: 4:  $succs.APPEND(w, e_{ind})$ 5: else for  $(w, w_{or}, e_{ind}) \in N^-_{\overline{u}}$  do 6:  $succs.APPEND(w, 1 - w_{or}, \overline{e_{ind}})$ 7: 8: return succs

### ► Algorithm 8: Iterate over the successors for BGU

**Require:** Graph G = (V, E), vertex  $v \in V$ , orientation of  $v v_{or} \in \{0, 1\}$ , empty list *succs*. **Ensure:** The returned list contains the successors of v in graph G. 1: function BGU\_SUCCS( $G, v, v_{or}, succs$ ) orientations  $\leftarrow (0, 1)$ ▷ forward/reverse orientations 2: for  $(w, e'_{ind}) \in N_v$  do 3: if v < w then 4: if  $v_{or} = 0$  then 5: if  $rel_{vw} = 0$  then  $\triangleright v_f \rightarrow w_f \text{ or } v_f \rightarrow w_r$ 6: succs. APPEND(w, orientations  $[or_{vw}], 2 \times e'_{ind}$ ) 7:  $\triangleright v_r \rightarrow w_f \text{ or } v_r \rightarrow w_r$ else if  $rel_{uv} = 1$  then 8: succs.APPEND(u, orientations  $[1 - or_{uv}], 2 \times e'_{ind} + 1)$ 9: else if  $v_{or} = 0$  then 10: if  $or_{uv} = 0$  then 11: 12: if  $rel_{uv} = 1$  then  $\triangleright v_f \rightarrow w_f$ succs. APPEND $(w, 0, 2 \times e'_{ind})$ 13: else if  $rel_{uv} = 0$  then 14:  $\triangleright v_f \rightarrow w_r$ 15:  $succs.APPEND(w, 1, 2 \times e'_{ind} + 1)$ else if  $or_{uv} = 0$  then 16: if  $rel_{uv} = 0$  then 17:  $\triangleright v_r \rightarrow w_r$  $succs.APPEND(w, 1, 2 \times e'_{ind} + 1)$ 18:  $\triangleright v_r \to w_f$ 19: else if  $rel_{uv} = 1$  then 20: succs. APPEND $(w, 0, 2 \times e'_{ind})$ 21: return succs

## 4.1.4 Adding a Vertex

### ► Algorithm 9: Add a new vertex in the graph for DGS

**Require:** Graph G = (V, E).

**Ensure:** Returns the new vertex' index (in forward orientation if there is the choice).

1: function DGS\_ADD\_VERTEX(G) 2:  $N_V^+$ .APPEND(EMPTY\_LIST()) 3:  $N_V^+$ .APPEND(EMPTY\_LIST()) 4: return  $|N_V^+| - 2$ 

► Algorithm 10: Add a new vertex in the graph for DGF

Require: Graph G = (V, E).
Ensure: Returns the new vertex' index (in forward orientation if there is the choice).
1: function DGF\_ADD\_VERTEX(G)
2: N<sub>V</sub><sup>-</sup>.APPEND(EMPTY\_LIST())
3: N<sub>V</sub><sup>+</sup>.APPEND(EMPTY\_LIST())

4: return  $|N_V^+| - 1$ 

### ▶ Algorithm 11: Add a new vertex in the graph for BGU

Require: Graph G = (V, E).
Ensure: Returns the new vertex' index (in forward orientation if there is the choice).
1: function BGU\_ADD\_VERTEX(G)
2: N<sub>V</sub>.APPEND(EMPTY\_LIST())
3: return |N<sub>V</sub>| - 1

### 4.1.5 Adding an Edge

### ► Algorithm 12: Add a new edge and its reverse in the graph for DGS

**Require:** Graph G = (V, E),  $(u, v) \in V^2$ . Note that the vertices are already in the graph. **Ensure:** Returns the new edge's index (in forward orientation if there is the choice). 1: function DGS\_ADD\_EDGE(G, u, v) ▷ *ind\_edges* is the number of edges. It is always even. 2:  $N_u^+$ .APPEND $(v, ind\_edges)$ 3:  $N_{\overline{u}}^+$ .APPEND $(\overline{u}, ind\_edges + 1)$ 4:  $ind\_edges \leftarrow ind\_edges + 2$ 5:  $card\_edges \leftarrow card\_edges + 2$ 6: return ind edges - 27:

### ► Algorithm 13: Add a new edge and its reverse in the graph for DGF

**Require:** Graph G = (V, E),  $(u, v) \in V^2$ , with their orientation  $(u_{or}, v_{or}) \in$  $\{0, 1\}^2$ . Note that the vertices are already in the graph. Ensure: Returns the new edge's index (in forward orientation if there is the choice). 1: function DGF\_ADD\_EDGE( $G, u, u_{or}, v, v_{or}$ ) ▷ *ind\_edges* is the number of edges. It is always even. 2: if  $u_{or} = 0$  then  $\triangleright u_f \rightarrow v_f \text{ or } u_f \rightarrow v_r$ 3:  $N_{u}^{+}$ .APPEND $(v, v_{or}, ind\_edges)$ 4:  $\triangleright u_f \leftarrow v_f \text{ or } u_f \leftarrow v_r$ 5: else  $N_u^-$ .APPEND $(v, 1 - v_{or}, ind\_edges + 1)$ 6: if  $v_{or} = 0$  then  $\triangleright u_f \rightarrow v_f \text{ or } u_r \rightarrow v_f$ 7:  $N_u^-$ .APPEND $(u, u_{or}, ind\_edges)$ 8:  $\triangleright u_f \leftarrow v_f \text{ or } u_r \leftarrow v_f$ 9: else  $N_{v}^{+}$ .APPEND $(u, 1 - u_{or}, ind\_edges + 1)$ 10:  $ind\_edges \leftarrow ind\_edges + 2$ 11:  $card\_edges \leftarrow card\_edges + 2$ 12: return  $ind\_edges - 2$ 13:

### ▶ Algorithm 14: Add a new edge and its reverse in the graph for BGU

**Require:** Graph G = (V, E),  $(u, v) \in V^2$ , with their orientation  $(u_{or}, v_{or}) \in \{0, 1\}^2$ . Note that the vertices are already in the graph.

**Ensure:** Returns the new edge's index (in forward orientation if there is the choice).

```
1: function BGU_ADD_EDGE(G, u, u_{or}, v, v_{or})
         \triangleright ind_edges is the number of edges. E_{attr} is a list of edges attributes. \triangleleft
 2:
         or \leftarrow |u_{or} - v_{or}|
 3:
          \  \  \, \text{if} \ u < v \ \text{then} \\
 4:
              rel \leftarrow u_{or}
 5:
 6:
         else
 7:
              rel \leftarrow 1 - v_{or}
 8:
          N_u.APPEND(v, ind\_edges)
 9:
          N_v.APPEND(u, ind\_edges)
          E_{attr}.APPEND(or, rel)
10:
         ind\_edges \leftarrow ind\_edges + 1
11:
         card\_edges \leftarrow card\_edges + 1
12:
13:
         return 2 \times (ind\_edges - 1)
```

### 4.1.6 Deleting a Vertex

### ► Algorithm 15: Delete a vertex for DGS

**Require:** Graph G = (V, E), vertex  $v \in V$  (in forward orientation). **Ensure:** Delete the vertex and its reverse such that  $V' = V \setminus \{v, \overline{v}\}$ , and  $\forall v \in V', 0 \le v_{ind} \le |V'| - 2.$ 1: function DGS\_DELETE\_VERTEX(G, v)> Delete it from its predecessors 2:  $\triangleleft$  $v\_rev \leftarrow v+1$ 3: for  $(u, e_{ind}) \in N_v^+_{rev}$  do 4:  $u\_rev \leftarrow \overline{u}$ 5:  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_u^+ _{rev}, \overline{e_{ind}}, 1)$ 6: if  $adj\_ind = \left| N_u^+ \right| - 1$  then 7: > Just delete the last element 8:  $\triangleleft$  $N_u^+_{rev}$ .POP() 9: 10: else ▷ Replace the edge by the last in the neighbour list 11:  $\triangleleft$ 

12:	$N_{u\_rev}^+[adj\_ind] \leftarrow N_{u\_rev}^+.$ POP()	
13:	$card\_edges \leftarrow card\_edges - 2$	
14:	$\text{DELETE}(N^+_{v\_rev})$	
15:	Delete it from its successors	$\triangleleft$
16:	for $(w, e_{ind}) \in N_v^+$ do	
17:	$w\_rev \leftarrow \overline{w}$	
18:	$adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N^+_{w\_rev}, \overline{e_{ind}}, 1)$	
19:	if $adj\_ind = \left N^+_{w\_rev}\right  - 1$ then	
20:	Just delete the last element	$\triangleleft$
21:	$N^+_{w\_rev}$ .pop( )	
22:	else	
23:	Replace the edge by the last in the neighbour list	$\triangleleft$
24:	$N_{w\_rev}^+[adj\_ind] \leftarrow N_{w\_rev}^+$ .POP()	
25:	$card\_edges \leftarrow card\_edges - 2$	
26:	$ ext{delete}(N_v^+)$	
27:	Delete the whole vertex	$\triangleleft$
28:	if $v = \left  N_V^+ \right  - 2$ then	
29:	▷ It is the last, just pop it and its reverse	$\triangleleft$
30:	$N_V^+$ .pop()	
31:	$N_V^+$ .pop()	
32:	else	
33:	Replace it and its reverse by the last and its reverse	$\triangleleft$
34:	$N_{v\_rev}^+ \leftarrow N_V^+.\text{POP}()$	
35:	$N_v^+ \leftarrow N_V^+$ .POP()	
36:	Update the vertex index	$\triangleleft$
37:	for $(w,e_{ind})\in N_v^+$ do	
38:	$w\_rev \leftarrow \overline{w}$	
39:	$e_{ind}\_rev \leftarrow \overline{e_{ind}}$	
40:	$adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N^+_{w\_rev}, e_{ind}\_rev, 1)$	
41:	$N^+_{w\_rev}[adj\_ind] \leftarrow (v\_rev, e_{ind}\_rev)$	
42:	for $(w, e_{ind}) \in N^+_{v\_rev}$ do	
43:	$w\_rev \leftarrow \overline{w}$	
44:	$e_{ind}\_rev \leftarrow \overline{e_{ind}}$	
45:	$adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N^+_{w\_rev}, e_{ind}\_rev, 1)$	
46:	$N_{w rev}^+[adj\_ind] \leftarrow (v, e_{ind\_rev})$	
	—	

► Algorithm 16: Delete a vertex for DGF

**Require:** Graph G = (V, E), vertex  $v \in V$  (in forward orientation). **Ensure:** Delete the vertex and its reverse such that  $V' = V \setminus \{v, \overline{v}\}$ , and  $\forall v \in V', 0 \le v_{ind} \le |V'| - 2.$ 1: function DGF\_DELETE\_VERTEX(G, v)> Delete it from its predecessors 2:  $\triangleleft$ for  $(u, u_{or}, e_{ind}) \in N_v^-$  do 3: if  $u_{or} = 0$  then 4:  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_u^+, e_{ind}, 1)$ 5: if  $adj_ind = |N_u^+| - 1$  then 6: > Just delete the last element 7:  $\triangleleft$  $N_{u}^{+}$ .POP() 8: 9: else ▷ Replace the edge by the last in the neighbour list 10:  $\triangleleft$  $N_{u}^{+}[adj\_ind] \leftarrow N_{u}^{+}.POP()$ 11: else 12:  $adj\_ind \leftarrow \text{GET\_INDEX}(N_u^-, \overline{e_{ind}}, 1)$ 13: if  $adj_{u} = |N_{u}| - 1$  then 14: > Just delete the last element 15:  $\triangleleft$  $N_u^-$ .POP() 16: else 17: ▷ Replace the edge by the last in the neighbour list 18:  $\triangleleft$  $N_{u}^{-}[adj\_ind] \leftarrow N_{u}^{-}.POP()$ 19:  $card\_edges \leftarrow card\_edges - 2$ 20: 21: DELETE $(N_v^-)$ > Delete it from its successors 22:  $\triangleleft$ for  $(w, w_{or}, e_{ind}) \in N_v^+$  do 23: if  $w_{or} = 0$  then 24: 25:  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_w^-, e_{ind}, 1)$ if  $adj_ind = |N_w^-| - 1$  then 26: > Just delete the last element 27:  $\triangleleft$ 28:  $N_w^-$ .POP() else 29: ▷ Replace the edge by the last in the neighbour list 30:  $\triangleleft$  $N_w^-[adj\_ind] \leftarrow N_w^-.POP()$ 31: else 32:  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_w^+, \overline{e_{ind}}, 1)$ 33: if  $adj_{ind} = |N_w^+| - 1$  then 34: > Just delete the last element 35:  $\triangleleft$ 

 $N_w^+$ .POP() 36: 37: else 38: ▷ Replace the edge by the last in the neighbour list  $\triangleleft$  $N_w^+[adj\_ind] \leftarrow N_w^+$ .POP() 39:  $card\_edges \leftarrow card\_edges - 2$ 40: DELETE $(N_v^+)$ 41: 42: > Delete the whole vertex  $\triangleleft$ if  $v = |N_V^+| - 1$  then 43: ▷ It is the last, just pop it and its reverse 44:  $\triangleleft$  $N_V^-$ .POP() 45:  $N_V^+$ .POP() 46: else 47: ▷ Replace it and its reverse by the last and its reverse 48:  $\triangleleft$  $N_v^- \leftarrow N_V^-$ .POP() 49:  $N_v^+ \leftarrow N_V^+$ .POP() 50: > Update the vertex index 51:  $\triangleleft$ for  $(u, u_{or}, e_{ind}) \in N_v^-$  do 52: if  $u_{or} = 0$  then 53:  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_u^+, e_{ind}, 1)$ 54:  $N_{u}^{+}[adj\_ind] \leftarrow (v, 0, e_{ind})$ 55: else 56: 57:  $u\_rev \leftarrow \overline{u}$ 58:  $e_{ind}$  rev  $\leftarrow \overline{e_{ind}}$  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_u^- _{rev}, e_{ind}\_rev, 1)$ 59:  $N_{u\_rev}^{-}[adj\_ind] \leftarrow (v, 1, e_{ind\_}rev)$ 60: for  $(w, w_{or}, e_{ind}) \in N_v^+$  do 61: if  $w_{or} = 0$  then 62:  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_w^-, e_{ind}, 1)$ 63:  $N_w^{-}[adj\_ind] \leftarrow (v, 0, e_{ind})$ 64: 65: else 66:  $w\_rev \leftarrow \overline{w}$ 67:  $e_{ind}$ \_rev  $\leftarrow \overline{e_{ind}}$  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_w^+ _{rev}, e_{ind}\_rev, 1)$ 68:  $N_{w rev}^+[adj\_ind] \leftarrow (v, 1, e_{ind\_rev})$ 69:

### ► Algorithm 17: Delete a vertex for BGU

**Require:** Graph G = (V, E), vertex  $v \in V$  (in forward orientation).

**Ensure:** Delete the vertex and its reverse such that  $V' = V \setminus \{v, \overline{v}\}$ , and  $\forall v \in V', 0 \le v_{ind} \le |V'| - 2.$ 1: function BGU\_DELETE\_VERTEX(G, v)2: for  $(w, e_{ind}) \in N_v$  do  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_w, e_{ind}, 1)$ 3: if  $adj\_ind = |N_w| - 1$  then 4: > Just delete the last element 5:  $\triangleleft$  $N_w$ .POP() 6: 7: else ▷ Replace the edge by the last in the neighbour list 8:  $\triangleleft$  $N_w[adj\_ind] \leftarrow N_w.POP()$ 9: DELETE $(N_v)$ 10: > Delete the whole vertex 11:  $\triangleleft$ if  $v = |N_V| - 1$  then 12: ▷ It is the last, just pop it 13:  $\triangleleft$  $N_V$ .POP() 14: else 15: ▷ Replace it by the last 16:  $\triangleleft$  $N_v \leftarrow N_V.\text{POP}()$ 17: Update the vertex index 18:  $\triangleleft$ for  $(w, e_{ind}) \in N_v$  do 19:  $adj_ind \leftarrow \text{GET}_iNDEX(N_w, e_{ind}, 1)$ 20:  $N_w[adj\_ind] \leftarrow (v, e_{ind})$ 21: if w > v then 22: > The last (the greatest) identifier becomes a fewer and 23: breaks the identifier order  $\triangleleft$  $E_{attr}[e_{ind}] \leftarrow (E_{attr}[e_{ind}][0], 1 - E_{attr}[e_{ind}][1])$ 24:

## 4.1.7 Deleting an Edge

### ► Algorithm 18: Delete an edge for DGS

**Require:** Graph G = (V, E), edge  $(u, v) \in E$  and the edge's index  $e_{ind}$ . **Ensure:**  $|N_u^+ \setminus edge| = |N_u^+| - 1$  and  $|N_v^- \setminus edge| = |N_v^-| - 1$ . 1: function DGS\_DELETE\_EDGE( $G, u, v, e_{ind}$ ) 2:  $\triangleright$  Remove v from u's successors 3:  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_u^+, e_{ind}, 1)$ 4: if  $adj\_ind = |N_u^+| - 1$  then

 $\triangleleft$ 

> Just delete the last element 5:  $\triangleleft$ 6:  $N_u^+$ .POP() 7: else ▷ Replace the edge by the last in the neighbour list 8:  $\triangleleft$  $N_{\mu}^{+}[adj\_ind] \leftarrow N_{\mu}^{+}.POP()$ 9:  $\triangleright$  Remove u from v's predecessors. 10:  $\triangleleft$ 11:  $v\_rev \leftarrow \overline{v}$  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N^+_{v\_rev}, \overline{e_{ind}}, 1)$ 12: if  $adj\_ind = \left|N_v^+\right| - 1$  then 13: > Just delete the last element 14:  $\triangleleft$ 15:  $N_v^+_{rev}$ .POP() 16: else ▷ Replace the edge by the last in the neighbour list 17:  $\triangleleft$  $N_{v\_rev}^+[adj\_ind] \leftarrow N_{v\_rev}^+$ .POP() 18:  $card\_edges \leftarrow card\_edges - 2$ 19:

### ► Algorithm 19: Delete an edge for DGF

**Require:** Graph G = (V, E), edge  $(u, v) \in E$ , with their orientation  $(u_{or}, v_{or}) \in E$  $\{0;1\}^2$ , and the edge's index  $e_{ind}$ . **Ensure:**  $|N_u^+ \setminus edge| = |N_u^+| - 1$  and  $|N_v^- \setminus edge| = |N_v^-| - 1$ . 1: function DGF\_DELETE\_EDGE( $G, u, u_{or}, v, v_{or}, e_{ind}$ ) 2:  $\triangleright$  Remove v from u's successors  $\triangleleft$ if  $u \quad or = 0$  then 3:  $list\_succs \leftarrow N_u^+$ 4:  $adj\_ind \leftarrow \text{GET\_INDEX}(list\_succs, e_{ind}, 2)$ 5: else 6:  $list\_succs \leftarrow N_u^-$ 7:  $adj\_ind \leftarrow \text{GET\_INDEX}(list\_succs, \overline{e_{ind}}, 2)$ 8: 9: if  $adj\_ind = |list\_succs| - 1$  then 10: > Just delete the last element  $\triangleleft$ 11: *list\_succs*.POP() 12: else ▷ Replace the edge by the last in the neighbour list 13:  $\triangleleft$  $list\_succs[adj\_ind] \leftarrow list\_succs.POP()$ 14:  $\triangleright$  Remove u from v's predecessors. 15:  $\triangleleft$ if  $v\_or = 0$  then 16:  $list\_preds \leftarrow N_n^-$ 17:  $adj\_ind \leftarrow \text{GET\_INDEX}(list\_preds, e_{ind}, 2)$ 18:

19:	else	
20:	$list\_preds \leftarrow N_v^+$	
21:	$adj\_ind \leftarrow \text{GET}\_\text{INDEX}(list\_preds, \overline{e_{ind}}, 2)$	
22:	if $adj\_ind =  list\_preds  - 1$ then	
23:	Just delete the last element	$\triangleleft$
24:	<i>list_preds</i> .POP()	
25:	else	
26:	Replace the edge by the last in the neighbour list	$\triangleleft$
27:	$list\_preds[adj\_ind] \leftarrow list\_preds.POP()$	
28:	$card\_edges \leftarrow card\_edges - 2$	

### ► Algorithm 20: Delete an edge for BGU

**Require:** Graph G = (V, E), edge  $(u, v) \in E$ , with their orientation  $(u_{or}, v_{or}) \in E$  $\{0;1\}^2$ , and the edge's index  $e_{ind}$ . **Ensure:**  $|N_u^+ \setminus edge| = |N_u^+| - 1$  and  $|N_v^- \setminus edge| = |N_v^-| - 1$ . 1: function BGU\_DELETE\_EDGE( $G, u, u_{or}, v, v_{or}, e_{ind}$ ) ▷ Euclidian division 2:  $e'_{ind} \leftarrow e_{ind} \div 2$  $\triangleright$  Remove v from u's neighbours. 3:  $\triangleleft$  $adj\_ind \leftarrow \text{GET}\_\text{INDEX}(N_u, e'_{ind}, 1)$ 4: if  $adj\_ind = |N_u| - 1$  then 5: > Just delete the last element 6:  $\triangleleft$ 7:  $N_u$ .POP() else 8: ▷ Replace the edge by the last in the neighbour list 9:  $\triangleleft$  $N_u[adj\_ind] \leftarrow N_u.POP()$ 10:  $\triangleright$  Remove u from v's neighbours. 11:  $\triangleleft$  $adj_ind \leftarrow \text{GET}_iNDEX(N_v, e'_{ind}, 1)$ 12: if  $adj\_ind = |N_v| - 1$  then 13: > Just delete the last element 14:  $\triangleleft$  $N_v$ .POP() 15: else 16: ▷ Replace the edge by the last in the neighbour list 17:  $\triangleleft$  $N_v[adj\_ind] \leftarrow N_v.POP()$ 18:  $card\_edges \leftarrow card\_edges - 1$ 19:

## 4.2 Time Complexities

## 4.2.1 Complexities Calculus Details

Table 1 details the calculus of algorithmic costs.

Table 1 –	Calculus detail	of basic of	operations costs.	c(x)	) is the cost of element $x$ .
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Operation	$\operatorname{Cost}$	Description
x	0	Memory access
$x \pm y$	1 + c(x) + c(y)	Basic operation
$x \leftarrow y$	c(y)	Affectation
x	1 + c(x)	Absolute value or element's length
$\mathbf{if} \ x \stackrel{\leq}{\leq} y$	1 + c(x) + c(y)	Conditional
EMPTY_LIST()	1	Empty list constructor
list.APPEND(x)	1 + c(x)	Add $x$ to the end of the list <i>list</i>
list.POP()	1	Delete the last element of the list $list$
DELETE(list)	list	Delete all the list
for $i \in \llbracket a; b \rrbracket$ do $x$	$(b-a+1) \times c(x)$	For loop

best, worst and average cases are respectively rather lower and upper bounds, and equiprobable independent event's costs

## 4.2.2 Costs for Subfunctions

Table 2 gives the algorithmic costs of subfunctions in Algorithms 1 and 2.

	Best	Worst	Average
REV		2	
GET_INDEX	3	$3 \times  list $	$3 \times \left\lceil \frac{ list }{2} \right\rceil$

## **Table 2** – Algorithmic costs for subfunctions.

## 4.2.3 Iterating Over the Neighbours

Table 3 gives the algorithmic costs of Algorithms 3 to 8.

**Table 3** – Algorithmic costs of iterating over the neighbours for DGS, DGF and BGU.

	(a) Iterate over the predecessors			
	Best	Worst	Average	
DGS		$5 \times o_v^- + 2$		
DGF	$o_{v}^{-} + 1$	$4 \times o_v^- + 3$	$2.5\times o_v^-+2$	
BGU	$3 \times o_v$	$6 \times o_v$	$4.75 \times o_v$	

## (a) Iterate over the predecessors

	(b) Iterate over the successors			
	Best	Worst	Average	
DGS		$o_v^+$		
DGF	$o_v^+ + 1$	$4 \times o_v^+ + 3$	$2.5 \times o_v^+ + 2$	
BGU	$3 \times o_v$	$6 \times o_v$	$4.75 \times o_v$	

# 4.2.4 Costs for Dynamics

Table 4 gives the algorithmic costs of Algorithms 9 to 14. Table 5 gives the algorithmic costs of Algorithms 18 to 20. Table 6 gives the algorithmic costs of Algorithms 15 to 17.

<b>Table 4</b> – Algorithmic costs c	of adding a vertex or a	an edge for DGS,	DGF and BGU.
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		Add a ver	tex		Add an ed	lge
	$\mathbf{Best}$	Worst	Average	Best	Worst	Average
DGS		5			8	
DGF		5		6	10	8
BGU		3			9	

<b>Table 5</b> – Algorithmic costs of de	ting an edge for DGS, DGF and BGU.
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	Best	Worst
DGS	17	$3 \times (o_u^+ + o_v^-) + 13$
DGF	17	$3 \times (o_u^- + o_v^+) + 17$
BGU	14	$3 \times (o_u + o_v) + 10$

(a) Best and	Worst cases

(b)	Average	case
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DGS	$3 \times \left( \left\lceil \frac{o_u^+}{2} \right\rceil + \left\lceil \frac{o_v^-}{2} \right\rceil \right) + 13 - \frac{1}{o_u^+} - \frac{1}{o_v^-}$
DGF	$\frac{3}{2} \times \left( \left\lceil \frac{o_u^-}{2} \right\rceil + \left\lceil \frac{o_u^+}{2} \right\rceil + \left\lceil \frac{o_v^-}{2} \right\rceil + \left\lceil \frac{o_v^+}{2} \right\rceil \right) + 13 - 2 \times \left( \frac{1}{o_u} + \frac{1}{o_v} \right)$
BGU	$3 \times \left( \left\lceil \frac{o_u}{2} \right\rceil + \left\lceil \frac{o_v}{2} \right\rceil \right) + 11 - \frac{1}{o_u} - \frac{1}{o_v}$

**Table 6** – Algorithmic costs of deleting a vertex for DGS, DGF and BGU.

(a) Best cases			
DGS	DGF	BGU	
5	4	3	

(b) Worst cases

$$\begin{array}{l} \mathbf{DGS} \qquad 9 \times o_v + 3 \times \left( \sum_{u \in N_v^-} o_u^+ + \sum_{w \in N_v^+} o_w^- + \sum_{x \in N_z^-} o_x^+ + \sum_{y \in N_z^+} o_y^- \right) + 5 \times (o_z + 1) \\ \mathbf{DGF} \qquad 9 \times o_v + 4 \times o_z + 3 \times \left( \sum_{u \in N_v^-} o_u^- + \sum_{w \in N_v^+} o_w^+ + \sum_{x \in N_z^-} o_x^- + \sum_{y \in N_z^+} o_y^+ \right) + 4 \\ \mathbf{BGU} \qquad 5 \times o_v + 3 \times o_z + 3 \times \left( \sum_{w \in N_v} o_w + \sum_{y \in N_z} o_y \right) + 4 \end{array}$$

(c) Average cases (DGS, DGF and BGU)

$$\begin{split} 10 \times o_v + \frac{10 \times \mathcal{R}_{aw} - 5}{2 \times \mathcal{R}_{aw}} \times o_z + 3 \times \left( \sum_{u \in N_v^-} \left\lceil \frac{o_u^+}{2} \right\rceil + \sum_{w \in N_v^+} \left\lceil \frac{o_w^-}{2} \right\rceil \right) \\ + \frac{6 \times \mathcal{R}_{aw} - 3}{2 \times \mathcal{R}_{aw}} \times \left( \sum_{x \in N_z^-} \left\lceil \frac{o_x^+}{2} \right\rceil + \sum_{y \in N_z^+} \left\lceil \frac{o_y^-}{2} \right\rceil \right) - \left( \sum_{u \in N_v^-} \frac{1}{o_u^+} + \sum_{w \in N_v^+} \frac{1}{o_w^-} \right) + 5 \\ \hline \frac{15}{2} \times o_v + \frac{6 \times \mathcal{R}_{aw} - 3}{2 \times \mathcal{R}_{aw}} \times o_z + \frac{3}{2} \times \sum_{u \in N_v^- \cup N_v^+} \left( \left\lceil \frac{o_u^-}{2} \right\rceil + \left\lceil \frac{o_u^+}{2} \right\rceil \right) \right) \\ + \frac{6 \times \mathcal{R}_{aw} - 3}{4 \times \mathcal{R}_{aw}} \times \sum_{x \in N_z^- \cup N_v^+} \left( \left\lceil \frac{o_x^-}{2} \right\rceil + \left\lceil \frac{o_x^+}{2} \right\rceil \right) \\ - \frac{1}{2} \times \left( \sum_{u \in N_v^-} \frac{1}{o_u^+} + \sum_{w \in N_v^+} \frac{1}{o_w^-} \right) + \frac{6 \times \mathcal{R}_{aw} - 1}{\mathcal{R}_{aw}} \\ \hline 5 \times o_v + \frac{3 \times \mathcal{R}_{aw} - 3}{\mathcal{R}_{aw}} \times o_z + 3 \times \sum_{w \in N_v} \left\lceil \frac{o_w}{2} \right\rceil + \frac{3 \times \mathcal{R}_{aw} + 3}{2 \times \mathcal{R}_{aw}} \times \sum_{y \in N_z} \left\lceil \frac{o_y}{2} \right\rceil \\ - \sum_{w \in N_v} \frac{1}{o_w} + \frac{4 \times \mathcal{R}_{aw} - 1}{\mathcal{R}_{aw}} \end{split}$$

# References

- [1] John Dimitri Kececioglu. Exact and Approximation Algorithms for DNA Sequence Reconstruction. The University of Arizona, 1991.
- [2] Chen-Shan Chin, Paul Peluso, Fritz J. Sedlazeck, Maria Nattestad, Gregory T. Concepcion, Alicia Clum, Christopher Dunn, Ronan O'Malley, Rosa Figueroa-Balderas, Abraham Morales-Cruz, Grant R. Cramer, Massimo Delledonne, Chongyuan Luo, Joseph R. Ecker, Dario Cantu, David R. Rank, and Michael C. Schatz. Phased diploid genome assembly with single-molecule real-time sequencing. *Nature Methods*, 13(12):1050–1054, December 2016.
- [3] Govinda M. Kamath, Ilan Shomorony, Fei Xia, Thomas A. Courtade, and David N. Tse. HINGE: Long-read assembly achieves optimal repeat resolution. *Genome Research*, 27(5):747–756, January 2017.
- [4] Rumen Andonov, Hristo Djidjev, Sebastien François, and Dominique Lavenier. Complete assembly of circular and chloroplast genomes based on global optimization. *Journal of Bioinformatics and Computational Biology*, 17(3):1950014, June 2019.
- [5] Kishwar Shafin, Trevor Pesout, Ryan Lorig-Roach, Marina Haukness, Hugh E. Olsen, Colleen Bosworth, Joel Armstrong, Kristof Tigyi, Nicholas Maurer, Sergey Koren, Fritz J. Sedlazeck, Tobias Marschall, Simon Mayes, Vania Costa, Justin M. Zook, Kelvin J. Liu, Duncan Kilburn, Melanie Sorensen, Katy M. Munson, Mitchell R. Vollger, Jean Monlong, Erik Garrison, Evan E. Eichler, Sofie Salama, David Haussler, Richard E. Green, Mark Akeson, Adam Phillippy, Karen H. Miga, Paolo Carnevali, Miten Jain, and Benedict Paten. Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*, 38(9):1044–1053, September 2020.
- [6] Haoyu Cheng, Gregory T. Concepcion, Xiaowen Feng, Haowen Zhang, and Heng Li. Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm. *Nature Methods*, 18(2):170–175, February 2021.
- [7] E. W. Myers. Toward simplifying and accurately formulating fragment assembly. Journal of Computational Biology: A Journal of Computational Molecular Cell Biology, 2(2):275–290, 1995.
- [8] Daniel D. Sommer, Arthur L. Delcher, Steven L. Salzberg, and Mihai Pop. Minimus: A fast, lightweight genome assembler. *BMC bioinformatics*, 8:64, February 2007.

- [9] David Hernandez, Patrice François, Laurent Farinelli, Magne Østerås, and Jacques Schrenzel. De novo bacterial genome sequencing: Millions of very short reads assembled on a desktop computer. *Genome Research*, 18(5):802–809, January 2008.
- [10] Leena Salmela, Veli Mäkinen, Niko Välimäki, Johannes Ylinen, and Esko Ukkonen. Fast scaffolding with small independent mixed integer programs. *Bioinformatics*, 27(23):3259–3265, December 2011.
- [11] Eugene W. Myers. The fragment assembly string graph. *Bioinformatics*, 21(suppl\_2):ii79–ii85, January 2005.
- [12] Veli Mäkinen, Djamal Belazzougui, Fabio Cunial, and Alexandru I. Tomescu. Genome-Scale Algorithm Design. Cambridge University Press, May 2015.
- [13] Heng Li. Minimap and miniasm: Fast mapping and de novo assembly for noisy long sequences. *Bioinformatics*, 32(14):2103–2110, July 2016.

# Acronyms

## B | C | D

B
BG Unoriented Fragments Bi-directed Graph 31, 32
C
CSC Compressed Sparse Column 9
CSR Compressed Sparse Row 9
D
DGA All Oriented Fragments Directed Graph 22, 23, 25, 27
DGF Forward Fragments Directed Graph 27, 28, 30, 31
DGS Only Oriented Fragments' Successors Directed Graph 25–27

DNA Deoxyribonucleic Acid 1, 5, 7

# Symbols

Attributes | Functions | Graph | Operations | Sets

## Attributes

f Forward orientation 6-8, 12, 13, 15, 18, 19, 22, 28, 34, 37, 38, 40, see forward

ind Index 22, 23, 25, 27, 28, 30, 31, 35-38, 41-47

indor Index with boolean orientation 27, 28

- or Orientation 11, 12, 15–17, 20, 22, 23, 27, 28, 36–38, 40, 41, 43, 44, 46, 47, see forward & reverse
- r Reverse orientation 6-8, 12, 13, 15, 18, 19, 22, 30, 34, 37, 38, 40, see reverse
- rid Read identifier 5, 6, 11, 12, 14, 16, 19, 20, 22, 27, 28, 31, 33, 34
- seq Nucleotide sequence 5–7

### Functions

strand\_iid Read identifier function 5-7

### Graph

- G Graph object 11–13, 15, 17, 20, 22, 36–41, 43–47, *see* undirected graph, directed graph, vertex & edge
- V Vertices set 11-17, 19, 20, 22, 23, 25-28, 30, 31, 34, 36-47, see vertex
- E Edges set 11-23, 27, 28, 30, 31, 36-41, 43-47, see edge
- N Neighbours set 31, 37–39, 41, 45, 47, 51, see edge
- $N^-$  Predecesors set 23, 28, 36, 38–40, 43–47, 51, see edge, N &  $N^+$
- $N^+$  Successors set 23, 25, 28, 36–47, 51, see edge,  $N \& N^-$

### Operations

→ Reverse operation 6-9, 12-14, 16, 17, 20, 21, 23, 27, 28, 30, 35, 36, 38, 40-47, see reverse & rev

### Sets

- ℕ The set of natural (positive) integer 5, 6, 11, 13, 14, 17, 19, 20
- O Set of overlaps 8, 9, 12, 14, 15, 19-23, 25, 28, 29, 31-33
- $\mathcal{R}_{aw}$  Set of raw reads 5–7, 12, 15, 20, 22, 23, 25, 27, 28, 30–34, 51
- $\mathcal{R}$  Set of reads 6–9, 12, 14, 15, 19–21
- $\mathcal{R}_{ev}$  Set of reversed raw reads 6
- $\Sigma$  Alphabet set 5

# Glossary

## A | B | C | D | E | F | G | N | O | P | R | S | U | V | W

## Α

**alignment** Nucleotide comparison between at least two sequences 7, 8 **assembly** Method used to reconstruct genomes from fragments 1, 6, 7, 11, 14 **assembly graph** One of the output of genome assembly method *see* assembler

### В

bi-directed graph Graph that contains 3 edge types 1, 11, 14–17, 20, 31, 32

## С

contig Merge, consensus of reads obtain by assembly method(s) see assembler

## D

**directed graph** Graph where the edges are directed 1, 11–13, 22–24, 26, 27, 29, 33, 34

## Ε

edge Component of a graph that connects two vertices 9, 11–23, 25, 27, 28, 30, 31, 33, 34, see graph & vertex

## F

forward Original sequence orientation 6–8, 11, 14, 15, 18, 19, 21, 27–29, 31, 32, 34, *see* reverse

fragment Generic nucleotide fragment 1, 5, 11-13, 20-22, 24, 26, 29

## G

genome Entire set of DNA instructions found in a cell 7

**graph** Object composed of vertices connected by edges 1, 9, 11–14, 16–18, 20–29, 31, 34, *see* vertex & edge

### Ν

neighbour Vertex connected to a given one 11, 27, 31-34

nucleotide Basic building block of nucleic acids (RNA and DNA) 5-8, see DNA

### 0

**overlap** Suffix-prefix alignment type between two sequences 1, 7–9, 11, 12, 14, 15, 18–27, 29, 31–34, *see* alignment

### Ρ

- **path** A sequence of vertices such that two consecutive vertices are connected by an edge in the graph 12, 13, 17, 20, 21, *see* walk, graph, vertex & edge
- predecessor In-vertex of one edge of one given vertex 23, 24, 26-31, 34, see successor

### R

- **read** DNA fragment from one DNA's strand, output by a sequencer 5–7, 9, 11, 12, 14, 15, 18–22, 27, 28, 30, 31, 33, 34, *see* sequencer
- **reverse** Reverse-complement sequence orientation 1, 6, 7, 9, 11–13, 16, 18–22, 25–27, 30, 31, *see* forward

### S

sequencer Sequencing technology machine 5

- sequencing Method to generate nucleotide fragments 5–7
- strand The DNA molecule is made up of two strands, each of which has a complementary sequence to the other 5-7
- string graph Graph structure that stores overlaps between reads see overlap
- **succession relationship** When moving from one to the other is feasible, two things have a succession relationship 1, 7, 8, 11, 15, 16

successor Out-vertex of one edge of one given vertex 23-31, 34, see predecessor

### U

undirected graph Graph where the edges are undirected 11, 16–21, 31

## V

vertex Component of a graph 9, 11–23, 25–28, 30, 31, 33, 34, see graph & edge

W

**walk** A sequence of vertices such that two consecutive vertices are connected by an edge in the graph 12, 13, 15–18, 20, 21, *see* path, graph, vertex & edge