An Efficient Algorithm for Chinese Postman Walk on Bi-directed de Bruijn Graphs

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Abstract. Sequence assembly from short reads is an important problem in biology. It is known that solving the sequence assembly problem exactly on a bi-directed de Bruijn graph or a string graph is intractable. However finding a Shortest Double stranded DNA string (SDDNA) containing all the k-long words in the reads seems to be a good heuristic to get close to the original genome. This problem is equivalent to finding a cyclic Chinese Postman (CP) walk on the underlying un-weighted bi-directed de Bruijn graph built from the reads. The Chinese Postman walk Problem (CPP) is solved by reducing it to a general bi-directed flow on this graph which runs in $O(|E|^2 \log^2(|V|))$ time.

In this paper we show that the cyclic CPP on bi-directed graphs can be solved without reducing it to bi-directed flow. We present a $\Theta(p(|V|+|E|)\log(|V|)+(d_{max}p)^3)$ time algorithm to solve the cyclic CPP on a weighted bi-directed de Bruijn graph, where $p = \max\{|\{v|d_{in}(v) - d_{out}(v) > 0\}|, |\{v|d_{in}(v) - d_{out}(v) < 0\}|\}$ and $d_{max} = \max\{|d_{in}(v) - d_{out}(v)\}$. Our algorithm performs asymptotically better than the bi-directed flow algorithm when the number of *imbalanced* nodes p is much less than the nodes in the bi-directed graph. From our experimental results on various datasets, we have noticed that the value of $p/|V|$ lies between 0.08% and 0.13% with 95% probability.

Many practical bi-directed de Bruijn graphs do not have cyclic CP walks. In such cases it is not clear how the bi-directed flow can be useful in identifying contigs. Our algorithm can handle such situations and identify maximal bi-directed sub-graphs that have CP walks. We also present a $\Theta((|V| + |E|)\log(V))$ time algorithm for the single source shortest path problem on bi-directed de Bruijn graphs, which may be of independent interest.

1 Introduction

Sequencing the human genome was one of the major scientific breakthroughs in the last seven years. Analysis of the sequenced genome can give us vital information about the expression of genes, which in turn can help scientists to develop drugs for diseases. Thus sequencing the genome of an organism is of fundamental importance in both medicine and biology. Unfortunately the

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technology used in major human genome sequencing projects – Human Genome Project (HGP) [1] and Celera [2], was too expensive to be adopted in a large scale. This led to the research on *next-generation sequencing* methods. *Pyrosequencing* technologies such as SOLiD, 454 and Solexa generate a large number of short reads which have acceptable accuracy but are several times cheaper compareted to the Sanger technology adopted in the HGP project.

Directed de Bruijn graph based sequence assembly algorithms such as [3] and [4] seem to handle these short read data efficiently compared to the string graph based algorithms (see e.g., [5]). Unfortunately solving the sequence assembly problem exactly on both these graph models seems intractable [6]. However heuristics such as finding a shortest string which includes all the k-mers (sub strings of length k) seem to yield results close to the original genome. In the case of directed de Bruijn graphs finding an Eulerian tour seems to yield good results. If the graph is not Eulerian then a Chinese Postman (CP) tour has been suggested in [4]. To account for the double strandedness of the DNA molecule we need to simultaneously search for two complimentary CP tours. In [6] the directed de Bruijn graphs are replaced with bi-directed de Bruijn graphs to find two complimentary CP tours simultaneously. A CP tour on the *un-weighted* bi-directed graph constructed from the reads serves as a solution to the *Shortest Double Stranded DNA* string (SDDNA) problem. The solution presented in [6] solves the SDDNA problem by reducing it to a general weighted bi-directed flow problem. This algorithm runs in $O(|E|^2 \log^2(V))$ time.

In this paper we present algorithms for SDDNA/CPP on bi-directed de Bruijn graphs without using a bi-directed flow algorithm. Our algorithms are based on identifying shortest bi-directed paths and use of weighted bi-partite matching. Our algorithms perform asymptotically better than the bi-directed flow algorithm when the *imbalanced* nodes in the bi-directed graphs are much smaller in number than $|V|$. This restriction seems to be true in practice from what we have observed in our experiments. On the other hand it turns out that in many practical situations these bi-directed de Bruijn graphs fail to have *cyclic* CP tours. In these cases it is not clear how the bi-directed flow algorithm [6] can help us in identifying a set of *contigs* covering every k-long word at least once. In contrast to this flow algorithm, our algorithm can be useful in obtaining a *minimal* set of contigs when a *cyclic* CP tour does no exist. We now summarize our results as follows. Firstly our deterministic algorithm to solve the *cyclic* CPP on a general bi-directed graph takes $\Theta(p(|V| + |E|)\log(|V|) + (d_{max}\,p)^3)$ time, where $d_{max} = \max\{|d_{in}(v) - d_{out}(v)|, v \in V\}$, $p = \max\{|V^+|, |V^-|\}$, $V^+ = \{v|v \in V, d_{in}(v) - d_{out} > 0\}$ and $V^- = \{v|v \in V, d_{in}(v) - d_{out} < 0\}$. Secondly we solve the SDDNA problem on an un-weighted bi-directed de Bruijn graph deterministically in $\Theta(p(|V|+|E|)+(d_{max}\,p)^3)$ time. As a consequence we also present a $\Theta((|V| + |E|)\log(V))$ time single source shortest bi-directed path algorithm, which may be of independent interest to some assembly algorithms such as Velvet [3] – TourBus heuristic.

The organization of the paper is as follows. In Section 2 we provide some preliminaries. Section 3 defines the CPP and SDDNA problems. In Section 4 we introduce our algorithm for single source shortest bi-directed paths, which is used as a component in our main algorithm. The main algorithm is introduced in Section 7 along with algorithms for several sub-problems. Section 8 briefly explains how we can handle situations when the bi-directed graphs do not have cyclic CP tours. Finally experimental studies are reported in Section 9.

2 Preliminaries

Let $s \in \Sigma^n$ be a string of length n. Any substring s_j (i.e., $s[j, \ldots j+k-1], n-k+1 \geq j \geq 1$) of length k is called a $k-$mer of s. The set of all $k-$mer's of a given string s is called the $k-$spectrum of s and is denoted by $\mathbb{S}(s,k)$. Given a $k-$mer s_j, $\bar{s_j}$ denotes the *reverse compliment* of s_j (e.g., if $s_j = AAGTA$ then $\bar{s_j} = TACTT$). Let $\leq$ be the partial ordering among the strings of equal length, then $s_i \leq s_j$ indicates that string s_i is lexicographically smaller than s_j. Given any $k-$mer s_i, let $\hat{s_i}$ be the lexicographically smaller string between s_i and $\bar{s_i}$. We call $\hat{s_i}$ the *canonical* $k-$mer of s_i. More formally, if $s_i \leq \bar{s_i}$ then $\hat{s_i} = s_i$ else $\hat{s_i} = \bar{s_i}$. A $k-$molecule of a given $k-$mer s_i is a tuple $(s_i, \bar{s_i})$ consisting of s_i and its reverse compliment $\bar{s_i}$, the first entry in this tuple is called the positive strand and the second entry is called the negative strand.

A *bi-directed* graph is a generalized version of a standard directed graph. In a directed graph every edge ($-\triangleright$ or $\triangleleft-$) has only one arrow head. On the other hand, in a bi-directed graph every edge ($\triangleleft-\triangleright$, $\triangleleft-\triangleleft$,$\triangleright-\triangleleft$ or $\triangleright-\triangleright$) has two arrow heads attached to it. Formally, let V be the set of vertices of a bi-directed graph, $E = \{(v_i, v_j, o_1, o_2) | v_i, v_j \in V \wedge o_1, o_2 \in \{\triangleleft, \triangleright\}\}$ is the set of bi-directed edges in a bi-directed graph $G(V,E)$. A *walk* $w(v_i, v_j)$ between two nodes $v_i, v_j \in V$ of a bi-directed graph $G(V,E)$ is a sequence $v_i, e_{i_1}, v_{i_1}, e_{i_2}, v_{i_2} \ldots v_{i_m}, e_{i_{m+1}}, v_j$, such that for every intermediate vertex $v_{i_l}, 1 \leq l \leq m$, the orientation of the arrow heads on either side is opposite. To make this more clear let $e_{i_l}, v_{i_l}, e_{i_{l+1}}$ be the sub-sequence in the walk $w(v_i, v_j)$, $e_{i_l} = (v_{i_{l-1}}, v_{i_l}, o_1, o_2), e_{i_{l+1}} = (v_{i_l}, v_{i_{l+1}}, o_1, o_2)$ then for the walk to be valid $e_{i_l}.o_2 = e_{i_{l+1}}.o_1$. If $v_j = v_i$ and $e_{i_1}.o_1 = e_{i_{m+1}}.o_2$ then the walk is called *cyclic*. A walk on the bi-directed graph is referred to as a *bi-directed walk*. We define an orientation function $\mathcal{O} : V^2 \rightarrow \{\triangleright, \triangleleft\}^2$ which gives the orientation of the bi-directed edge between a pair of vertices – if one exists . For instance if $(v_i, v_j, \triangleleft, \triangleright)$ is a bi-directed edge between v_i and v_j then $\mathcal{O}(v_i, v_j) = \triangleleft-\triangleright$. An edge which is adjacent on a vertex with an orientation $\triangleright$ ($\triangleleft$) is called an *incoming* (*outgoing*) edge. The incoming(outgoing) degree of a vertex v is denoted by $d_{in}(v)$ ($d_{out}(v)$). A vertex v is called *balanced* iff $d_{in}(v) - d_{out}(v) = 0$. A vertex is called *imbalanced* iff $|d_{in}(v) - d_{out}(v)| > 0$. The imbalance of a vertex is called *positive* iff $d_{in}(v) - d_{out}(v) > 0$. Similarly a vertex is *negative* imbalanced iff $d_{in}(v) - d_{out}(v) < 0$. A bi-directed graph is called *connected* iff every pair of vertices have a bi-directed walk between them.

A de Bruijn graph $D^k(s)$ of the order k on a given string s is defined as follows. The vertex set V of $D^k(s)$ is defined as the $k-$spectrum of s (i.e., $V = \mathbb{S}(s,k)$). We use the notation $\text{suf}(v_i, l)(\text{pre}(v_i, l))$ to denote the suffix(prefix) of length l in string v_i. The symbol . denotes concatenation between two strings. Finally the set of directed edges E of $D^k(s)$ is defined as follows $E = \{(v_i, v_j) | \operatorname{suf}(v_i, k-1) = \operatorname{pre}(v_j, k-1) \wedge v_i[1].\operatorname{suf}(v_i, k-1).v_j[k] \in \mathbb{S}(s, k+1)\}$. We can further generalize the definition of a de Bruijn graph $B^k(S)$ on a set $S = \{s_1, s_2 \dots s_n\}$ of strings, $V = \cup_{i=1}^{n} \mathbb{S}(s_i, k)$ and $E = \{(v_i, v_j) | \operatorname{suf}(v_i, k-1) = \operatorname{pre}(v_j, k-1) \wedge \exists\, l : v_i[1].\operatorname{suf}(v_i, k-1).v_j[k] \in \mathbb{S}(s_l, k+1)\}$.

To model the double strandedness of the DNA molecules we should also consider the reverse compliments ($\bar{S} = \{\bar{s_1}, \bar{s_2} \dots \bar{s_n}\}$) while we build the de Bruijn graph. To address this a bi-directed de Bruijn graph $BD^k(S \cup \bar{S})$ has been suggested in [6]. The set of vertices V of $BD^k(S \cup \bar{S})$ consists of all the possible $k-$molecules from Σ^k. For every $k+1-$mer $z \in S \cup \bar{S}$, if x, y are the two $k-$mer's of z then an edge is introduced between the $k-$molecules (v_i, v_j) corresponding to x and y. The orientations of the arrow heads on the edges is chosen as follows. If both x, y are the positive strands in v_i, v_j an edge $(v_i, v_j, \rhd, \rhd)$ is introduced. If x is a positive strand in v_i and y is a negative strand in v_j an edge $(v_i, v_j, \rhd, \lhd)$ is introduced. Finally if x is a negative strand in v_i and y is a positive strand in v_j an edge $(v_i, v_j, \lhd, \rhd)$ is introduced.

3 Problem Definitions

A *Chinese Postman walk* in a bi-directed graph is a bi-directed walk which visits every edge at least once. A *cyclic Chinese Postman walk* of minimum cost on a weighted bi-directed graph is denoted as CPW. The problem of finding a CPW is referred to as CPP. The problem of finding a CPW on an un-weighted bi-directed de Bruijn graph (of order k) constructed from a set of reads is called the *Shortest Double stranded DNA* string (SDDNA) problem. In this paper we give algorithms for the cyclic CPP and SDDNA problems.

4 Single Source Shortest Path Algorithm on a Bi-directed de Bruijn Graph

We first present an algorithm for the single source shortest path problem on a bi-directed de Bruijn graph. The bi-directed de Bruijn graph in the context of sequence assembly has non-negative weights on the edges. This makes it possible to extend the classic Dijkstra's single source shortest path algorithm to these graphs. In our algorithm we attach two labels for each vertex in the bi-directed graph.

Given a source vertex s, the algorithm initializes all the labels similar to Dijkstra's algorithm. In each stage of the algorithm a label with the smallest cost is picked and some of labels corresponding to adjacent nodes are updated. The only major difference between Dijkstra's algorithm and our algorithm is the way we update the labels. Dijkstra's algorithm updates all the labels/nodes which are adjacent to the smallest label/node currently picked. However our algorithm updates only those labels/nodes which are consistent with the bi-directed walk property. We now give details of our algorithm and prove its correctness.

Let $G = (V, E)$ be the bi-directed graph of interest. Also let s be the source and t be the destination. We are interested in finding a *shortest bi-directed* walk from s to t. We introduce two labels $dist^+[u]$, $dist^-[u]$ for every vertex $u \in V$. The algorithm first initializes labels corresponding to the source (i.e. $dist^+[s]$ and $dist^-[s]$) to zero. Along with these labels of all the nodes adjacent to s are also initialized with the corresponding edge weight. The orientation of the edge determines the label we use for initialization. For instance, if (s, v) is a bi-directed edge with $\triangleright\!\!-\!\!\triangleleft$ as the orientation, the label $dist^-[v]$ is initialized with $w_{s,v}$ and $dist^+[v]$ is left uninitialized. In contrast, if the orientation of the edge is $\triangleright\!\!-\!\!\triangleright$ then $dist^+[v]$ is initialized to $w_{s,v}$ and $dist^-[v]$ is left uninitialized. All the uninitialized labels contains ∞ by default.

In each iteration of the algorithm a label with the minimum cost is picked. Since we have two types of labels, the minimum label can come from either $dist^+$ or $dist^-$. In the first case let u^+ be the node corresponding to the minimum label during the iteration. This intuitively means that we have a path from s to u^+ and the orientation of the edge adjacent to u^+ in this path is either $\triangleleft\!\!-\!\!\triangleright$ or $\triangleright\!\!-\!\!\triangleright$. We are going to prove this fact later in the correctness. On the other hand if u^+ is different from the destination t, then u^+ may possibly appear as an internal node in the shortest bi-directed walk between s and t. In this case the path through u^+ should satisfy *bi-directed walk constraint.* Thus we should explore only those node(s) adjacent to u^+ with an edge(s) orientated as $\triangleright\!\!-\!\!\triangleleft$ or $\triangleright\!\!-\!\!\triangleright$. The orientation of the edge determines the type of the label we need to update – similar to the label initialization. For instance let (u^+, v) be an edge adjacent on u^+ with an orientation of $\triangleright\!\!-\!\!\triangleleft$. In this case we should use label $dist^-[v]$ to make an update. Similarly if the orientation of the same edge is $\triangleright\!\!-\!\!\triangleright$ then $dist^+[v]$ is used in the update process. Consistent with the classical terminology of the Dijkstra's algorithm, we refer to the minimum cost label picked in each iteration as the *permanent label.* For instance if a label $dist^-[v]$ is picked to be the minimum label in an iteration then we call $dist[v]$ as the *permanent label* of node v. Now to prove the correctness of the algorithm. It is sufficient to show that the cost on the permanent label of a node in each iteration is the weight of the shortest bi-directed path from s to that node.

Theorem 1. *The permanent label of a node $u \in V$ in each iteration of* **Algorithm 1** *is the weight of the shortest bi-directed path from s to u.*

Proof. We prove the statement by induction on the number (n) of iterations in Algorithm 1. We now prove the base case when $n = 1$. Since we have initialized $dist^+[s] = dist^-[s] = 0$ and the values of the remaining both initialized and uninitialized nodes are > 0; the first iteration picks s and zero is trivially the cost of shortest bi-directed path form s to s.

Assume that the statement is true for $n = 1 \dots k$. As per the induction hypothesis the permanent labels $dist[s], dist[v_{i_2}] \dots dist[v_{i_k}]$ correspond to the costs of the shortest bi-directed paths between s and $s, v_{i_2} \dots v_{i_k}$.

Now let $dist'[v_{i_{k+1}}] < dist[v_{i_{k+1}}]$ be the cost of the shortest bi-directed walk from s to $v_{i_{k+1}}$. Also let $s, v_{j_2} \dots v_{j_k}, v_{i_{k+1}}$ be the path corresponding to the cost $dist'[v_{i_{k+1}}]$. Note that v_{j_k} cannot be one of the nodes with a permanent label. If

Algorithm 1. Algorithm to find the shortest bi-directed path from s to t

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INPUT   : Bi-directed graph $G = (V, E)$ and two vertices $s, t \in V$
OUTPUT: Cost of the shortest bi-directed path between $s$ and $t$

$dist^+[s] = dist^-[s] = 0$
$dist^+[v] = dist^-[v] = \infty \ \forall v \in V \wedge v \neq s$

while $dist^+ \neq \phi$ or $dist^- \neq \phi$ do
    $u^+ = \min_u\{dist^+\}$
    $u^- = \min_u\{dist^-\}$

    if $u^+ = t$ or $u^- = t$ then
        return $\min\{dist^+[u^+], dist^-[u^-]\}$


    if $dist^+[u^+] < dist^-[u^-]$ then
        $U^+ = \{v|(u^+, v) \in E \wedge (\mathcal{O})(u^+, v) = \lhd\!-\!\lhd)\}$
        $U^- = \{v|(u^+, v) \in E \wedge (\mathcal{O})(u^+, v) = \lhd\!-\!\rhd)\}$
        $dist[u^+] = dist^+[u^+]$
        $dist^+ = dist^+ - \{u^+\}$
    else
        $U^+ = \{v|(u^-, v) \in E \wedge (\mathcal{O})(u^-, v) = \rhd\!-\!\lhd)\}$
        $U^- = \{v|(u^-, v) \in E \wedge (\mathcal{O})(u^+, v) = \rhd\!-\!\rhd)\}$
        $dist[u^-] = dist^-[u^-]$
        $dist^- = dist^- - \{u^-\}$


    foreach $u \in dist^+$ do
        $dist^+[u] = \min\{dist^+[u], dist^+[u^+] + w[u^+, u]\}$
    foreach $u \in dist^-$ do
        $dist^-[u] = \min\{dist^-[u], dist^-[u^-] + w[u^-, u]\}$


return $\infty$
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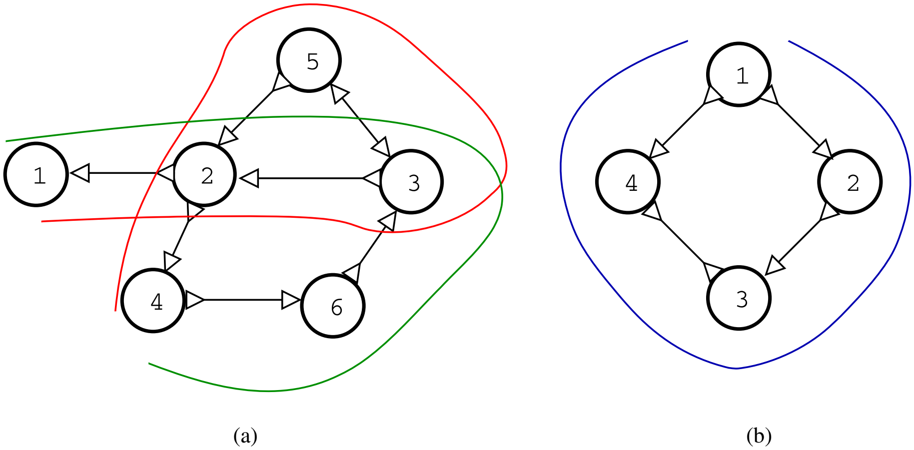
not, we would have $dist'[v_{i_{k+1}}] = dist[v_{i_{k+1}}]$ (because we should have updated v_{k+1} when the v_{j_k} was given a permanent label) which is a contradiction. Now let $dist'[v_{j_k}]$ be the cost of the shortest path from s to v_{j_k}. Clearly, $dist'[v_{j_k}] < dist[v_{i_{k+1}}]$ and this means that none of the nodes $v_{j_2}, v_{j_3} \dots v_{j_k}$ haa a permanent label. Since in the iteration $n = 1$ the algorithm updated the labels adjacent to all the nodes this means that either $dist^+[v_{j_2}]$ or $dist^-[v_{j_2}]$ should have a cost $0 < w_{s,j_2}$ and $dist'[v_{i_{k+1}}] \geq w_{s,j_2}$. In each iteration from $n = 1, \dots, (k+1)$ we picked the globally minimum label $dist[v_{i_{k+1}}] < w_{s,j_2} \leq dist'[v_{i_{k+1}}]$ which is a contradiction. $\square$



(a) (b)

Fig. 1. (a) node 4 contains two bi-directed walks from node 1, the green colored path is the shortest.**(b)** the walk starting from node 1 and ending at node 1 is a Chinese walk but not a cyclic Chinese walk.

We now give a simple example to illustrate the algorithm. Consider the bi-directed graph in Figure 1(a), with a unit weight on every edge. Let $s = 1$ and $t = 4$ for instance. From Figure 1(a) we see two bi-directed walks – *red*, *green*. The *green* path is the shortest path of length 4 units.

5 Terminal Oriented Shortest Bi-directed Walks

In the previous section we have seen how to find a shortest bi-directed walk between two nodes in a given bi-directed graph. We now define a *terminal oriented bi-directed walk* as follows. Let $w(v_i, v_j) = v_i, e_{i_1}, v_{i_1}, e_{i_2}, v_{i_2} \dots v_{i_m}, e_{i_{m+1}}, v_j$ be any bi-directed walk between two nodes v_i and v_j in a bi-directed graph. Then this bi-directed walk $w(v_i, v_j)$ is called *terminal oriented bi-directed walk* iff $e_{i_1}.o_1 = \triangleright$ and $e_{i_{m+1}}.o_2 = \triangleright$. For example in Figure 1(a) there are two bi-directed walks between nodes 4 and 1 – marked with green and red. However only the green bi-directed walk is terminally oriented. A terminal oriented bi-directed walk w is called the *shortest terminal oriented bi-directed walk* iff there is no other terminal oriented bi-directed walk shorter than w.

5.1 An Algorithm for Finding a Terminal Oriented Shortest Bi-directed Walk

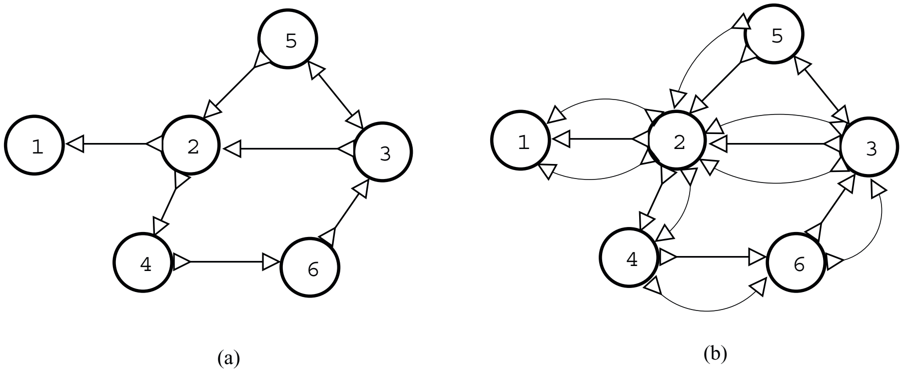
It is easy to modify Algorithm 1 to find a terminal oriented shortest path between s and t. We only have to modify the initialization step and the step which checks if the target node has been reached. During the initialization at line 2 of Algorithm 1 we make $dist^{+}[s] = 0$ and $dist^{-}[s] = \infty$. This avoids the exploration of bi-directed walks which does not start with $\triangleright$. In line 9, we stop our exploration only if $u^{+} = t$. These changes ensure that the bi-directed walk at s starts with $\triangleright$ and ends with $\triangleright$ at t.

6 A Sufficient Condition for an Eulerian Tour on a Bi-directed Graph

The following Lemma 1 [6] is a sufficient condition for a cyclic Eulerian tour in a bi-directed graph. A bi-directed graph which has a cyclic Eulerian tour is called an Eulerian bi-directed graph.

Lemma 1. *A connected bi-directed graph is Eulerian if and only if every vertex is balanced.*

Note that if a bi-directed graph is Eulerian then a cyclic CP walk is the same as a cyclic Eulerian walk. We emphasize the cyclic adjective for the following reason. Figure 1(b) has a CP walk starting and ending at vertex 1. However the CP walk is not cyclic because the walk starts with $\triangleright$ and ends with $\triangleleft$. The bi-directed graph in Figure 1(b) is not balanced. If the bi-directed graph is not Eulerian, the key strategy to find a cyclic CP walk is to make it Eulerian by introducing multi-edges into the original graph. The hope is that introducing multi-edges would make the bi-directed graph balanced. Thus a cyclic Eulerian walk on a balanced multi-edge bi-directed graph would give a cyclic CP walk on the original graph. Since we are interested in finding a shortest cyclic CP walk, we would like to minimize the number of multi-edges we introduce in the original graph.



(a) (b)

Fig. 2. **(a)** a simple bi-directed graph, **(b)** a multi-bi-directed graph. Notice that orientations of the multi-edges is the same as the orientation of the original edge.

7 A Deterministic Algorithm to Find a Cyclic CP Walk on a Bi-directed Graph

We now describe our deterministic algorithm to find a cyclic CP walk on a weighted bi-directed graph. First we define a *multi-bi-directed graph* as a bi-directed graph in which an edge between two nodes is overlaid at least once, without changing its orientation. Figure 2(a) shows a bi-directed graph; Figure 2(b) shows a valid multi-bi-directed graph. Notice that while overlaying the edge we did not change its orientation. Since the orientation of the multi-edges is the same as the original edges, any bi-directed walk involving multi-edges is consistent with the bi-directed walk in the original graph. Another important property of the multi-bi-directed graphs is their ability to make the nodes balanced. Notice that the vertex 3 in the original bi-directed graph is positively imbalanced – $d_{in}(v_3) = 2, d_{out}(v_3) = 1$. However in the multi-bi-directed graph in Figure 2(b) we are able to balance vertex 3 by introducing some multi-edges into the original graph. Given a bi-directed graph $G = (V, E)$, let $G^m = (V, E^m)$ be some multi-bi-directed graph corresponding to G. The following Lemma 2 gives a characterization for G to have a cyclic CP walk.

Lemma 2. *A non Eulerian bi-directed graph $G = (V, E)$ has a cyclic Chinese Postman walk $\iff \exists$ a corresponding multi-bi-directed graph $G^m = (V, E^m)$ which is Eulerian.*

Given a multi-bi-directed graph $G^m(V, E^m)$ corresponding to some bi-directed graph $G = (V, E)$, we define the *multi-bi-directed graph weight* as $\mathcal{W}(G^m) = \sum_{e \in E^m} c(e)$, where $c : e \in E \rightarrow \mathbb{R}^+$ is a cost function on the bi-directed graph $G(V, E)$. We denote $G^*(V, E^*)$ as the minimum weight Eulerian multi-bi-directed graph corresponding to $G(V, E)$ if at all one exists. The following Lemmas are easy to prove.

Lemma 3. *Finding a cyclic CP walk on a bi-directed graph $G(V, E)$ is equivalent to finding a minimum weight Eulerian multi-bi-directed graph $G^*(V, E^*)$ corresponding to G.*

Lemma 4. *If a bi-directed-graph $G(V, E)$ has a cyclic CP walk then the cost of that walk is equal to the weight of $G^*(V, E^*)$.*

7.1 Balancing Bi-partite Graph

Given a bi-directed de Bruijn graph $G(V, E)$ we define a corresponding *Balancing Bi-partite Graph*, $B(P, Q, E^b)$ as follows. Let $V^+ = \{v | \, d_{in}(v) - d_{out}(v) > 0\}$, $V^- = \{v | \, d_{in}(v) - d_{out}(v) < 0\}$. $P = \cup_{p \in V^+} \{p^{(1)}, p^{(2)} \ldots p^{(|d_{in}(p) - d_{out}(p)|)}\}$, $Q = \cup_{q \in V^-} \{q^{(1)}, q^{(2)} \ldots q^{(|d_{in}(q) - d_{out}(q)|)}\}$. We now introduce an edge between $p^(i) \in P$ and $q^{(j)} \in Q$ iff $p, q \in V$ are connected by a *terminal oriented bi-directed walk* from p to q. Let $dist^t(p, q)$ be the weight of this walk. Then $E^b = \{(p^{(i)}, q^{(j)}) | \, dist^t(p, q) \neq \infty \, \wedge \, p, q \in V\}$. The weight of the edge $(p^{(i)}, q^{(j)}) \in E^b$ is the weight of terminal oriented bi-directed walk $dist^t(p, q)$.

Lemma 5. *A non Eulerain bi-directed graph* $G(V, E)$ *has a cyclic CP walk* $\Longleftrightarrow$ *the balancing bi-partite graph* $B(P, Q, E^b)$ *has a perfect match.*

7.2 Constructing a Family of Eulerian Multi-bi-directed Graphs

We now give a construction for generating Eulerian multi-bi-directed graphs corresponding to a given non Eulerian bi-directed graph which has a cyclic CP walk. We call this a *Balancing Match Family* denoted by $\mathcal{F}$. Lemma 5 can be used to generate $\mathcal{F}$. Assume that $G(V, E)$ is a non Eulerian bi-directed graph that has a cyclic CP walk. The following construction generates a family of Eulerian multi-bi-directed graphs corresponding to $G(V, E)$.

- STEP-1: Create a balancing bi-partite graph $B(P, Q, E^m)$ corresponding to $G(V, E)$ by choosing some terminal oriented bi-directed walk between $p^{(i)} \in P$ and $q^{(j)} \in Q$.
- STEP-2: Find a perfect match M_b in $B(P, Q, E^m)$. For each edge in M_b overlay the corresponding terminal oriented bi-directed walk on $G(V, E)$. This generates a Eulerian multi-bi-directed graph $G^m(V, E^m)$.

The following Lemma 6 is easy to see.

Lemma 6. *If* $G(V, E)$ *is a non Eulerian bi-directed graph that has a cyclic CP walk, then every corresponding Eulerian multi-bi-directed graph* $G^m(V, E^m)$ *belongs to the family* $\mathcal{F}$.

The following Lemma gives an expression for the weight of any $G^m(V, E^m) \in \mathcal{F}$.

Lemma 7. *Let* $G(V, E, c)$ *be a non Eulerian weighted bi-directed graph which has a cyclic CP walk* $c : E \rightarrow \mathbb{R}^+$. *Let* $G^m(V, E^m, c) \in \mathcal{F}$ *be some Eulerian multi-bi-directed graph. Then,* $\mathcal{W}(G^m) = \sum_{e \in E} c(e) + \sum_{(p^{(i)}, q^{(j)}) \in M_b} dist^t(p, q)$, *where* M_b *is a perfect match in* $B(P, Q, E^b)$.

7.3 An Algorithm for Finding an Optimal Cyclic CP Walk

We now put together all the results in the preceding sub-section(s) to give an algorithm to find $G^*(V, E^*)$. The algorithm is summarized in the following steps.

- STEP-1: We first identify positive and negative imbalanced nodes in G. Let $V^+ = \{v | d_{in}(v) - d_{out}(v) > 0\}$, $V^- = \{v | d_{in}(v) - d_{out}(v) < 0\}$
- STEP-2: Find the cost of a *terminal oriented shortest bi-directed walk* between every pair $(v, u) \in V^+ \times V^-$. Let this cost be denoted as $dist^t(v, u)$.
- STEP-3: Create a *balancing bi-partite graph* $B(P, Q, E^b)$ as follows. Let $P = \cup_{v \in V^+} \{v^{(1)}, v^{(2)}, \ldots, v^{(|d_in(v) - d_out(v)|)}\}$, $Q = \cup_{u \in V^-} \{u^{(1)}, u^{(2)}, \ldots, u^{(|d_{in}(u) - d_{out}(u)|)}\}$, $E = \{(v^{(i)}, u^{(j)}) | v^{(i)} \in P \wedge u^{(j)} \in Q\}$. The cost of an edge $c(v^{(i)}, u^{(j)}) = dist^t(v, u)$.

- STEP-4: Find a minimum cost perfect match in B. Let this match be M_b. If B does not have a perfect match then G does not have a cyclic CP walk.
- STEP-5: For each edge $(v^{(i)}, u^{(j)}) \in M_b$, overlay the terminal oriented shortest bi-directed walk between v and u in the $G(V, E)$. After overlaying all the terminal oriented bi-directed walks from M_b on to $G(V, E)$ we obtain $G^*(V, E^*)$. We will prove that it is optimal in Theorem 2.

Theorem 2. *If $G(V, E)$ is a bi-directed graph that has a cyclic CP walk, then the cost of this cyclic CP walk is equal to $\mathcal{W}(G^*) = \sum_{e \in E} c(e) + \sum_{(v^{(i)}, u^{(j)}) \in M_b} dist^t(v, u)$. Here M_b is the min-cost perfect match in the balancing bi-partite graph B.*

7.4 Runtime Analysis of the Algorithm to Find a Cyclic CP Walk

Let $p = \max\{|V^+|, |V^-|\}$ and $d_{max} = \max_{v \in V}\{|d_{in}(v) - d_{out}(v)\}$. STEP-2 of the algorithm runs in $\Theta(p(|V|+|E|)\log(|V|))$ time to compute $dist^t(v, u)$. In STEP-3 $|P| \leq d_{max}p$, $|Q| \leq d_{max}p$. For STEP-4 Hungarian method can be applied to solve the weighted matching problem in $\Theta((d_{max}p)^3)$ time. So the total runtime of this deterministic algorithm is $\Theta(p(|V| + |E|)\log(|V|) + (d_{max}p)^3)$. As mentioned before if p is much smaller than $|V|$ this algorithm performs better than the bi-directed flow algorithm.

7.5 Runtime Analysis of the Algorithm to Find SDDNA

Since SDDNA runs on a bi-directed de Bruijn graph which is un-weighted, STEP-2 of the algorithm runs in $\Theta(p(|V| + |E|))$ time – because we don't need to use a Heap, we just do a BFS on the bi-directed graph. The rest of the analysis for the runtime remains the same and the total run time of the algorithm is $\Theta(p(|V| + |E|) + (d_{max}p)^3)$.

8 Dealing with Practical Bi-directed de Bruijn Graphs with no Cyclic CP Walks

As we have mentioned earlier most of the bi-directed de Bruijn graphs constructed from the reads do not satisfy the sufficient condition for cyclic CP walks. In such cases our algorithm can still be used, by modifying it to find a *maximum* match in the balancing bi-partite graph rather than perfect match. We can introduce a hypothetical node h and connect all the un-matched nodes in the balancing bi-partite graph to h with appropriate bi-directed edges and thus make all the original nodes balanced. We can now find a cyclic CP walk in this hypothetical graph. Every sub-walk in the cyclic CP walk that starts from h and ends at h can be reported as a *contig*. Thus our algorithm is capable of handling cases when the bi-directed graph cannot have a cyclic CP walk.

9 Experimental Results

As we have mentioned in the previous sections the asymptotic complexity of our algorithm depends on p – the maximum of positively and negatively imbalanced nodes. In the case of de Bruijn graphs $d_{max} \leq |\Sigma|$, where $|\Sigma|$ is the size the alphabet from which the strings are drawn. In our case this is exactly four. So we can safely ignore d_{max} in the case of de Bruijn graphs and just concentrate on p. In the rest of the discussion we would like to refer to p as the number of imbalanced nodes. It is clear that p is a random variable with support in $[0, |V|]$. So we would like to estimate the expected number of imbalanced nodes in a graph with $|V|$ bi-directed edges. We estimated the mean of the random variable $\frac{p}{|V|}$ from several samples of bi-directed de Bruijn graphs constructed from reads from a plant genome. A simple $t-$test is applied to to estimate the 95% confidence interval of $\frac{p}{|V|}$. See Table 1 for the details of the samples used. Notice that as we increase the size of k (de Bruijn graph order) from 21 to 25, the number of imbalanced nodes in columns corresponding to $|V^+|$ and $|V^-|$ reduces. This is because increasing k reduces the number of edges which may reduce the number of imbalanced nodes. On the other hand for a fixed value of k the number of imbalanced nodes increases consistently with the nodes. However the rate of growth is very slow compared to the rate of growth of the number of nodes. Finally we use this evidence to hypothesize that the number of imbalanced nodes in practical bi-directed graphs is only between 0.087% to 0.133% of the number of nodes in the graph, with a probability of 95%.

Table 1. The value of p on short read data from a plant genome sequencing data from CSHL

READS	k	NODES	P-IMBAL	N-IMBAL	BAL-BI-GRAPH			
			$\lvert V^+\rvert$	$\lvert V^-\rvert$	$\lvert P\rvert$	$\lvert Q\rvert$	p	$\frac{p\times100}{\lvert V\rvert}$
102400	21	1588569	1157	1133	1186	1173	1186	0.075
153600	21	2353171	2240	2141	2298	2211	2298	0.098
204800	21	3097592	3509	3492	3601	3590	3601	0.116
256000	21	3825101	4953	5004	5074	5131	5131	0.134
307200	21	4538734	6719	6748	6878	6912	6912	0.152
358400	21	5235821	8586	8603	8789	8802	8802	0.168
409600	21	5917489	10665	10693	10914	10934	10934	0.185
102400	25	1202962	569	521	588	540	588	0.049
153600	25	1788533	1104	1026	1139	1062	1139	0.064
204800	25	2362981	1744	1708	1788	1759	1788	0.076
256000	25	2927656	2521	2523	2579	2592	2592	0.089
307200	25	3484849	3370	3414	3451	3517	3517	0.101
358400	25	4032490	4333	4369	4441	4485	4485	0.111
409600	25	4571554	5390	5467	5518	5613	5613	0.123
$\left[\bar{x} - z_{\frac{\alpha}{2}}\frac{S}{\sqrt{n}}, \bar{x} + z_{-\frac{\alpha}{2}}\frac{S}{\sqrt{n}}\right]$: 95% C.I for average $\frac{p\times100}{\lvert V\rvert}$ is $[0.0872\%, 0.1330\%]$								

9.1 Implementation and Data

An implementation of the algorithms discussed is available at `http://trinity.engr.uconn.edu/~vamsik/fast_cpp.tgz`.

10 Conclusion and Further Research

In this paper we have given an algorithm for cyclic Chinese Postman walk on a bi-directed de Bruijn graph. Our algorithm is based on identifying shortest bi-directed walks and weighted matching. This algorithm performs asymptotically better than the bi-directed flow algorithm when the number of imbalanced nodes are much smaller than the nodes in the bi-directed graph. On the other hand this algorithm can also handle the instances of bi-directed graphs which does not have a cyclic CP walk and provide a minimal set of walks, cyclic walks which cover every edge in the bi-directed graph at least once.

There are several research directions which can be pursued. Firstly, we need to address how the addition of paired reads may impose new constraints on the cyclic CPP walk. Secondly, while Eulerization of the bi-directed graph we have chosen the shortest path bi-directed path, however this may not correspond to the repeating region in the genome. Other strategy to make the graph Eulerian is to choose the path with maximum read multiplicity. This on other hand may increase the length of the Chinese walk, can we simultaneously optimize these two objectives ?.

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