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Almost Parallel Strong Trace Model of Self–Assembly Polypeptide Nanostructure

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Abstract

Polypeptides are programmable natural polymers, which can be self-assembled into ordered nanostructures. The stable trace and strong trace have been introduced in [17] and [19], respectively, to provide the underlying mathematical model for self-assembly of polypeptide nanostructures. In this paper, we introduce the E_1 -antiparallel strong trace of a graph G = (V, E), which is a strong trace of G with only the edges of $E_1 \subset E$ are traversed in the opposite direction. Given a graph G and its edge subset E_1 , the main purpose of the paper is to consider under which conditions G has an E_1 -antiparallel strong trace, and we solve it in the case that E_1 is an independent edge set, E_1 induces a path and E_1 induces a cycle of G, respectively. Furthermore, we discuss the molecular design of polypeptide nanostructures based on almost parallel strong trace model.

1 Introduction

Polynucleotides and polypeptides are two kinds of programmable natural polymers, which have long been recognized as building blocks in nanotechnology [1]. Due to the basepairing rules, DNA is a tractable molecule in designing defined complex 3D structures [2], from the first DNA cube [3] to the largest DNA prism [4]. More recently, some symmetrical polypeptide nanostructures have been self-assembled by fusing protein oligomerization domains [5], and designing new protein-protein interacting surfaces [6]. On the other hand, the mathematical model of DNA polyhedra was proposed and the invariant of corresponding polyhedral links was computed to reveal the structural properties of DNA polyhedra [7–11]. Designing the principle of self-assembly represents a major challenge, not only for DNA but also for protein nanostructures [12].

In comparison with DNA nanostructures [13], the self-assembling of polypeptides into protein nanostructures is based on cooperative and long-range interactions, and hence developed more slowly but provides more versatile functionality [14]. However, a simple topology-based method was proposed for self-assembling a single-chain polypeptide tetrahedron [15]. In this approach, coiled-coil dimers were used to mimic DNA duplexes as building modules. Unlike with DNA duplexes which are always antiparallel, coiledcoil dimers adopt either a parallel or antiparallel orientation, expanding the number of reachable designed topologies. These landmark discoveries could lead to significant development in biotechnology since they provide a foundation for constructing new topological polypeptide folds based on the set of orthogonal interacting polypeptide segments [16]. Therefore, the study of underlying mathematical model is of great importance in designing of self-assembly polypeptide nanostructures.

The stable trace introduced in [17] provides a general mathematical support for selfassembly polypeptides, and it has been proved that the structure created from its stable trace could be guaranteed to be stable. But in [19], Fijavž, Pisanski and Rus observed that this model has two deficiencies: firstly it does not account for vertices of degree ≤ 2 , and secondly, a stable trace of G may fold to a graph different from G when G contains a vertex of degree ≥ 6 . They further introduced the strong trace which overcomes the two deficiencies. And the authors in [17–19] investigated the necessary and sufficient conditions of graphs that admit a parallel proper trace, parallel stable trace and parallel strong trace, respectively. Graphs which admit an antiparallel strong trace were also studied in [19].

It has been proved that a single-chain tetrahedron cannot be constructed without the use of both parallel and antiparallel strands, which means that the strong trace of a topfold can be constructed by polypeptide rather than DNA [16]. In addition, more parallel coiled-coil dimers have been characterized for the molecular design than antiparallel dimers [20]. For example, the experimentally obtained single-chain tetrahedron is the topofold with the largest number of parallel segments, comprising four parallel and two antiparallel coiled-coil dimeric edges [15]. This motivated us to study the almost parallel strong trace model, which may give new insight into the folding of polypeptide nanostructures.

To this aim, we introduce the notion of E_1 -antiparallel strong trace of a graph G = (V, E) with $E_1 \subset E$, which is an almost parallel strong trace with only the edges in E_1 of G are traversed in the opposite direction. Usually, E_1 is a subset with fewer edges compared with edges of G, which justifies the notion of almost parallel strong trace. Throughout this paper, we will assume that all graphs are finite, connected and simple (i.e. no loops and no multiple edges) unless stated otherwise. We use $A \subseteq B$ and $A \subset B$ to denote A is a subset of B and A is a proper subset of B, respectively. This paper is organized as follows. Section 2 is devoted to present some basic definitions and some known results. In Section 3, we consider the case that E_1 is an independent edge set of G, E_1 induces a path and a cycle of G, respectively. We discuss some biological implications of the molecular design of polypeptide nanostructures base on almost parallel strong trace model in the last Section 4.

2 Definitions and some known results

We shall first give some necessary definitions and notations, for those not given here we refer the readers to [21,22].

Let G = (V, E) be a graph with vertex set V and edge set E. For $v \in V$, we denote by N(v) (resp. E(v)) the set of vertices adjacent to (resp. edges incident with) v, and we denote by $d_G(v)$ the degree of v in G, i.e. $d_G(v) = |N(v)| = |E(v)|$. We use $\delta(G)$ to denote the minimum degree of G, i.e. $\delta(G) = \min_{v \in V} \{ d_G(v) \}$. A graph G is called to be even if $d_G(v)$ is even for each $v \in V$. For $E_1 \subset E$, we denote by $G \setminus E_1$ the graph obtained from G by deleting edges in E_1 . An edge e of G is said to be a *cut edge* of G if its deletion results in a disconnected graph.

A tour of a graph G is a closed walk that traverses each edge of G at least once, and an *Euler tour* one that traverses each edge exactly once. A graph is *Eulerian* if it admits an Euler tour. A fundamental theorem of graph theory, known as Euler's theorem, states that G is Eulerian if and only if it is connected and even.

A double trace in G is a closed walk which traverses each edge of G exactly twice, we say that a double trace contains a *retracing* if it has an immediate succession of an edge e by its parallel copy, see Figure 1. Moreover, if v is a vertex of a graph G with a double trace T, then we say that T contains a *repetition through* v if the vertex sequence $u \to v \to w$ appears twice in T in any direction $(u \to v \to w \text{ or } w \to v \to u)$, where $u, w \in N(v)$, see Figure 2. A double trace that with no retracing is a *proper trace*, and a proper trace that with no repetitions through all vertices is a *stable trace*.



Figure 1. Retracing of the edge e.



Figure 2. Repetition through the vertex v.

Let T be a double trace of length l, and let $N \subseteq N(v)$, we say that T has an N-repetition at v if the following condition holds:

for every $i \in \{0, \dots, l-1\}$: if $v = v_i$ then $v_{i+1} \in N$ if and only if $v_{i-1} \in N$.

Clearly if T has an N-repetition at v, then it also has an $N(v) \setminus N$ -repetition at v. An N-repetition at v is a d-repetition if |N| = d, and a d-repetition will also be called a repetition of order d. An N-repetition at v is trivial if $N = \emptyset$ or N = N(v). A strong trace is a double trace without nontrivial repetitions, and a d-stable trace is a double trace without repetitions of order i for all $1 \le i \le d$. It is easily seen that a proper trace (respectively, stable trace) is a 1-stable trace (respectively, 2-stable trace).

Let T be a double trace in G and $v \in V$, the vertex figure of v, denoted by $F_{v,T}$, is a graph having E(v) as its vertex set by making edges $e, e' \in E(v)$ adjacent if e and e' are consecutive edges along T. Observe that $F_{v,T}$ is a 2-regular graph, and it contains a loop as a subgraph if and only if T contains a retracing at v, and contains a pair of parallel edges as a subgraph if and only if T contains a repetition through v. The following theorem will be used in the paper. **Theorem 2.1** [19] Let T be a double trace in G. Then T is a strong trace of G if and only if $F_{v,T}$ is a single cycle for each $v \in V$.

The characterization of graphs that admit proper trace, stable trace and strong trace were studied in [23,24], [17] and [19], respectively.

Theorem 2.2 (1) [19] Every graph admits a strong trace.

(2) [19] A graph G admits a d-stable trace if and only if $\delta(G) > d$.

Let T be a double trace of G and $e \in E$. Then e is traversed exactly twice along T, if in both cases e is traversed in the same direction, we say that e is a parallel edge (with respect to T), and say that e is an antiparallel edge (with respect to T) otherwise. Furthermore, a double trace T is said to be a parallel double trace if every edge of G is parallel and an antiparallel double trace if every edge of G is antiparallel. The authors in [17–19] investigated the necessary and sufficient conditions of graphs that admit parallel double trace and parallel strong trace, respectively.

- **Theorem 2.3** (1) [19] A graph G admits a parallel strong trace if and only if G is Eulerian.
 - (2) [19] A graph G admits a parallel d-stable trace if and only if G is Eulerian and δ(G) > d.

In [19], Fijavž, Pisanski and Rus also characterized graphs that admit an antiparallel strong trace, and they obtained:

Theorem 2.4 [19] A graph G admits an antiparallel strong trace if and only if G has a spanning tree ST such that each connected component of $G \setminus E(ST)$ has an even number of edges.

Let $E_1 \subseteq E$, and T be a double trace of a graph G = (V, E), we say that T is an E_1 -antiparallel double trace of G if exactly the edges of E_1 are traversed in the opposite direction in T. Furthermore, T is said to be an E_1 -antiparallel strong (respectively, d-stable) trace if T is not only a strong (respectively, d-stable) trace but also an E_1 -antiparallel double trace. Observe that the parallel double trace and the antiparallel double trace are both special cases of E_1 -antiparallel double trace for $E_1 = \emptyset$ and $E_1 = E$, respectively. The following lemma is quite useful in the subsequent section. **Lemma 2.1** Let $E_1 \subseteq E$, the edge set of G. If G admits an E_1 -antiparallel double trace, then $G \setminus E_1$ is even.

Proof Suppose that T is an E_1 -antiparallel double trace of G and DG is the multi-graph obtained from G by doubling each of its edges. It follows from the definition of T that edges of G inside E_1 are antiparallel and edges of G outside E_1 are parallel. In addition, the double trace T viewed as an oriented closed walk induces an orientation of edges of DG. Let $v \in V$. Suppose that the number of antiparallel edges of G incident with v is x and the number of parallel edges of G whose heads (resp. tails) are v is y_1 (resp. y_2). Note that the in-degree $d^-(v)$ of v will be equal to its out-degree $d^+(v)$ in DG, and $d^-(v) = x + 2y_1, d^+(v) = x + 2y_2$. Hence $y_1 = y_2$, which implies $d_{G\setminus E_1}(v)$ is even.

In next section we are going to study when the necessary condition will also be sufficient and only consider $E_1 \subset E$.

3 A little theoretical result

3.1 E_1 is an independent set

Lemma 3.1 Suppose that $E_1 \subset E$ is an independent set of a connected graph G = (V, E). If $G \setminus E_1$ is even, then G admits an E_1 -antiparallel strong trace.

Proof For simplicity, let $|E_1| = k$. We shall prove the lemma by induction on k. By Theorem 2.3 (1), the lemma holds for k = 0. Now suppose that k > 0, assume that the lemma is true for l < k, and that E_1 is an independent set with k edges of G and $G \setminus E_1$ is even. Choose an arbitrary edge, say $e = u_1u_2$, from E_1 , let $G' = G \setminus e$ and $E_2 = E_1 \setminus e$. It is obvious that $E_2 \subset E(G')$ with (k-1) independent edges, and that $G' \setminus E_2 = G \setminus E_1$, is even.

Case 1 e is not a cut edge of G.

In this case G' is connected and $d_{G\setminus E_1}(u_i) \ge 2$ for i = 1, 2. By our induction hypothesis, G' admits an E_2 -antiparallel strong trace T'.

Then all the edges incident with u_i (i = 1, 2) except e must be parallel in T'. Furthermore, there must exist an edge, say $e_2 = u_2v_2$, that is traversed twice both towards u_2 in T'. Without loss of generality, we may describe T' as

$$T' = v_1 e_1 u_1 f_1 w_1 t_1 v_2 e_2 u_2 f_2 w_2 t_2 v_2 e_2 u_2 h_2 y_2 t_3,$$

such that $e_1 = u_1v_1$, $f_1 = u_1w_1$ are two edges incident with vertex u_1 , and $f_2 = u_2w_2$, $h_2 = u_2y_2$ are edges incident with vertex u_2 , whenever $h_2 = f_2$ if and only if $d_{G'}(u_2) = 2$, and t_i (i = 1, 2, 3) is a segment of T' and doesn't contain e_2 , see Figure 3(1). By Theorem 2.1, the vertex figure $F_{v,T'}$ is a single cycle for each $v \in V(G)$.

Now let

$T = v_1 e_1 u_1 e u_2 f_2 w_2 t_2 v_2 e_2 u_2 e u_1 f_1 w_1 t_1 v_2 e_2 u_2 h_2 y_2 t_3$

obtained from T' by interchanging its two interior segments between u_1 and u_2 with direction preserved and by adding the edge e twice in the opposite direction. See Figure 3(2). It is easy to see that T is an E_1 -antiparallel double trace of G. For any vertex $v \in V(G) \setminus \{u_1, u_2\}$, note that the vertex figure $F_{v,T}$ is exactly the same as $F_{v,T'}$, which is a single cycle. For the vertex u_i (i = 1, 2), it is not difficult to see that $F_{u_i,T}$ is obtained from $F_{u_i,T'}$ by replacing the edge $e_i f_i$ with two adjacent edges $e_i e$ and ef_i , which means that $F_{u_i,T}$ is also a single cycle, see Figure 4. Hence T is an E_1 -antiparallel strong trace of G.



Figure 3. (1)The double trace T' of G'. (2)The double trace T of G.



Figure 4. The vertex figures: $(1)F_{u_1,T'}$ $(2)F_{u_2,T'}$ $(3)F_{u_1,T}$ and $(4)F_{u_2,T}$.

Case 2 e is a cut edge of G.

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Let G_1 and G_2 be the two connected components of G' with $u_i \in V(G_i)$. Then at most one of G_i (i = 1, 2) is trivial, otherwise, $G = K_2$ and $E_1 = \{e\}$ is not a proper edge subset of G. We shall suppose that G_2 is not trivial. For $i \in \{1, 2\}$, let $E_{1i} = E_1 \cap E(G_i)$. Obviously, $|E_{11}| + |E_{12}| = k - 1$. Notice that E_{12} is a proper independent edge subset of G_2 satisfying $G_2 \setminus E_{12}$ is even. Similar to Case 1, we may describe the E_{12} -antiparallel strong trace T_2 of G_2 as

$$T_2 = v_2 e_2 u_2 f_2 w_2 t_2 v_2 e_2 u_2 h_2 y_2 t_2',$$

such that $f_2 = u_2 w_2$, $h_2 = u_2 y_2$ are edges incident with u_2 , whenever $h_2 = f_2$ if and only if $d_{G_2}(u_2) = 2$, and t_2, t'_2 are segments of T_2 , which do not contain e_2 . See Figure 6(2).



Figure 5. (1)The strong trace T, (2)the vertex figure F_{u_2,T_2} , (3)the vertex figure $F_{u_2,T}$ and (4)the vertex figure $F_{u_1,T}$.

Subcase 2.1 G_1 is trivial.

In this case we can construct T as follows:

$$T = v_2 e_2 u_2 e u_1 e u_2 f_2 w_2 t_2 v_2 e_2 u_2 h_2 y_2 t'_2.$$

See Figure 5(1). By Figures 5(2)-(4)we know that T is an E_1 -antiparallel strong trace of G.

Subcase 2.2 G_1 is not trivial.

In this case E_{11} is also a proper independent edge subset of G_1 satisfying $G_1 \setminus E_{11}$ is even. Hence we may describe T_1 as

$$T_1 = v_1 e_1 u_1 f_1 w_1 t_1 v_1 e_1 u_1 h_1 y_1 t_1',$$

such that $f_1 = u_1 w_1$, $h_1 = u_1 y_1$ are edges incident with u_1 , whenever $h_1 = f_1$ if and only if $d_{G_1}(u_1) = 2$, and that t_1, t'_1 are segments of T_1 , which do not contain e_1 . See Figure 6(1).

Now we construct a double trace T of G as follows:

$$T = v_1 e_1 u_1 e u_2 f_2 w_2 t_2 v_2 e_2 u_2 h_2 y_2 t'_2 v_2 e_2 u_2 e u_1 f_1 w_1 t_1 v_1 e_1 u_1 h_1 y_1 t'_1 .$$

See Figure 6(3). By checking changes of vertex figures (also see Figure 4) we know that T is an E_1 -antiparallel strong trace of G.



Figure 6. The double traces: $(1)T_1$, $(2)T_2$ and (3)T.

By combining Lemma 2.1 and Lemma 3.1, we obtain:

Theorem 3.1 Suppose that $E_1 \subset E$ is an independent set of a connected graph G = (V, E). Then G admits an E_1 -antiparallel strong trace if and only if $G \setminus E_1$ is even.

As a consequence we have:

Corollary 3.1 Let G be a connected graph. Then G admits an $\{e\}$ -antiparallel strong trace if and only if $G \setminus e$ is even.

3.2 The subgraph induced by E_1 is a path and a cycle

Firstly, we present some lemmas which are necessary in the later proofs.

Lemma 3.2 Let G = (V, E) be a graph, $x \in V$, and G' be the graph obtained from G by splitting x into two adjacent vertices x' and x'' such that $d_{G'}(x') \ge 3$ and $d_{G'}(x'') \ge 3$. Let T' be a double trace of G', and T be a double trace of G obtained from T' by ignoring the edge e = x'x'' and by identifying both the vertices x' and x'' with a single x. If the vertex figure $F_{x',T'}$ and $F_{x'',T'}$ are both a single cycle, then the vertex figure $F_{x,T}$ is also a single cycle. **Proof** Firstly, we assume that the edge e is traversed twice in the same direction and without loss of generality, we assume the direction is from x' to x'' in T', and hence we may describe $T' = \cdots e'x'ex''e'' \cdots f'x'ex''f'' \cdots$, where e' and f' (respectively, e'' and f'') are edges incident with vertex x' (respectively, x''), see Figure 7(1). Then $T = \cdots e'xe'' \cdots f'xf'' \cdots$, as shown in Figure 7(2). Furthermore, since $d_{G'}(x') \ge 3$ (respectively, $d_{G'}(x'') \ge 3$) and $F_{x',T'}$ (respectively, $F_{x'',T'}$) is a single cycle, we have $e' \neq f'$ (respectively, $e'' \neq f''$). Note that $F_{x,T}$ is obtained from two disjoint single cycles $F_{x',T'}$ and $F_{x'',T'}$ by removing four edges e'e, ef', e''e, ef'' and adding two new edges e'e'', f'f''. Hence $F_{x,T}$ is also a single cycle. See Figure 8. Secondly, if e is traversed exactly once in



Figure 7. (1) The double trace T' of G' and (2) the double trace T of G.

each direction in T', then we can also obtain that $F_{x,T}$ is a single cycle, and we leave the details to the readers.



Figure 8. The vertex figures: (1) $F_{x',T'}$, (2) $F_{x'',T'}$ and (3) $F_{x,T}$.

Lemma 3.3 Let G = (V, E) be a connected graph and $E_1 \subset E$. Suppose that the subgraph induced by E_1 is a path of length $k \ge 2$. If $G \setminus E_1$ is even, then G admits an E_1 -antiparallel strong trace.

Proof We first consider the case of k = 2, then the general case of $k \ge 3$.

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Case 1 k = 2.

Suppose that $E_1 = \{a, b\}$, where $a = u_1 x$ and $b = u_2 x$. Then $d_G(x)$ is even and $d_G(u_i)$ are both odd for i = 1, 2.

Subcase 1.1 $d_G(x) = 2$.

Let G' be the graph obtained from G by merging a and b into a single edge e as shown in Figure 9. Then $G' \setminus e$ is even.



Figure 9. (1) The graph G and (2) the graph G'.

Therefore G' admits an $\{e\}$ -antiparallel strong trace T' by Corollary 3.1. This means that each vertex figure $F_{v,T'}$ is a single cycle by Theorem 2.1. Now we construct a double trace T of G from T' by replacing u_1eu_2 with u_1axbu_2 , and by replacing u_2eu_1 with u_2bxau_1 . Note that only a and b are traversed in the opposite direction in T. Moreover, it is clear that $F_{v,T}$ is isomorphic to $F_{v,T'}$ for each $v \neq x$, and there is no retracing appeared at the vertex x. Thus T is an E_1 -antiparallel strong trace of G.

Subcase 1.2 $d_G(x) \ge 4$.

For convenience, let $d = d_G(x)$. We assume that $N(x) = \{u_1, u_2, x_1, x_2, \cdots, x_{d-2}\}$. We construct G' from G as shown in Figure 10. Let $E_2 = \{a', b'\}$. Then $E_2 \subset E(G')$ and $G' \setminus E_2$ is even. By Theorem 3.1, G' admits an E_2 -antiparallel strong trace T'. Note that $d_{G'}(x') = 2\lfloor \frac{d}{4} \rfloor + 1 \ge 3$, $d_{G'}(x'') = d - 2\lfloor \frac{d}{4} \rfloor + 1 \ge 3$ and let T be the double trace of G obtained from T' by ignoring the edge e firstly and then identifying the vertices x' and x'' to become x. By Lemma 3.2, T is an E_1 -antiparallel strong trace G.

Case 2 k > 2.

Let $E_1 = \{z_1, \dots, z_k\}$ with $z_i = x_{i-1}x_i$ for $i \in \{1, \dots, k\}$. Then only the vertices x_0 and x_k are of odd degrees in G. Let $1 \leq i_1 < i_2 < \dots , < i_l \leq k-1$ such that $d_G(x_i) > 2$ if $i \in \{i_1, i_2, \dots, i_l\}$ and $d_G(x_i) = 2$ otherwise. Let $E'_1 = \{x_0x_{i_1}, x_{i_1}x_{i_2}, \dots, x_{i_l}x_k\}$. Let G' be the graph obtained from $(G \setminus E_1)$ by adding the edges in E'_1 firstly and then by deleting the isolated vertices (if there exist isolated vertices). Let G'' be the graph obtained from G' by splitting each x_{i_i} for $j \in \{1, 2, \dots, l\}$ as shown in Figure 10. Applying Subcase 1.2



Figure 10. (1) The graph G and (2) the graph G'.

to G'', we obtain G' admits an E'_1 -antiparallel strong trace. Applying Subcase 1.1 to G', we obtain G admits an E_1 -antiparallel strong trace.

Combining Lemma 2.1 and Lemma 3.3, we obtain:

Theorem 3.2 Let G = (V, E) be a connected graph and $E_1 \subset E$. Suppose that the subgraph induced by E_1 is a path. Then G admits an E_1 -antiparallel strong trace if and only if $G \setminus E_1$ is even.

As a consequence we have:

Corollary 3.2 Let G = (V, E) be a connected graph and $\{a, b\} \subset E$. Then G admits $\{a, b\}$ -antiparallel strong trace if and only if $G \setminus \{a, b\}$ is even.

Furthermore, it is not difficult to combine Theorem 3.1 and Theorem 3.2 into the case that E_1 forms several disjoint paths. Now we consider the case that E_1 forms a cycle.

Theorem 3.3 Let G = (V, E) be a connected graph and $E_1 \subset E$. Suppose that the subgraph induced by E_1 is a cycle. Then G admits an E_1 -antiparallel strong trace if and only if $G \setminus E_1$ is even.

Proof It suffices to prove its sufficiency. Since $E_1 \subset E$, there must exist an edge, say $e \in E_1$, such that one of its two endpoints is of degree ≥ 2 in $G \setminus E_1$. Let $G' = G \setminus e$, $E_2 = E_1 \setminus e$. Then G' is connected with $E_2 \subset E(G')$ and $G \setminus E_1 = G' \setminus E_2$. Similar to the proof of Lemma 3.3, G' admits an E_2 -antiparallel strong trace T'. An E_1 -antiparallel strong trace T of G can be obtained just like Case 1 in Lemma 3.1.



Figure 11. (1) The tetrahedron designed from a single polypeptide chain comprising 12 concatenated coiled coil-forming segments [15]. It has two independent antiparallel edges. Theory suggests that this is one of the three possible topologies with two others having three parallel and three antiparallel edges. (2) A strong trace of the cube such that only the edges in its perfect matching are traversed oppositely. It has four independent antiparallel edges.

4 Implications and discussions for the molecular design

Based on the mathematical model of polyhedral links, some topological operations have been introduced for the molecular design of DNA nanostructures [25,26]. Compared to the elaborate field of structural DNA nanotechnology, the field of designed modular polypeptide nanotechnology is at the very beginning. Herein, we suggest that almost parallel strong trace model may provide novel insight into the molecular design of polypeptide nanostructures.

A tetrahedron is of degree 3, removing a single edge leaves a non-even graph. By Corollary 3.1, there is no strong trace for the tetrahedron such that only one edge is traversed in the opposite direction for this trace. By Corollary 3.2, there is a strong trace for the tetrahedron such that exactly two edges are traversed in the opposite direction for this trace, and these two edges should be independent and can not be connected to be a path. This confirms that the largest number of parallel edges in the previous experimentally realized single-chain polypetptide tetrahedron is 4. See Figure 11(1).

According to Corollaries 3.1 and 3.2, it is easy to determine where a graph admits a strong trace with only 1 or 2 antiparallel edges. Theorems 3.1, 3.2 and 3.3 could be used to design almost parallel strong trace. There is no strong trace for regular polyhedron



Figure 12. (1) For a 3-cycle of the octahedron, we can realize a strong trace such that only the edges of the cycle are traversed oppositely. (2) For a 4-cycle of the octahedron, we can realize a strong trace such that only the edges of the cycle are traversed oppositely.

such that only edges on a path are traversed oppositely. A *perfect matching* of a graph is a set of independent edges covering every vertex of the graph. For a regular polyhedron of degree 3, we can realize a strong trace with only edges in its perfect matching traversed oppositely. Figure 11(2) illustrates a strong trace of the cube such that only the edges in its perfect matching are traversed in the opposite direction. An octahedron is a regular polyhedron of degree 4, for a given cycle of this polyhedron with length 3, 4, 5, or 6, we can realize a strong trace with only edges on the cycle traversed oppositely, see Figure 12 and Figure 13.



Figure 13. (1) For a 5-cycle of the octahedron, we can realize a strong trace such that only the edges of the cycle are traversed oppositely. (2) For a 6-cycle of the octahedron, we can realize a strong trace such that only the edges of the cycle are traversed oppositely.

It is easier for the self-assembling of polypeptide nanostructures with largest number of parallel edges, because there is a larger number of known orthogonal parallel coiled-coil dimers than antiparallel dimers as the building blocks. We leave the following mathematical question for further study.

Question 4.1 Given a graph, determine the minimum number of edges such that there is a strong trace with only these edges traversed oppositely.

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References

- H. Gradišar, R. Jerala, Self-assembled bionanostructures: proteins following the lead of DNA nanostructures, J. Nanobiotech. 12 (2014) #4.
- [2] M. R. Jones, M. C. Seeman, C. A. Mirkin, Nanomaterials, programmable materials and the nature of the DNA bond, *Science* 347 (2015) #1260901.
- [3] J. H. Chen, N. C. Seeman, Synthesis from DNA of a molecule with the connectivity of a cube, *Nature* **350** (1991) 631–633.
- [4] R. Iinuma, Y. Ke, R. Jungmann, T. Schlichthaerle, J. B. Woehrstein, P. Yin, Polyhedra self-assembled from DNA tripods and characterized with 3D DNA-PAINT, *Science* 344 (6179) (2014) 65–69.
- [5] Y. T. Lai, D. Cascio, T. O. Yeates, Structure of a 16-nm cage Designed by using protein oligomers, *Science* **336** (2012) 1129–1129.
- [6] N. P. King, W. Sheffler, M. R. Sawaya, B. S. Vollmar, J. P. Sumida, I. Andre, T. Gonen, T. O. Yeates, D. Baker, Computational design of self-assembling protein nanomaterials with atomic level accuracy, *Science* **336** (2012) 1171–1174.
- [7] G. Hu, X. D. Zhai, D. Lu, W. Y. Qiu, The architecture of Platonic polyhedral links, J. Math. Chem. 46 (2009) 592–603.
- [8] G. Hu, W. Y. Qiu, A. Ceulemans, A new Euler's formula for DNA polyhedra, PLoS One 6 (2011) #e26308.
- X. Jin, F. Zhang, The architecture and the Jones polynomial of polyhedral links, J. Math. Chem. 49 (2011) 2063–2088.
- [10] X. Cheng, X. Jin, The braid index of complicated DNA polyhedral links, *PLoS One* 7 (11) (2012) #e48968.

- [11] M. Li, Q. Deng, X. Jin, A general method for computing the Homfly polynomial of DNA double crossover 3-regular links, *PLoS One* **10** (2015) #e0125184.
- [12] A. Ljubetič, I. Drobnak, H. Gradišar, R. Jerala, Designing the structure and folding pathway of modular topological bionanostructures, *Chem. Commun.* 52 (2016) 5220– 5229.
- [13] V. Kočar, J. S. Schreck, S. Čeru, H. Gradišar, N. Bašić, T. Pisanski, J. P. Doye, R. Jerala, Design principles for rapid folding of knotted DNA nanostructures, *Nat. Commun.* 7 (2016) #10803.
- [14] J. Zhang, F. Zheng, G. Grigoryan, Design and designability of protein-based assemblies, Curr. Opin Struct. Biol. 27 (2014) 79–86.
- [15] H. Gradišar, S. Božič, T. Doles, D. Vengust, I. Hafner-Bratkovič, A. Mertelj, B. Webb, A. Šali, S. Klavžar, R. Jerala, Design of a single–chain polypeptide tetrahedron assembled from coiled–coil segments, *Nat. Chem. Biol.* **9** (2013) 362–366.
- [16] V. Kočar, S. A. Božič, T. Doles, N. Bašić, H. Gradišar, T. Pisanski, R. Jerala, TOPOFOLD, the designed modular biomolecular folds: polypeptide-based molecular origami nanostructures following the footsteps of DNA, WIREs Nanomed. Nanobiotech. 7 (2015) 218–237.
- [17] S. Klavžar, J. Rus, Stable traces as a model for self-assembly of polypeptide nanoscale polyhedrons, MATCH Commun. Math. Comput. Chem. 70 (2013) 317–330.
- [18] J. Rus, Parallelism of stable traces, preprint.
- [19] G. Fijavž, T. Pisanski, J. Rus, Strong traces model of self-assembly of polypeptide structures, MATCH Commun. Math. Comput. Chem. 71 (2014) 199–212.
- [20] H. Gradišar, R. Jerala, De novo design of orthogonal peptide pairs forming parallel coiled-coil heterodimers, J. Pept. Sci. 17 (2011) 100–106.
- [21] H. Fleischner, Eulerian Graphs and Related Topics, Elsevier, Amsterdam, 1991.
- [22] J. A. Bondy, U. S. R. Murty, Graph Theory, Springer, New York, 2008.
- [23] G. Sabidussi, Tracing graphs without backtracking, Operations Research Verfahren XXV, Symp. Heidelberg, Teil 1 (1977) 314–332.
- [24] R. B. Eggleton, D. K. Skilton, Double tracings of graphs, Ars Comb. 17 (1984) 307–323.
- [25] J. W. Duan, W. Li, X. W. Li, G. Hu, W. Y. Qiu, Molecular design of DNA polyhedra based on genus, J. Math. Chem. 52 (2014) 2380–2394.
- [26] G. Hu, Z. Wang, W. Y. Qiu, Topological analysis of enzymatic actions on DNA polyhedral links, *Bull Math Biol.* 73 (2011) 3030–3046.