Reconfiguration of Plane Trees in Convex Geometric Graphs

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Abstract

A non-crossing spanning tree of a set of points in the plane is a spanning tree whose edges pairwise do not cross. Avis and Fukuda in 1996 proved that there always exists a flip sequence of length at most $2n-4$ between any pair of non-crossing spanning trees (where n denotes the number of points). Hernando et al. proved that the length of a minimal flip sequence can be of length at least $\frac{3}{2}n$. Two recent results of Aichholzer et al. and Bousquet et al. improved the Avis and Fukuda upper bound by proving that there always exists a flip sequence of length respectively at most $2n - \log n$ and $2n - \sqrt{n}$ when the points are in convex position.

We pursue the investigation of the convex case by improving the upper bound by a linear factor for the first time in 30 years. We prove that there always exists a flip sequence between any pair of non-crossing spanning trees T_1, T_2 of length at most cn where $c \approx 1.95$. Our result is actually stronger since we prove that, for any two trees T_1, T_2, there exists a flip sequence from T_1 to T_2 of length at most $c|T_1 \setminus T_2|$.

We also improve the best lower bound in terms of the symmetric difference by proving that there exists a pair of trees T_1, T_2 such that a minimal flip sequence has length $\frac{5}{3}|T_1 \setminus T_2|$, improving the lower bound of Hernando et al. by considering the symmetric difference instead of the number of vertices.

We generalize this lower bound construction to non-crossing flips (where we close the gap between upper and lower bounds) and rotations.

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1 Introduction

Let C be a set of n points in the plane in convex position. A *spanning tree* T on the set of points C is a subset of edges that forms a connected acyclic graph on C. A spanning tree T on C is *non-crossing* if every pair of edges of T (represented by the straight line interval between their endpoints) are pairwise non-crossing.

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Let us denote by $\mathcal{S}(C)$ the set of all non-crossing spanning trees on the point set C. Let $T \in \mathcal{S}(C)$. A *flip* on T consists of removing an edge e from T and adding another edge f so that the resulting graph $(T \cup f) \setminus e$ is also a non-crossing spanning tree. A *flip sequence* is a sequence of non-crossing spanning trees such that consecutive spanning trees in the sequence differ by exactly one flip. Equivalently, one can define the *configuration graph* on the vertex set $\mathcal{S}(C)$ where two trees T, T' are adjacent if they differ in exactly one edge (that is $|T \setminus T'| = |T' \setminus T| = 1$). A (minimal) flip sequence is a (shortest) path in the configuration graph.

1.1 Flips between non-crossing spanning trees

Avis and Fukuda [4] proved that there always exists a flip sequence between any pair of non-crossing spanning trees of length at most $2n-4$ by showing that there is a *star* (that is a spanning tree with at most one vertex of degree at least 2) S on C such that T_1 and T_2 can be turned into S with at most $n-2$ flips. In fact, they showed that this flip sequence exists even if the point set C is in general position.

Given two spanning trees T_1, T_2, the *symmetric difference* between T_1 and T_2 is denoted by $\Delta(T_1, T_2) = (T_1 \setminus T_2) \cup (T_2 \setminus T_1)$. We denote by $\delta(T_1, T_2) = |\Delta(T_1, T_2)|/2$ the number of edges in T_1 and not in T_2, which is a trivial lower bound on the length of a flip sequence from T_1 to T_2.

It is well-known that the set of spanning trees of a graph G forms a matroid. In particular, for any possible pair of spanning trees T_1, T_2, there is a (non geometric) flip sequence that transforms T_1 into T_2 in exactly $\delta(T_1, T_2)$ flips. So if we do not care about geometric properties of the representation of the spanning trees, it is always possible to transform a spanning tree T_1 into T_2 using at most $n-1$ flips. One can wonder if the same holds if we want to keep non-crossing spanning trees all along the flip sequence. Hernando et al. [9] answered this question in the negative by providing, for every n, two non-crossing spanning trees T_1, T_2 on a convex set of n points whose minimal flip sequence needs $\frac{3}{2}n - 5$ flips (we give their example in Figure 1).

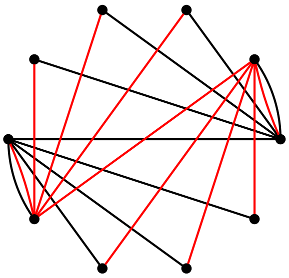

Figure 1 A minimal flip sequence between T_1 (in black) and T_2 (in red) has length exactly $\lfloor \frac{3}{2}n \rfloor - 5 = 10$.

During 30 years, no improvement of the lower or upper bound has been obtained until a recent result of Aichholzer et al. [2]. They showed that the upper bound of Avis and Fukuda can be improved when points are in convex position by proving that there exists a flip sequence between any pair of non-crossing spanning trees of length at most $2n - \Omega(\log n)$. Their result has been further improved by Bousquet et al. [5] who proved that $2n - \Omega(\sqrt{n})$ flips are enough. However, until now, there does not exist any general proof that there always exists a flip sequence of length at most $(2-\epsilon)n$ for some $\epsilon > 0$.

In both papers, the authors prove as well the existence of shorter flip sequences when one (or both) of the trees has a special shape. Aichholzer et al. [2] proved that when the points are in convex position and T_1 is a path then there exists a flip sequence of length at most $\frac{3}{2}n - 2 - |T_1 \cap T_2| = \frac{n+|\Delta(T_1,T_2)|}{2} - 1$. Bousquet et al. [5] proved that there exists a flip sequence of length at most $\frac{3}{2}n$ when the points are in convex position and T_1 is a path or a nice caterpillar[1].

Bousquet et al. [5] conjectured that the lower bound of Hernando et al. [9] is essentially tight:

▶ **Conjecture 1.** *Let C be a set of n points in convex position. There exists a flip sequence between any pair of non-crossing spanning trees of length at most $\frac{3}{2}n$.*

One can easily prove that there exists a flip sequence of length at most $2\delta(T_1, T_2)$ between any pair of non-crossing spanning trees in convex position. The improvement of Aichholzer et al. [2] also holds in that setting. Since in the example of Hernando et al. the intersection is reduced to two edges, one can wonder if Conjecture 1 can be extended to the symmetric difference, namely:

▶ **Conjecture 2.** *Let C be a set of n points in convex position. There exists a flip sequence between any pair of non-crossing spanning trees T_1, T_2 of length at most $\frac{3}{2}\delta(T_1, T_2)$.*

Our main results, discussed in more details in the next paragraphs, first consist in (i) improving the best known upper bound by breaking the linear factor 2 of the threshold on the length of a minimal flip sequence (even in terms of the symmetric difference) and (ii) disproving Conjecture 2 by proving that the best upper bound factor we can hope for is $\frac{5}{3}$. We complete these results by providing improved upper and lower bounds on the length of transformations in the non-crossing and rotation models defined later. In particular, we close the gap between upper and lower bounds in the case of non-crossing flips.

Improved upper bound. The first main result of this paper is to improve the best upper bound of [5] by a linear factor by proving that the following holds:

▶ **Theorem 3.** *Let C be a set of n points in convex position. There exists a flip sequence between any pair of non-crossing spanning trees T_1 and T_2 of length at most $c \cdot \delta(T_1, T_2)$ with $c = \frac{1}{12}(22 + \sqrt{2}) \approx 1.95$.*
In particular, there exists a flip sequence of length at most $cn \approx 1.95n$ between any pair of non-crossing spanning trees.

One can note that our result is expressed in terms of the symmetric difference, which is also the case for the upper bound of [2]. Note that some of the partial results obtained in [2] depend on both n and Δ.

Our proof technique is completely different from the previous approach of [5] whose goal is to transform at least one spanning tree into a very rigid structure that does not really take into account the specific structure of both trees. On the contrary, our approach depends on the local structure of both trees. This idea stems from [2] and works along the following lines: if two non-crossing trees T, T' contain a common chord, we divide our problem into two sub-problems: the “left” and the “right” problem where the common chord becomes an

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[1] A *caterpillar* is a tree such that the set of nodes that are not leaves induces a path. Without giving the exact definition, a nice caterpillar is a caterpillar such that every chord cuts in a nice way the geometric representation.

edge of the convex hull in both cases. In particular, if we can create a common chord with few modifications, we can apply induction. This approach is safe since our upper bound depends on the size of the symmetric difference and not on n. Unfortunately, this cannot work in general since we may have to modify a lot of edges until we can create a common edge (see e.g. the example of Figure 1). We prove that we can find a chord e in T and one side of that chord (say "left") such that T' has not too many endpoints in that side. The difference with the argument above is that the "not too many" here is not a universal constant but depends on the size of the side. We then prove that, by only modifying a small linear fraction of these edges, we can transform "left" into what we call a very good side. Informally speaking, "left" is a very good side if (i) no edge of T' has both endpoints in "left" (in other words, all the edges with one endpoint in left have the other endpoint in the right part) and, (ii) the number of such edges in T' is equal to the size of "left". We then prove that, in that case, we can perform flips in order to be sure that both trees agree on the left of e in at most $\frac{5}{3}$ times the number of vertices[2] to the left of e.

Our proof is self-contained and is algorithmic. So a flip sequence of length at most cn can be obtained in polynomial time. Moreover, it is robust since it can be adapted to improve the best upper bounds for rotations for instance. Note that we did not try to optimize the constant c to keep the proof as simple as possible.

Lower bound in terms of the symmetric difference. Our second set of results consists in proving stronger lower bounds in terms of the symmetric difference. In particular, we disprove Conjecture 2:

▶ **Theorem 4.** *For every $k > 0$, there exist two trees T_k and T'_k such that $\delta(T_k, T'_k) = 3k$ and every flip sequence between T_k and T'_k has length at least $5k = \frac{5}{3}\delta(T_k, T'_k)$.*

The proof of Theorem 4 consists in first proving the case $k = 1$ by providing two spanning trees T_1, T'_1 on 8 vertices for which $\delta(T_1, T'_1) = 3$ and such that the minimal flip sequence between T_1 and T'_1 needs 5 flips (see Figure 13). One of the reasons of the hardness comes from the fact that, for every common edge e of the convex hull, the endpoint of e that is used to connect this edge to the rest of the tree is different in both trees. This allows us to increase the number of crossings between the trees, and then the length of the flip sequence. Note that our example is not a counterexample to Conjecture 1 since the pair of trees contains a lot of common edges.

We then prove that if we glue many instances of (T_1, T'_1) appropriately, we can obtain a similar example with arbitrarily large value of k. The idea is as follows. If we assume that there always exists a minimal flip sequence that does not break common edges, the conclusion immediately follows. Unfortunately, this statement, known as the Happy Edge conjecture [2], is only known to be true for common edges of the convex hull but not for chords. So we have to prove that it is never worthwhile to break a common edge which we succeed to do in this particular case (in other words, the Happy Edge Conjecture holds in this case).

We have not found any example for trees T_1, T_2 for which a flip sequence of length more than $\frac{5}{3}\delta(T_1, T_2)$ is necessary. We therefore leave the following as an open problem:

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[2] Actually, the size of a side will be defined as the number of non-edges of the convex hull and not simply of vertices in the side which explains why we obtain a bound in terms of the symmetric difference.

▶ **Question 5.** Let C be a set of points in convex position and T_1, T_2 two non-crossing spanning trees on C. Does there always exist a flip sequence between T_1 and T_2 of length at most $\frac{5}{3}\delta(T_1, T_2)$?

Improved lower bounds for the other models. Several other types of flips have been introduced in the literature (see e.g. [14] for an overview of the results in the different models). We proved that we can strengthen the best lower bounds in terms of the symmetric difference for two other types of flips: non-crossing flips and rotations.

Let T be a spanning tree, e be an edge of T and f be an edge such that $(T \cup f) \setminus e$ is non-crossing. We say that the flip is *non-crossing* if $T \cup f$ does not contain any crossings. In other words, we restrict to flips where the new edge does not cross the edge that is deleted. We say that the flip is a *rotation* if e and f share an endpoint. In other words, every flip must rotate an edge around a point in that case.

Upper and lower bounds in terms of n for the longest minimal transformation have already been studied (see [14]). Note that the best known lower bounds for all the models are the same and are given by the construction of Hernando et al. which gives a lower bound (in terms of n) of size $\frac{3}{2}n$. We improved the lower bounds in terms of the symmetric difference for both non-crossing flips and rotations.

For non-crossing flips, one can easily remark that, by flipping edges on the convex hull, we can always find a non-crossing flip sequence between any pair of trees of length at most $2\delta(T_1, T_2)$ (see Lemma 10 for a formal proof). We prove that this bound is tight by giving a pair of trees that reach this bound, which completely closes the gap between lower and upper bounds for non-crossing spanning trees in terms of symmetric difference. Namely we prove that the following holds:

▶ **Theorem 6.** *For every $k > 0$, there exist two trees T_k and T'_k such that $\delta(T_k, T'_k) = k$ and every flip sequence between T_k and T'_k has length at least $2k = 2\delta(T_k, T'_k)$.*

We finally consider the rotation model. One can easily remark that there is always a rotation sequence between T_1 and T_2 of length at most $4\delta(T_1, T_2)$ by flipping edges on the convex hull. Actually one can prove that this 4 can be improved into a 3 with a simple clever analysis.

Our last result consists in improving the best lower bound for rotation by showing that the following holds:

▶ **Theorem 7.** *For every $k > 0$, there exist two trees T_k and T'_k such that $\delta(T_k, T'_k) = 3k$ and every rotation sequence between T_k and T'_k has length at least $7k = \frac{7}{3}\delta(T_k, T'_k)$.*

While the family of trees reaching that bound is similar to the family constructed for flips, the analysis that this family works is much more involved. We end this part with a last open problem:

▶ **Question 8.** Let C be a set of points in convex position and T_1, T_2 two non-crossing spanning trees on C. Does there always exist a rotation sequence from T_1 to T_2 of length at most $\frac{7}{3}\delta(T_1, T_2)$?

1.2 Related work

Flip distance between geometric structures. Flips between combinatorial structures have been widely studied in computational geometry and combinatorics. One of the most studied problem, known as the Flip Distance problem, aims at computing the minimum number of flips needed to transform one triangulation into another (a flip in that case consists in replacing one diagonal of a quadrilateral into the other). The problem has been proven to be NP-complete when considering n points in non-convex position [16, 13], and in that case, the flip graph of triangulations of a point set may have diameter $\Theta(n^2)$ [11]. When the n points are in convex position, the maximum flip distance between triangulations is linear and equal to $2n-10$ when $n \geq 9$. A first proof for n large was found using hyperbolic geometry [18], while a combinatorial proof for all $n \geq 9$ was only given decades later [17]. However, the complexity of the FLIP DISTANCE problem is, as far as we know, still an open problem in that case.

Flip graphs and their diameter for other geometric objects have been studied, such as non-crossing perfect matchings or rectangulations. For both of these objects there are several natural notions of flips, yielding various flip graphs. A natural way of defining a flip for perfect matchings is by allowing two edges to be removed and two other edges to be added such that the resulting matching is still non-crossing. When the n points are in convex position and n is even, Hernando, Hurtado and Noy [8] showed that the flip graph of non-crossing perfect matchings has diameter $\frac{n}{2}-1$. Houle et al. [10] gave a result on general point sets when using the notion of flip where M_1 is connected to M_2 in the flip graph where the symmetric difference of M_1 and M_2 contains a single non-crossing cycle. They showed that there is a transformation of linear length between any pair of non-crossing matchings, whereas Aichholzer et al. [3] showed that, if multiple non-crossing cycles are allowed in a flip, then any minimal transformation has length at most $O(\log n)$.

Ackerman et al. [1] considered flips of rectangulations with two elementary flip operations, where one flip changes a horizontal line to a vertical line and vice versa and the other flip is a rotation around a point (by splitting the line segment into two parts). They showed that the maximum flip sequence over all n points is of the order $\Theta(n \log n)$. A natural point set for rectangulations to consider is a diagonal point set, for which Ackerman et al. showed that the flip graph has diameter at most $11n$.

Combinatorial Reconfiguration. In the last decade, an important line of work has consisted in finding transformations between solutions of a problem such as graph colorings or independent sets (see e.g. [15] for a recent survey). Amongst all these works, some of them studied transformations between restricted spanning trees. While we focus in this work on a restriction to the geometric representation of the spanning trees (non-crossing), these works focus on combinatorial properties of the spanning trees such as their maximum degree [7] or their number of leaves [6]. In these cases, the existence of a transformation is not guaranteed and the goal is to design efficient algorithms determining, given a pair of spanning trees, whether one can transform one into the other. These works focus on the token jumping model which essentially corresponds to flips and very little is known on the token sliding model (which is an analogue of rotations).

As a final remark, spanning trees are, as we already mentioned, a particular case of matroids (called graphic matroids). Other reconfiguration results related to generalizations of matroids have also been studied in the literature, see e.g. [12].

Organization of the paper. After giving some definitions and simple observations in Section 2, we prove Theorem 3 in Section 3. In Section 4 we prove Theorems 4, 6 and 7. Due to space constraints, we only sketch the main ideas of each proof. The full versions can be found on arXiv.

2 Basic definitions and observations

Let C be a set of points in convex position and T be a non-crossing spanning tree on C. We say two points of a convex set C are *consecutive* if they appear consecutively on the convex hull of C. We say we *perform* $e \rightsquigarrow e'$ *in* T if we perform the flip consisting in removing e and adding e' in T.

Let $A \subseteq C$. We denote by $T[A]$ the induced subgraph of T on A, that is the subforest of T with vertex set A where uv is an edge if and only if uv is an edge of T. Note that $T[A]$ is a non-crossing forest. A *border edge* (for T) is an edge between consecutive points. An edge of T which is not a border edge is called a *chord*. A *hole* of T is a pair of consecutive points that is not a border edge. We will say that we *fill a hole* when we apply a flip where the created edge joins the pair of points of the hole.

One can remark that, for each chord e of T, the line containing e splits the convex hull of C in two non-trivial parts. A *side of a chord* e is the subset of points of C contained in one of the two closed half-planes defined by the line containing the two endpoints of e (see Figure 2 for an illustration). A *side of* T is a side of a chord e for some $e \in T$. We say an edge (or a hole) is *in a side* A if both its endpoints are in A.

In the following, for every side A of a chord, we will denote by k_A the number of holes in A, which is also the number of chords of T in A. Since T is acyclic, we also have $k_A > 0$. Note that each chord e of T defines two sides A and B whose intersection is exactly the endpoints of e. Moreover, T has exactly $k_A + k_B$ holes.

Let e be a chord of T and A be a side of e. For every chord e' in A, the side of e' (w.r.t. A) is the side of e' that is contained in A. Note that for every pair of chords e_1, e_2 in A, the sides of e_1 and e_2 (w.r.t. A) are either disjoint or contained in each other. The chord e_1 is *inclusion-wise minimal* if no side of a chord e' in A is included in the side of e_1 w.r.t. A. By connectivity, we can easily note the following.

▶ Remark 9. Let e be a chord of T and A be a side of e. Let A' be the side of an inclusion-wise minimal chord e' in A. Then $k_{A'} = 1$.

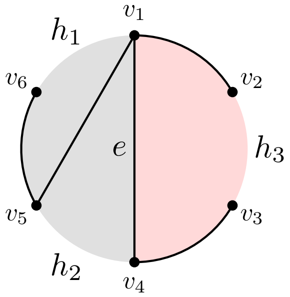

Figure 2 The side A (in grey) of the chord e is is the subset of vertex $\{v_1, v_4, v_5, v_6\}$ and the other side B (in red) of e is $\{v_1, v_4, v_2, v_3\}$. The edges of T in A are the edges v_5v_6, v_1v_5 and v_1v_4. The holes h_1 and h_2 of T are in A and h_3 is in B. So we have $k_A = 2$ and $k_B = 1$.

Let A be a side of a chord e of T. We define the *degree* of a side A in a tree T' as the number of chords of T' crossing e plus twice the number of chords of T' with both endpoints in A (see Figure 3 for an illustration). Note that, if T' has no chords with both endpoints in A, then the degree of A in T' is equal to the number of chords of T' crossing e.

The following lemma appeared in [5].

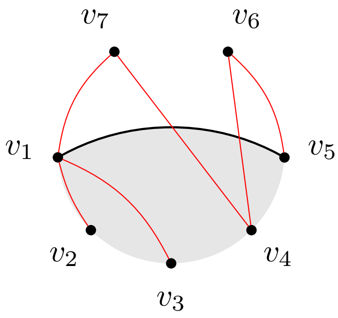

Figure 3 The side A of the edge v_1v_5 highlighted in grey contains v_1, v_2, v_3, v_4 and v_5. The degree of A in the red tree is equal to 4 : v_4v_6 and v_4v_7 cross v_1v_5, and v_1v_3 has both endpoints in A. Note that v_1v_2 is not a chord, thus it does not increase the degree of A in T'.

▶ **Lemma 10.** *Let T be a tree and e be a border edge not in T. Then there exists a non-crossing flip that adds e in T without removing any border edge of T (except if T only contains border edges).*

3 Upper bounds

This section aims at proving Theorem 3 by induction. Let T_I, T_F be two trees on a convex point set C, and assume that Theorem 3 holds for every pair of trees T'_I and T'_F, which are either defined on the same set of points and $\delta(T'_I, T'_F) < \delta(T_I, T_F)$ or on a smaller set of points.

Before giving all the details of the proof, let us first explain the main steps of the proof (see Figure 4 for an illustration). First, we prove in Section 3.1 that we may assume that T_I and T_F have the same border edges and no common chord. In Section 3.2 we define a τ-extremal side, which is a side which always exists in a nice pair of trees (and hence which we can also find in T_I and T_F). We give tools in Section 3.3 to transform a τ-extremal side to what we call a very good side without using too many flips. In Section 3.4, we will observe that in very good sides, we can match the k_A chords in the side using at most $\frac{5}{3}k_A$ flips in total.

3.1 Basic properties of T_I, T_F

Cutting the pair T_I, T_F along a common chord gives two smaller pairs of trees. We may then reconfigure T_I into T_F applying a minimal flip sequence on each smaller pair separately. This yields the following.

▶ **Lemma 11.** *If T_I and T_F share a common chord, there exists a flip sequence from T_I to T_F of length at most $c \cdot \delta(T_I, T_F)$.*

Observe that every border edge appearing only in one of T_I, T_F can be added to the other tree using only one flip. Therefore, we get:

▶ **Lemma 12.** *If there is a border edge in the symmetric difference of T_I and T_F, there exists a flip sequence from T_I to T_F of length at most $c \cdot \delta(T_I, T_F)$.*

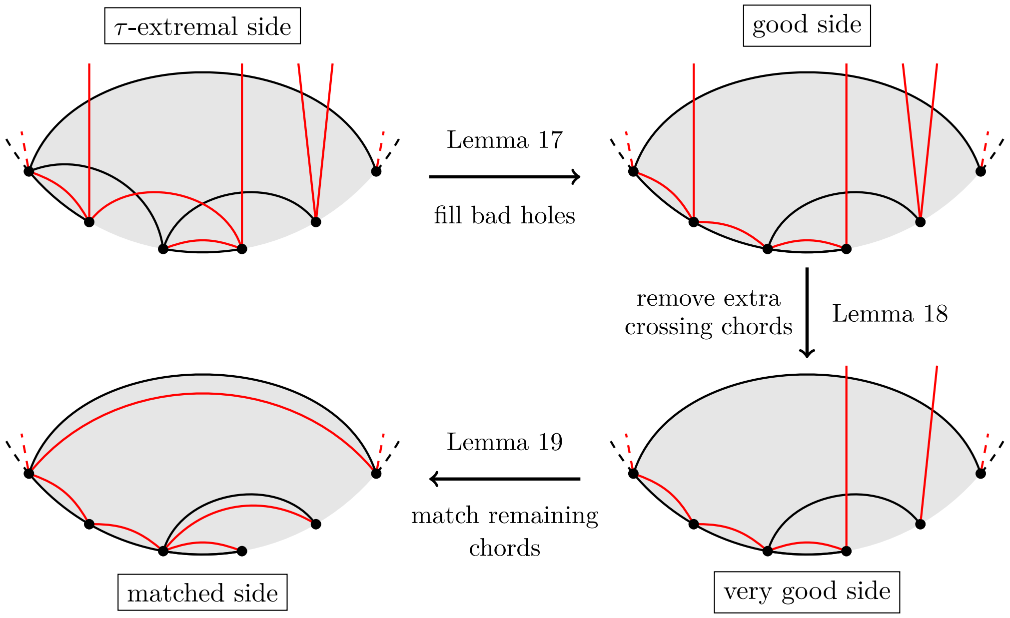

Figure 4 The main steps in the proof of Theorem 3. The goal is to match the chords in a side using few steps. (We define τ-extremal, bad, good and very good later).

We say that two trees T and T' form a *nice pair* of trees if the two trees have no common chord and have the same border edges. Note that for a nice pair of trees, every pair of consecutive points is either a common hole or a common border edge. Thus, for a nice pair of trees (T, T'), we will refer to a hole of T or T' simply as a hole. Lemmas 11 and 12 ensure that the following holds:

▶ **Corollary 13.** *If T_I and T_F is not a nice pair of trees, there exists a flip sequence from T_I to T_F of length at most $c \cdot \delta(T_I, T_F)$.*

Using this result, we may now assume for the rest of the proof that (T_I, T_F) form a nice pair of trees.

3.2 τ-extremal sides

The goal of this section is to define and state the existence of the so-called τ-*extremal* sides that are the starting point of the transformation sketched above.

Let T, T' be a nice pair of trees and $\tau > 2$. We say a side A of a chord e of T is τ-*extremal* for a tree T' if the degree of A in T' is at most $\tau \cdot k_A$, and, for every side $A' \subsetneq A$ of T', the degree of A' in T is more than $\tau \cdot k_{A'}$. We first prove that such a side exists in T_I or T_F. To this end, we start from an arbitrary side and use an iterative greedy argument until we get a τ-extremal side.

▶ **Lemma 14.** *Let T_1 and T_2 be a nice pair of trees that are not border paths and $\tau > 2$, then either T_1 or T_2 contains a τ-extremal side.*

Our process starts from a τ-extremal side and refines it until we can show it can be matched using few flips. This refinement starts by removing *bad holes*. A hole h in a side A of T w.r.t. T' is *bad* if it is also in a side $B \subsetneq A$ of T', see Figure 5. For our process to yield the desired number of flips, we need to show that the refinement process is not too expensive, and in particular that a τ-extremal side has not too many bad holes. This is summarized in the following lemma, whose proof relies on double counting the degrees of sides included in a τ-extremal side. Containing too many bad holes would violate the τ-extremality.

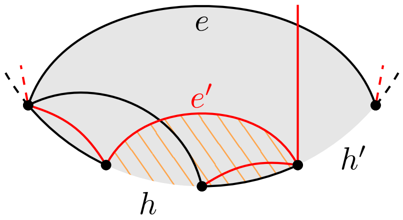

Figure 5 Let T_1 be the black tree and T_2 the red tree. The hole h is a bad hole of the side A (in grey) w.r.t T_2 since it is inside the side of e' included in A.

▶ **Lemma 15.** *Let T_1 and T_2 be a nice pair of trees, and A be a τ-extremal side of a chord e of T with $\tau > 2$. Then the side A contains at most $\frac{2}{\tau}k_A$ bad holes w.r.t. T_2.*

3.3 Refining a τ-extremal side

By Lemma 14, a τ-extremal side S exists in T_I or T_F, say T_I by symmetry. Moreover, informally speaking, it does not have too large degree (by definition) and does not contain too many bad holes by Lemma 15.

Let T and T' be a nice pair of trees. We say that a side of T is good w.r.t. T' when it contains no bad hole, or equivalently no chord in T'. Our goal in this section is first to make S good w.r.t. T_F by removing its bad holes, and then by reducing its degree. The former step relies on the following observation.

A *face* f of a tree T is a face, different from the outer face, of the plane graph obtained by filling the holes of T with edges. Note that, since T is connected, every face contains exactly one hole on its boundary and every hole is on the boundary of exactly one face. Thus, there is a bijection between holes and faces of a tree. The face *containing* a hole h of a tree T is the face f such that h belongs to the boundary of f. We say that the hole h is *contained in* the face f in T.

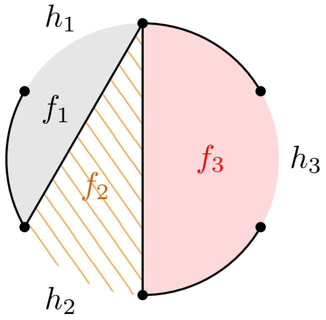

Figure 6 The tree T has three faces f_1, f_2 and f_3. The face f_i contains the hole h_i in T.

▶ **Observation 16.** *For every hole h, we can fill h in T by flipping any chord on the boundary of the face of T containing h.*

Lemma 17 explains how we can fill one bad hole in S, and our goal is to apply it several times to obtain a good side.

▶ **Lemma 17.** *Let T_1, T_2 be a nice pair of trees, A be a side of a chord e of T_1 that contains at least two holes including at least one bad hole h w.r.t T_2. Then, we can fill h in T_1 by flipping a chord different from e and we can fill h in T_2 by flipping a chord with both endpoints in A, see Figure 7.*

Moreover, the resulting pair of trees after these two flips is still nice, and A has one less bad hole.

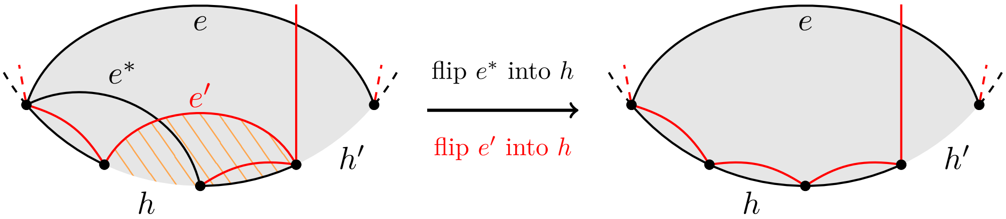

Figure 7 An example of a side A (in grey) of the chord e in the tree T_1 (in black) contains two holes h and h', with h a bad hole of A w.r.t the tree T_2 (in red) because of the chord e'. We fill h in both trees by flipping e' in T_2, and by finding a chord $e^* \neq e$ in T_1.

By Lemma 15, S contains at most $\frac{2k_S}{\tau} < k_S$ bad holes, hence it contains a good hole. Therefore, each time we update T_I, T_F applying Lemma 17 on S, the good holes in S are not filled, which ensures we can repeatedly apply the lemma until no bad hole remains. Let T'_I, T'_F be the resulting trees after this process. Observe that we filled $m \leq \frac{2k_S}{\tau}$ bad holes w.r.t. T_F in $2m$ flips, and S is now a good side of T'_I w.r.t. T'_F of size $k'_S = k_S - m$.

Our goal is now to reduce the degree of S in order to transform S into a very good side. Given a pair of trees (T, T'), a good side A of T is *very good* (w.r.t. T') if the degree of A in T' is at most k_A, see Figure 8. Note that, for a good side A of an edge e of T, the degree of A in T' is equal to the number of chords of T' crossing e.

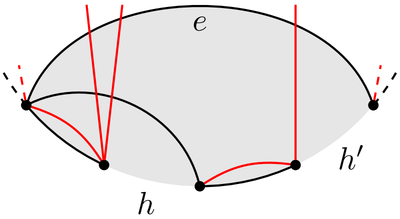

Figure 8 Let T_1 be the black tree and T_2 the red tree. The side A (in grey) of e is a good side of T_1 w.r.t. T_2 since there is no chord of T_2 inside A, but A is not very good w.r.t T_2 since the degree of A in T_2 is $3 > k_A = 2$.

For now, if S is not very good, then there are too many chords of T'_F crossing the unique chord e on the boundary of S. The goal of Lemma 18 is to remove these extra crossings. To make S very good, we will apply it iteratively until we reach the right amount of chords.

▶ **Lemma 18.** *Let T_1, T_2 be a nice pair of trees, A be a good side of a chord e of T_1 w.r.t T_2 which is not very good w.r.t. T_2. Then there exists a hole h not in A such that: (i) we can fill h in T_1 by flipping a chord distinct from e and (ii) we can fill h in T_2 by flipping a chord crossing e, see Figure 9.*

Moreover, the resulting pair of trees after these two flips is still nice.

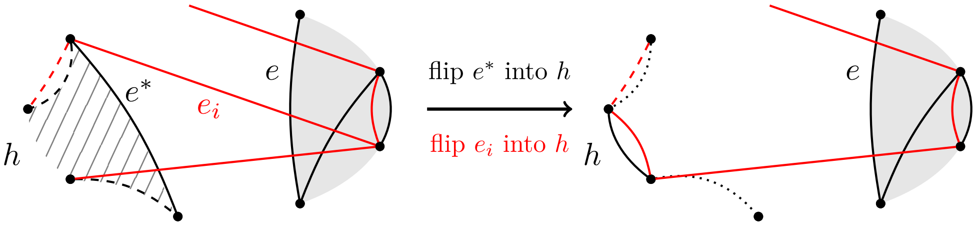

Figure 9 An example of a nice pair T_1 (in black) and T_2 (in red) with the side A of e (in grey) being good w.r.t T_2. We can fill h in T_1 by flipping a chord $e^* \neq e$ on the face (hatched in grey) of T_1 containing h, and in T_2 by flipping a chord e_i which crosses e and on the face of T_2 containing h.

Let d_S be the degree of S in T_F. Since we filled m bad holes in S to obtain T'_F, the degree of S in T'_F is $d_S - 2m \leq \tau k_S - 2m$. Applying Lemma 18 until S gets degree k'_S transforms (T'_I, T'_F) into (T''_I, T''_F) using $2(d_S - 2m - k'_S) \leqslant 2(\tau - 1)k_S - 2m$ flips and we get that S is a very good side of T''_I w.r.t. T''_F of size $k''_S = k'_S$.

3.4 Very good sides

Using Lemma 17 and Lemma 18, we are able to ensure that S is a very good side. However, at each step, we use 2 flips and fill only one hole. We now show that we can compensate for this costly procedure using the fact that S is very good. More precisely, we show the following.

▶ **Lemma 19.** *Let T_1 and T_2 be a nice pair of trees, e be a chord of T_1, and A be a very good side of e (w.r.t. T_2). Then, we can match k_A pairs of chords of T_1 and T_2 using at most $\frac{5}{3}k_A$ flips in total.*

This result heavily relies on the structure of very good sides in a nice pair of trees. The full description can be found in the full version, but we summarize here their main properties (see Figure 10). The set of border edges in a very good side A of T_1 induces $k_A + 1$ paths (possibly reduced to a single point), two of which contain an endpoint of e. Each of the $k_A - 1$ remaining paths contains one endpoint of a chord of T_2 crossing e. Except these chords, there may be at most one *extra chord* e^* of T_2 crossing e. In particular, we use that a minimal side of T_1 contained in A has degree at most 3.

With this information, we may now sketch the proof of Lemma 19. The main idea consists in applying inductively the following result (proved in the full version) on a minimal side $A' \subseteq A$ of T_1, defined by a chord e'. Recall that A' has degree $d \leq 3$ in T_2:

▷ Claim 20. If $d > 0$ (resp. $d = 0$), in at most $\frac{5}{3}d$ (resp. 1) flips, we can obtain from T_1 and T_2 a nice pair of trees T'_1, T'_2 that agree on A' by filling $d - 1$ (resp. 0) holes of A in both T_1 and T_2 and creating the chord e' in T_2, see Figure 11. Moreover, if $k_A > d$, then we do not flip e and the number of edges in T'_2 crossing e decreases by d (resp. 1).

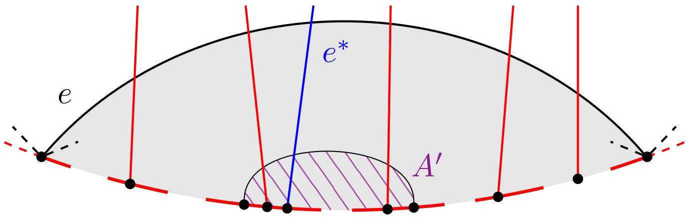

Figure 10 In a nice pair, the very good side A of T_1 (in black) w.rt. T_2 (in red), defined by a chord e, with a possible extra chord e^* (in blue). Then, a minimal side A' of T_1 (hatched) contained in A has degree at most 3. Note that border edges are common.

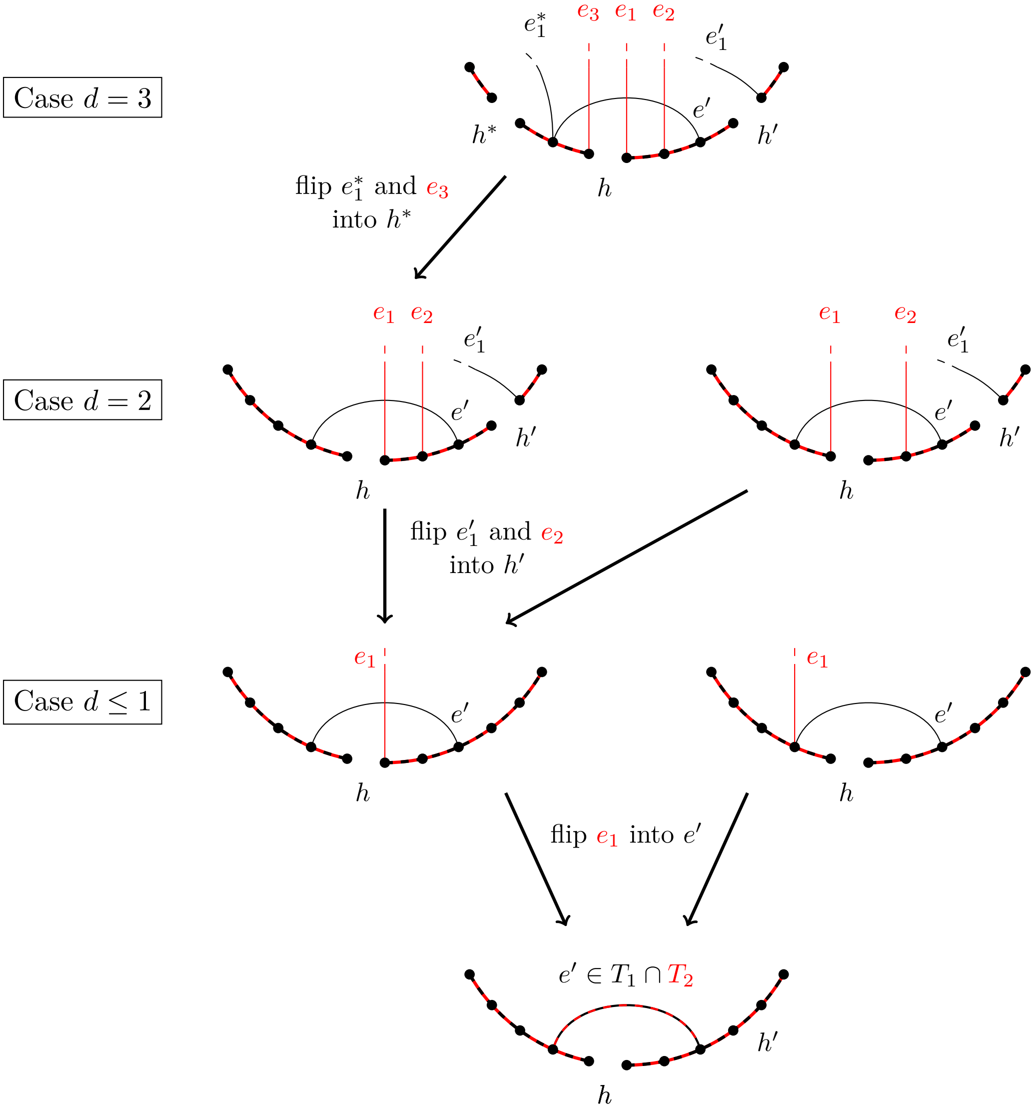

Figure 11 Illustration of Claim 20 on some examples T_1 (in black) and T_2 (in red). We consider several cases according to the degree d of A' w.r.t. T_2.

After applying Claim 20 on the minimal side A', we can forget the points and edges inside A' (where both resulting trees now agree). This makes e' a common border edge, and A remains a very good side with fewer holes, so the induction carries out and we obtain Lemma 19.

Since there is at most one extra chord in a very good side, observe that the case $d = 3$ in Claim 20 only happens once during the whole induction process. Hence, with a deeper analysis, the $\frac{5}{3}k_A$ bound of Lemma 19 can be improved to $\lceil \frac{3}{2}k_A \rceil$. However, there is an example of a small very good side A of T_1 w.r.t T_2, such that we cannot match the k_A chords in A of T_1 with chords of T_2 in less than $\frac{5}{3}k_A = \lceil \frac{3}{2}k_A \rceil$ flips, see Figure 12. This example was the base on which we built the lower bounds of Section 4.

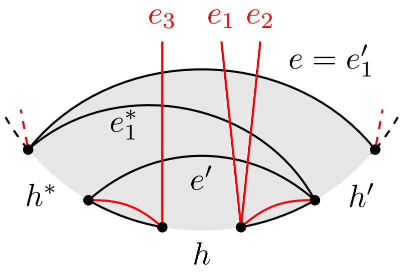

Figure 12 An example of a very good side A where $\frac{5}{3}k_A = 5$ flips are required to make the two trees agree on A.

3.5 Bounding the number of flips

Let (T^*_I, T^*_F) be the pair of trees obtained after applying Lemma 19 to S. We are now ready to conclude the proof of Theorem 3. Our transformation is as follows: first, we transform (T_I, T_F) into (T^*_I, T^*_F) by matching $m + (d_S - 2m - k'_S) + k''_S = d_S - m$ pairs using $2m + 2(d_S - 2m - k'_S) + \frac{5}{3}k''_S = 2d_S - k_S/3 - 5m/3$ flips. Then, we apply induction on (T^*_I, T^*_F) and get a transformation from T^*_I to T^*_F using at most $c\delta(T^*_I, T^*_F)$ flips.

In order to conclude the proof of Theorem 3, we need to make sure that we save enough using Lemma 19 to compensate for the expensive use of Lemmas 17 and 18. More precisely, we need that the total number of flips we used to get (T^*_I, T^*_F) is at most $c(d - m)$. Using that $d_S \leqslant \tau k_S$ (since S is τ-extremal) and that $m \leqslant \frac{2k_S}{\tau}$ by Lemma 15, this boils down to an inequality implying only c and τ, which is satisfied when plugging in the values $\tau = 2 + \sqrt{2}$ and $c = \frac{1}{12}(22 + \sqrt{2})$.

4 Lower bounds

This section aims at presenting several lower bounds. We provide three results, whose proofs share a similar structure and rely on counting arguments. We first present in Section 4.1 the family of pairs of trees providing the lower bound for flips from Theorem 4. We then briefly explain in Section 4.2 how to adapt the arguments to obtain lower bounds for the other types of flips considered in Theorems 6 and 7.

4.1 Flips and Theorem 4

Construction of the trees. Let us denote by T_1 and T'_1 the pair of non-crossing spanning trees on a convex set C of size 8 represented in Figure 13. Note that we have $\delta(T_1, T'_1) = 3$. For every k, we denote by T_k, T'_k the pair of non-crossing spanning trees obtained by taking

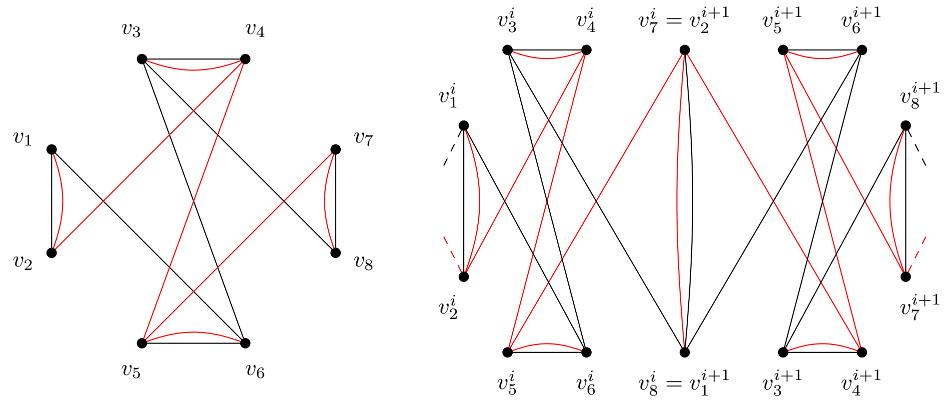

Figure 13 On the left, the tree T_1 in black and the tree T_1' in red. On the right, the subgraph induced by C_i and C_{i+1} in a pair T_k (in black) and T_k' (in red).

k disjoint copies of T_1, T_1' and identifying the points v_7 and v_8 of the i-th copy respectively with the points v_2 and v_1 in the $(i+1)$-th copy for $i < k$. (Note that the identification is performed upside down, which will be of importance in the proof, see Figure 13 for an illustration of two successive copies). We define C_i as the set of points of the i-th copy, and v_j^i the point corresponding to v_j in C_i. Observe that $\delta(T_k, T_k') = 3k$ for all $k \geq 1$.

Properties of a minimal flip sequence. We first claim that for every $k \geq 1$, there is a flip sequence from T_k to T_k' of length $\frac{5}{3}\delta(T_k, T_k') = 5k$. Indeed, the following flip sequence gives a transformation from T_1 to T_1': we perform in order the flips $v_6v_1 \rightsquigarrow v_2v_5$, $v_3v_8 \rightsquigarrow v_4v_7$, $v_3v_6 \rightsquigarrow v_4v_5$, $v_2v_5 \rightsquigarrow v_2v_4$, and finally $v_4v_7 \rightsquigarrow v_5v_7$. We can adapt this flip sequence for every $k > 1$ between T_k and T_k' into a sequence of length $5k$ by applying the former in each copy of T_1 and T_1' independently. The rest of the proof of Theorem 4 consists in proving by induction on k that the above mentioned sequences are minimal. First, we obtain the base case $k = 1$ by observing that, regardless of the two first flips, a transformation needs at least three additional flips.

▶ **Lemma 21.** *A minimal flip sequence between T_1 and T_1' has length at least 5.*

Let $k > 1$ be such that for $\ell < k$, a minimal flip sequence from T_ℓ to T_ℓ' has length at least 5ℓ. First, we prove the following by observing that if a common chord is not modified, every minimal flip sequence can be split into two minimal ones that independently modify each side of the chord.

▶ **Lemma 22.** *If there exists a common chord e that is not modified during a flip sequence $\mathcal{S}$ from T_k to T_k', then $\mathcal{S}$ has length at least $5k$.*

Therefore, it only remains to show that flip sequences that modify every common chord of T_k and T_k' have length at least $5k$. Let $\mathcal{S}$ be such a sequence. We use a double counting argument. More precisely, we distribute one unit of weight to a subset of $\{C_1, \ldots, C_k\}$ for every flip of $\mathcal{S}$. The core of our counting argument consists in proving that some intermediate edges are created during $\mathcal{S}$ due to connectivity. The flips in $\mathcal{S}$ involving these edges will provide extra weight to every set C_i. We essentially show that the total weight given by $\mathcal{S}$ to every set C_i is at least 5, which ensures that $\mathcal{S}$ has length at least $5k$.

To sum up, we finally obtain the following, which concludes the proof of Theorem 4.

▶ **Lemma 23.** *Let $\mathcal{S}$ be a minimal flip sequence between T_k and T'_k such that all the common chords are modified. Then, $\mathcal{S}$ has length at least $5k$.*

4.2 Other models

Non-crossing flips. To prove Theorem 6, we provide a construction similar to the previous section but with a much simpler base tree (see Figure 14). The proof goes along similar lines, but the counting is easier.

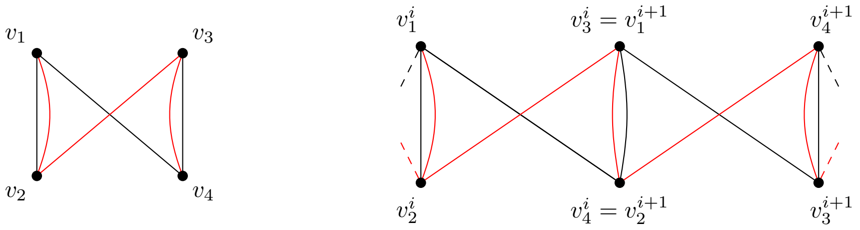

Figure 14 On the left, the tree T_1 in black and the tree T'_1 in red. On the right, the subgraph induced by C_i and C_{i+1} in a pair T_k (in black) and T'_k (in red).

Rotations. For rotations, we show that the construction of the previous section (see Figure 13) actually satisfies also the conclusion of Theorem 7. However, the arguments we use are more involved and the proof is overall more technical.

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