RESOLUTION DEPTH OF POSITIVE BRAIDS

ELLIOT KAPLAN, DAVID KRCATOVICH, AND PATRICIA O'BRIEN

ABSTRACT. The depth of a link measures the minimum height of a resolving tree for the link whose leaves are all unlinks. We show that the depth of the closure of a strictly positive braid word is the length of the word minus the number of distinct letters.

1. Introduction

It was shown by Conway [3] that the Alexander polynomial of an oriented link can be computed through a skein relation. If L_+ , L_- and L_0 are three link diagrams which are identical except in the neighborhood of a point, where they differ as in Figure 1, then the relationship

$$\Delta_{L_{\perp}}(t) - \Delta_{L_{\perp}}(t) = (t^{-1/2} - t^{1/2})\Delta_{L_0}(t), \tag{1}$$

along with the fact that $\Delta_{\text{unknot}}(t) = 1$, determines the Alexander polynomial for any oriented link. Similar



FIGURE 1. Three types of crossings and three link projections with these crossings

skein relations can be used to compute the Jones and HOMFLY-PT polynomials of a link.

Iterating this skein relation to compute a link polynomial leads one to construct a resolving tree [1] (also called a skein tree [10], or computation tree [4]). A resolving tree for a link L is a binary tree with L as the root. A diagram D is chosen, and a crossing is selected, so that D serves as L_{\pm} ; the left child is the diagram with the crossing changed, L_{\mp} , and the right is the diagram with the crossing resolved, L_0 . After possibly isotoping the resulting links at each node, this is repeated at each node which is not an unlink. With a deliberate choice of crossings, this process terminates, giving a finite tree. The depth of a leaf is the length of the (shortest) path from it to the root. The depth of a resolving tree is the maximum depth among all leaves. An example of a resolving tree with depth 6 is given in Figure 2. The depth of a link is the minimal depth among all resolving trees for the link. As such, it gives a measure of the complexity of computing link polynomials via this skein relation.

The leftmost branch of a resolving tree consists entirely of crossing changes, and therefore the unlinking number is a lower bound on the depth of a link. Note also that the skein relation (1) implies that the breadth of the Alexander polynomial is also a lower bound on the depth. Finding the depth of a particular link may require finding a resolving tree whose depth agrees with one of these lower bounds, which is not generally easy.

Links which have depth 1 were classified in [8]; those of depth 2 were classified in [10]. In this paper, we determine the depth of any link which is the closure of a positive (or negative) braid, by finding an explicit way to construct a resolving tree whose depth agrees with the lower bound coming from the Alexander polynomial.

Theorem 1. Suppose that an oriented link L is the closure of a strictly positive (negative) braid in B_n which is represented by a word of length ℓ . Then the depth of L is $\ell - n + 1$.

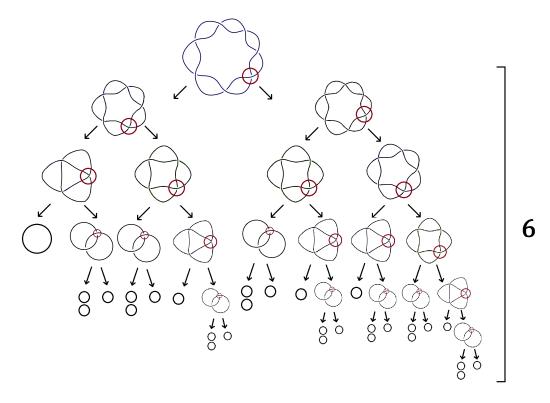


FIGURE 2. A resolving tree for the (7, 2)-torus knot

Section 2 gives the necessary background on braid closures and describes the effect which crossing changes and resolutions have on the corresponding braid word. Section 3 shows how to construct a particular resolving tree, giving an upper bound on the depth in Lemma 3. Section 4 shows (Lemmas 4 and 5) that this agrees with a lower bound coming from the Alexander polynomial, which proves Theorem 1.

2. Braids

2.1. Manipulating Braids. Let B_n denote the braid group on n strands, with generators $\sigma_1, \ldots, \sigma_{n-1}$. It will be convenient for an inductive argument in Section 3 to let $B_n[p]$ denote the subgroup of B_n generated by $\sigma_1, \ldots, \sigma_{p-1}$ (i.e., n-stranded braids where at most the first p strands are braided). For future reference we recall the relations of B_n :

 $\begin{array}{lll} \textbf{Rule 1:} \ \sigma_i \ \sigma_i^{-1} = 1 = \sigma_i^{-1} \ \sigma_i \\ \textbf{Rule 2:} \ \sigma_i \ \sigma_{i+1} \ \sigma_i = \ \sigma_{i+1} \ \sigma_i \ \sigma_{i+1} \\ \textbf{Rule 3:} \ \text{If} \ |\ i-j\ |>1, \ \text{then} \ \sigma_i \ \sigma_j = \ \sigma_j \ \sigma_i \ . \end{array}$

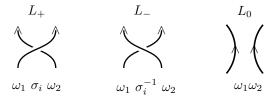
Further, if ω is a word in B_n , let $\widehat{\omega}$ denote its closure, a link in S^3 . The following ways [6] of changing ω do not change the isotopy class of $\widehat{\omega}$:

Rule 4 ((De-)stabilization): If $\omega \in B_n$ and $\omega' = \omega \sigma_n \in B_{n+1}$, then $\widehat{\omega}$ is equivalent to ω' as a link. More generally, if $\omega \in B_n[p]$ and $\omega' = \omega \sigma_p \in B_{n+1}[p+1]$, then $\widehat{\omega}$ is equivalent to $\widehat{\omega'}$.

Rule 5 (Conjugation): For any $\omega, \eta \in B_n$, $\widehat{\eta \omega \eta^{-1}}$ is equivalent to $\widehat{\omega}$ as a link.

Remark 1. An occurrence of σ_i in a braid word ω represents an L_+ crossing in the standard diagram of the link $\hat{\omega}$, and similarly σ_i^{-1} represents an L_- crossing. A crossing change results in the switching of the exponent from 1 to -1, or vice versa. A crossing resolution results in the elimination of this occurrence of σ_i from ω .

This remark is justified by the following diagram, where ω_1 and ω_2 are arbitrary braid words in B_n (for some $n \geq 2$).



By construction, all strands of a braid are oriented in the same direction, so this picture is sufficiently general.

Remark 2. Let ω be a braid word in which, for some i, σ_i appears two consectutive times (i.e., we have σ_i^2). If we target the crossing in $\widehat{\omega}$ which is represented by one of these σ_i 's and change the diagram from L_+ to L_- , the braid word representing our new link is the result of removing σ_i^2 from ω . If we instead resolve the crossing, this amounts to replacing σ_i^2 with σ_i .

2.2. Strictly Positive Braids. A positive braid word is one with no negative exponents, for example, $\sigma_3\sigma_1\sigma_3\sigma_2$. A positive braid is one which can be represented by a positive braid word. For example, $\sigma_3^{-1}\sigma_1\sigma_3\sigma_2$ represents a positive braid (because it is equivalent to $\sigma_1\sigma_2$), although it is not a positive braid word. A strictly positive braid is a braid which can be represented by a positive braid word in B_n such that σ_i appears at least once for each $1 \le i \le n-1$. Note that strict positivity is a characteristic of the braid closure – the closure of a positive braid is the closure of a strictly positive braid if and only if it is a non-split link. An essentially strictly positive braid is one which can be represented by a positive braid word $\omega \in B_n[p]$ for some p, such that σ_i appears at least once for each $1 \le i \le p-1$. In this case, we will say ω is strictly positive in $B_n[p]$. Note that essentially strict positivity is also a characteristic of the braid closure – the closure of a positive braid is the closure of an essentially strictly positive braid if and only if the first p strands form a non-split link and each of the remaining n-p strands is an unknot, for some p.

The following Lemma, paired with Remark 2, is the key to finding a resolving tree whose complexity decreases at each step. It is a slight variation of Lemma 2.1 of [4] (cf. [7, p. 34]).

Lemma 1. Suppose $\omega \in B_n$ is an essentially strictly positive braid whose closure $\widehat{\omega}$ is not an unlink. Then $\widehat{\omega}$ is the closure of an essentially strictly positive braid word in $B_m[p]$ (for some $p \leq m \leq n$) which contains σ_i^2 for some i. Further, such a word can be chosen so that either i = p - 1, or there are more than two occurrences of σ_i .

Proof of the first claim: It is clear that we may assume ω is strictly positive, for if a word in $B_n[p]$ contains a square, so does the same word in B_p (and this word's closure is either an unlink in both cases or in neither case).

So, let ω_0 be a strictly positive braid word which represents $\omega \in B_n$. Without loss of generality we assume that we have at least two σ_{n-1} 's in ω_0 , for if this is not the case, we can destabilize to get an strictly positive braid word in B_{n-1} , and then destabilize repeatedly, as many times as possible. A sequence of such destabilizations gives either the empty braid word in B_1 , whose closure is the unknot, or a positive braid word in B_i in which σ_{i-1} appears at least twice.

We begin by targeting two σ_{n-1} 's which have no other σ_{n-1} 's between them in ω_0 . Using Rule 3, we will move our σ_{n-1} 's as close together as possible. After this is done, we are left with three possible configurations:

Case 1: $\cdots \sigma_{n-1} \sigma_{n-1} \cdots$

In this case, a series of Rule 3 moves was sufficient to bring our σ_{n-1} 's together. Our first claim is satisfied.

Case 2: $\cdots \sigma_{n-1} \sigma_{n-2} \sigma_{n-1} \cdots$

Here, we apply Rule 2 to change ω to \cdots σ_{n-2} σ_{n-1} σ_{n-2} \cdots . If the resulting σ_{n-1} is the only σ_{n-1} left, we remove it through destabilization, resulting in \cdots σ_{n-2}^2 \cdots . Otherwise, we repeat the process with two of the remaining σ_{n-1} 's (again with no other σ_{n-1} 's between them). Note that the number of σ_{n-1} 's in ω has decreased by one, so after some number of repetitions, we will no longer have to consider this case.

Case 3: $\cdots \sigma_{n-1} \sigma_{n-2} \cdots \sigma_{n-2} \sigma_{n-1} \cdots$

Here our two σ_{n-1} 's are separated by a word in B_{n-1} , which we will refer to as ω_1 , and ω_1 has at

least two σ_{n-2} 's. We choose two σ_{n-2} 's with no other σ_{n-2} 's between them, and attempt to bring these together using Rule 3.

We can iterate this process, either finding a square (Case 1 or 2) or representing $\widehat{\omega}$ by a word $\omega_i \in B_{n-i}$ for successively larger i. Eventually, if we have not produced a square at a previous step, we end up with $\omega_{n-2} \in B_2$ containing at least two σ_1 's, so we have σ_1^2 .

Proof of the second claim:

Suppose we have represented $\widehat{\omega}$ by a strictly positive word $\omega' \in B_n$ which contains σ_i^2 for some i < n - 1, and no other occurences of σ_i . By conjugating, we may assume $\omega' = \sigma_i^2 \eta$, where η is a braid word in B_n not containing σ_i . Then, using Rule 3, we may write $\omega' = \sigma_i^2 \eta_- \eta_+$, where η_- is a word consisting of letters σ_j for j < i, and η_+ is a word consisting of letters σ_j for j > i. Since ω' is strictly positive, η_+ is not the empty word, and in fact contains all letters $\sigma_{i+1}, \dots, \sigma_{n-1}$. Applying the argument in the proof of the first claim to η_+ , we can either destabilize all of η_+ or we can find σ_i^2 for some j > i.

3. An Upper Bound on Depth

Let $\widehat{\omega_0}$ be the closure of a strictly positive braid word in $B_n[p]$. The aim of this section is to show that we can construct a resolving tree for which the "complexity" decreases each step down from the root. Recursively, if $\widehat{\omega_i^{\alpha}}$ is the closure of a strictly positive braid word in $B_n[p_i^{\alpha}]$, where α is a binary sequence of length i, then after choosing a crossing, define $\widehat{\omega_{i+1}^{\alpha,0}}$ to be the closure of a braid word resulting from an $L_+ \to L_-$ crossing change, and $\widehat{\omega_{i+1}^{\alpha,1}}$ the closure resulting from an $L_+ \to L_0$ resolution. Note that by Lemma 1 and Remark 2, a crossing can always be chosen so that both $\widehat{\omega_{i+1}^{\alpha,1}}$ and $\widehat{\omega_{i+1}^{\alpha,0}}$ are also closures of essentially strictly positive braid words. Let ℓ_i^{α} denote the length of ω_i^{α} , and let $\chi_i^{\alpha} = \ell_i^{\alpha} - p_i^{\alpha} + 1$. We will view χ as the complexity of the word, since it is merely the length minus the number of distinct letters. Note that if $\widehat{\omega_i^{\alpha}}$ is the closure of a strictly positive braid in B_n , then $p_i^{\alpha} = n$.

Lemma 2. Let $\widehat{\omega_i^{\alpha}}$ be the closure of a strictly positive braid word in $B_n[p_i^{\alpha}]$ which contains σ_j^2 for some j, such that either there are more than two σ_j 's or $j = p_i^{\alpha} - 1$. If we select a crossing which corresponds to one of these σ_j 's, then

$$\max\left\{\chi_{i+1}^{\alpha,0},\chi_{i+1}^{\alpha,1}\right\} \le \chi_i^{\alpha} - 1.$$

Paired with Lemma 1, this says we can construct a resolving tree for the closure of an essentially strictly positive braid for which the complexity decreases by at least one at each step.

Proof. For the left child, we change one of these σ_j 's to σ_j^{-1} We have three cases for this braid closure and its left child:

- (1) There are exactly two σ_j 's remaining. By our premise, $j = p_i^{\alpha} - 1$. We change one of the remaining σ_j 's to σ_j^{-1} , which then cancels with the last σ_j . The result is the closure of a strictly positive braid in $B_n[p_i^{\alpha} - 1]$. In this case, $\ell_{i+1}^{\alpha,0} = \ell_i^{\alpha} - 2$ and $p_{i+1}^{\alpha,0} = p_i^{\alpha} - 1$.
- (2) There are exactly three σ_j 's remaining and $j = p_i^{\alpha} 1$. We change one σ_j to σ_j^{-1} , which then cancels with another σ_j , and the third σ_j can be eliminated through destabilization, resulting in the closure of a strictly positive braid in $B_{n-1}[p_i^{\alpha} - 1]$. So, $\ell_{i+1}^{\alpha,0} = \ell_i^{\alpha} - 3$ and $p_{i+1}^{\alpha,0} = p_i^{\alpha} - 1$.
- (3) There are more than three σ_j 's remaining (or at least three if $j \neq p_i^{\alpha} 1$). We change one σ_j to σ_j^{-1} , which then cancels with another σ_j , but there are still at least two σ_j 's remaining. If $j \neq p_i^{\alpha} 1$ and there is only one σ_j remaining, this still can not be eliminated through destabilization, so $\ell_{i+1}^{\alpha,0} = \ell_i^{\alpha} 2$ and $p_{i+1}^{\alpha,0} = p_i^{\alpha}$.

In the second and third cases, χ decreases by 2. In the first case, χ decreases by 1. We have two cases for this braid closure and its right child:

- (1) There are exactly two σ_j 's remaining. By assumption, $j = p_i^{\alpha} - 1$. We remove one σ_j and the other σ_j can be eliminated through destabilization, so $\ell_{i+1}^{\alpha,1} = \ell_i^{\alpha} - 2$ and $p_{i+1}^{\alpha,1} = p_i^{\alpha} - 1$. (2) There are more than two σ_j 's remaining. We remove one σ_j and there are still at least two σ_j 's
- remaining, so $\ell_{i+1}^{\alpha,1} = \ell_i^{\alpha} 1$ and $p_{i+1}^{\alpha,1} = p_i^{\alpha}$.

In both cases, χ decreases by 1.

Lemma 3. Every link arising from the closure of a strictly positive braid word $\omega \in B_n[p]$ has a resolving tree of depth less than or equal to $\ell-p+1$, where ℓ is the length of ω . Thus, the depth of the closure $\widehat{\omega}$ has an upper bound of $\ell - p + 1$.

Proof. After using the first claim of Lemma 1 to find squares, Lemma 2 allows us to construct a tree for $\widehat{\omega}$ of depth less than or equal to $\chi = \ell - p + 1$, such that for each leaf we have $\chi_i^{\alpha} = 0$. It remains to see that this is a complete resolving tree – in other words, that these leaves are in fact all unlinks. But $\chi_i^{\alpha}=0$ implies that each letter $\sigma_1, \ldots, \sigma_{p_i^{\alpha}-1}$ is used exactly once, so successive destabilizations result in a braid closure with no crossings.

4. A Lower Bound on Depth

The skein relation (1) implies that if L' is a link which appears as a child of L in a resolving tree, then

$$Br(\Delta_L(t)) \le Br(\Delta_{L'}(t)) + 1,$$
 (2)

where Br is the breadth of a polynomial (the difference between the greatest and least exponents of its nonzero terms). Since an unlink has an Alexander polynomial of breadth zero, it follows that

$$Br(\Delta_L(t)) \le \operatorname{depth}(L).$$
 (3)

Therefore, to prove our main result, it is only necessary to show that if L is the closure of a strictly positive braid, represented by a braid word ω of length ℓ in B_n , then

$$Br(\Delta_L(t)) \ge \ell - n + 1.$$

This is a well-known fact, because closures of positive braids are fibered [9], but we present a proof here for the sake of self-containment. The proof relies on Kauffman's state sum model for the Alexander polynomial [5], which we review here.

Alexander gave the following method of computing $\Delta_L(t)$ from an oriented non-split link diagram [2]. At each crossing, each of the four adjacent regions is labelled with ± 1 or $\pm t$, as in Figure 3, depending on the handedness of the crossing. If the diagram has n crossings, it has n+2 regions, so one can construct an $n \times (n+2)$ -matrix A by setting a_{ij} to be the label assigned to region j at crossing i if region j is adjacent to crossing i, and otherwise 0. After removing any two columns to get a square matrix A',

$$\det(A') \doteq \Delta_L(t),$$

where " \doteq " symbolizes equality up to multiplication by $\pm t^i$ for some half-integer i.

A Kauffman state is an assignment of markings to each of these n crossings so that for each crossing, exactly one of the adjacent regions is marked, and so that each region has no more than one mark (n regions will be marked and 2 will be unmarked – in Figures 4, 6, and 7 the unmarked regions are starred, to clearly distinguish them). Once the diagram has been marked, values are assigned to each crossing according to which adjacent region is marked, as in Figure 3. The product of all n of these values is the weight of the state, and the Alexander polynomial of the oriented link (up to multiplication by $\pm t^i$) is equal to the sum of the weight of all states for a fixed diagram of the link with choice of two unmarked (or starred) regions. Each state is simply a term in det(A'), and the choice of 2 unmarked regions corresponds to the choice of 2 columns to remove.

We now set out to prove that $Br(\Delta_L(t)) \geq \ell - n + 1$. We will accomplish this by showing that, after a choice of starred regions, there is a unique Kauffman state with weight ± 1 , and a unique Kauffman state with weight $\pm t^{\ell-n+1}$. In order to do so, we introduce some notation, with Figure 4 as an illustration. Let n_i be the number of occurrences of σ_i in ω . Let c_i^j denote the crossing which corresponds to the jth occurrence

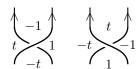


FIGURE 3. How values are assigned in a Kauffman state.

of σ_i . Let R_i^j denote the region which has c_i^j at the top and c_i^{j-1} at the bottom, if j > 1, and R_i^1 the region which connects $c_i^{n_i}$ to c_i^1 . Finally, R_0 is the exterior region, and R_n is the interior region. Star the adjacent regions R_0 and R_1^1 .

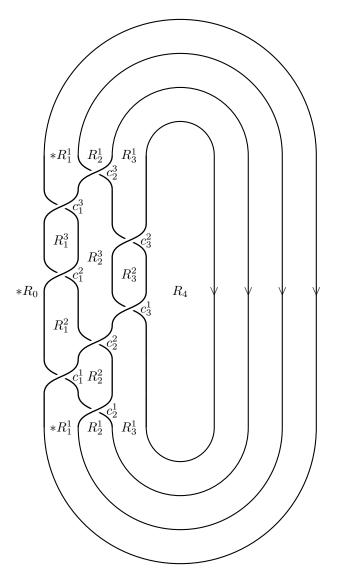


FIGURE 4. The closure of the braid $\sigma_2\sigma_1\sigma_2\sigma_3\sigma_1\sigma_3\sigma_1\sigma_2$

Lemma 4. There is a unique state with weight ± 1 .

Proof. Figure 5 shows a generic region R_i^j . Note that it has a single -1 at its bottom crossing, a single -t at its top crossing, 1 at each of its left crossings, and t at each of its right crossings. Start with the crossing

 $c_1^{n_1}$. Since the two starred regions are adjacent to this crossing, its only remaining labels are 1, in region R_2^j for some j, and -t. Therefore, to get a weight of ± 1 , we must assign the region R_2^j to this crossing. Next, consider the crossing c_2^{j-1} . It has a label of -1 in region R_2^j , but we have already used this region; therefore we are forced to use the label 1 in region R_3^k , for some k. This process repeats, forcing us to use a label 1 in region R_n at some crossing c_{n-1}^l . To this point, we have positioned the black circles in Figure 6.

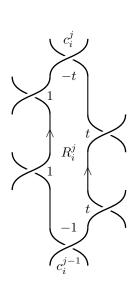


FIGURE 5. A generic region R_i^j

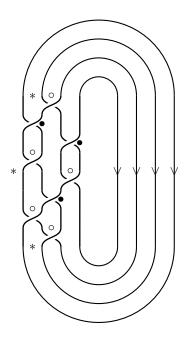


FIGURE 6. The Kauffman state with weight ± 1

Next we position the white circles in Figure 6. Observe that the regions R_1^j have no "left" crossings, so they have no 1 labels. It follows that we must assign R_1^j to crossing c_1^{j-1} , at which it has its unique -1 label. Now move to the regions R_2^j . We have used all of the c_1^j crossings, so there are no more "left" crossings available. So again, assign R_2^j to c_2^{j-1} , at which it has its unique -1 label. Iterating this procedure yields a state with (n-1) '1' labels, and $(\ell-n+1)$ '-1' labels. At each step, the choice is forced, so this is a unique state.

Lemma 5. There is a unique state with weight $\pm t^{\ell-n+1}$.

Proof. We begin by noting that, for fixed i, we cannot consistently choose $\pm t$ at crossing c_i^j for all j. Such a choice would use R_i^k or R_{i-1}^k regions. Then, to the right of these crossings, there would be only

$$s_i := n_{i+1} + n_{i+2} + \dots + n_{n-1}$$

crossings, but $s_i + 1$ adjacent regions to be matched. Since this cannot happen, it follows that for each i, at least one of the c_i^j must have a ± 1 label 1 . Therefore, the highest power of t which can be assigned to a state is $\ell - n + 1$. In order to achieve this, it is necessary that exactly one c_i^j has a ± 1 label for each i.

Consider first the crossings c_1^j . All of the t labels at these crossings are in the starred region R_0 . The only way to get the maximum $n_1 - 1$ labels of $\pm t$ is to assign c_1^j to R_1^j for all j > 1. In this case, the only remaining choice at the crossing c_1^1 , which we will denote by $c_1^{k_1}$, is the label +1, coming from some region, which we will call $R_2^{k_2}$.

¹Actually, a similar argument shows that at least one must have a +1 label, but we do not need this distinction.

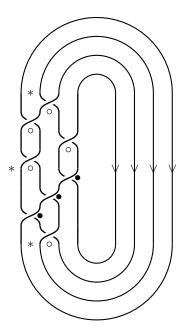


FIGURE 7. The Kauffman state with weight $\pm t^{\ell-w+1}$

Then consider the crossings c_2^j . Again, since all of the R_1^j regions have already been assigned to crossings, there are no t labels available. The best we can do is get n_2-1 labels of -t, by assigning crossing c_2^j to region R_2^j . This can be done for all but one j, because one of the regions, $R_2^{k_2}$, was already assigned to crossing $c_1^{k_1}$. This leaves the crossing $c_2^{k_2}$ without a label, and the only remaining choice is the +1 label coming from a region which we will call $R_3^{k_3}$.

The same process uniquely determines the assignments for all other crossings. Eventually we get a crossing $c_{n-1}^{k_{n-1}}$, which can only be assigned to the region R_n . This state has (n-1) labels of +1, where the crossing $c_i^{k_i}$ is assigned to region $R_{i+1}^{k_{i+1}}$, and $(\ell-n+1)$ labels of -t, where the remaining crossings c_i^j are assigned to regions R_i^j . This is the unique state with weight $\pm t^{\ell-n+1}$, shown in Figure 7.

PROOF OF THEOREM 1. Lemma 3 shows that $\ell-n+1$ is an upper bound for the depth. Lemmas 4 and 5 together show that

$$Br(\Delta_L(t)) = \ell - n + 1,$$

and so by inequality (3), this quantity is also a lower bound for the depth.

More generally, the closure of a positive – but not strictly positive – braid is a split link, splitting into closures of strictly positive braids, whose depths are determined by Theorem 1. Note also that the same argument applies to closures of negative braids.

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Ohio University, Athens, Ohio 45701

MICHIGAN STATE UNIVERSITY, EAST LANSING, MICHIGAN 48824

University of Texas, Austin, Texas 78712

 $Email\ address: \ {\tt ek432210@ohio.edu}$ $Email\ address: {\tt krcatov6@msu.edu}$ $Email\ address \hbox{: pjobrien@utexas.edu}$