Knots, Isotopies, and Khovanov Homology

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Declaration

The mathematics in this thesis is well known and certainly not of my own creation. I also owe much credit to my supervisor, Scott Morrison, for explaining many of the concepts and proofs to me. What remains is my own except where otherwise stated.

Hilary Hunt

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I have a lot of people to thank for their help in making this thesis:

First and foremost, my supervisor, Scott. Thank you for suggesting such a fun topic and for all your advice and patience in teaching me this year.

Thanks also go to the Vigleik, Joan and Zsuzsanna who have spared the time to help me with some of the many questions I've had.

My many fantastic teachers, some of whom have been mentioned but who also include Tony, Brian and Conrad. Thanks for teaching me so much this year.

My friends and fellow honours students.

And lastly, my supportive family — Mum, Dad, Phoebe and Jane whose delicious dinners I couldn't have done without.

Abstract

In this thesis, we aim to investigate the action of the centraliser of a braid on the Khovanov homology of its trace closure. To this end, we explore the theory of knots and braids. We define both objects and clarify the relationship between them. We investigate link invariants including the Jones polynomial and Khovanov homology and look at the uniqueness of isotopies on both braids and links.

Contents

Introduction

The aim of this thesis is to investigate the action of the centraliser of a braid on the Khovanov homology of its trace closure. Khovanov homology (described in Chapter 7) is a knot invariant that assigns vector spaces to links [24, 5, 6]. These vector spaces are the homology groups of graded chain complexes and are put together in a manner reminiscent of Kauffman's state sum bracket [19]. The construction of the Khovanov homology also gives explicit isomorphisms between the Khovanov homologies of isotopic links.

The fact that isotopies between links can be described as a sequence of a finite number of generating isotopies, the Reidemeister moves, makes this quality particularly exciting. If two links are isotopic, we can explicitly compute the corresponding isomorphism between the Khovanov homologies as the composition of the isomorphisms induced by the Reidemeister moves. Should two links not be isotopic but have isomorphic Khovanov homologies, knowing how self isotopies act on their Khovanov homologies could help to distinguish them. Thus, they could be used to make Khovanov homology a stronger invariant.

Every link can be represented by a braid closure [1]. This braid representative of the link is not unique however each braid does represent a unique link. We can take an element of the centraliser of the braid representative to construct a well-defined isotopy of the braid closure (see Definition 2.2.1 and Theorem 2.3.1). This will induce an automorphism of the Khovanov homology of the link. Hence Khovanov homology gives a representation of the centraliser of a braid on the Khovanov homology of its closure.

The isomorphisms associated to individual Reidemeister moves have been described previously, but not in a manner compatible with algorithms for computing Khovanov homology. Thus, to date, there are no explicit computations of the isomorphism associated to a non-trivial self-isotopy of a link. These calculations

would lead to a greater understanding of Khovanov homology. To this end, we explore the theory behind Khovanov homology and the main concepts in knot theory necessary to derive these relationships.

In Chapter 1, we go over precise definitions of what a mathematical knot is, what it means for two knots to be the same and how to depict them for easier analysis. In Chapter 2, we introduce braids. It is a useful fact that the trace closure of a braid is a link. We look at the aspects of the braid that determine what this link is and the relationship between any two braids with the same trace. Another important section of Chapter 2 is the introduction of the centraliser of a braid. We will be using elements of the centraliser later in this thesis to generate automorphisms of links that differ from the identity. These will give us insight into the specific isomorphisms between the Khovanov homologies of related knots.

In Chapter 3, we discuss Alexander's theorem on the relationship between knots and braids. A proof of the theorem is covered in some detail. This is because the connection is one of the central relations we will exploit when analysing Khovanov homology. It is also particularly suited to implementation as it provides a purely algorithmic approach to find the braid representatives of knots.

Chapter 4 returns to the topic of knots and links and introduces knot invariants. We look particularly at the Jones polynomial, one of the most famous invariants and Kauffman's contribution in the state sum calculation. Again, the algorithmic nature of calculating the Jones polynomial via a state sum lends itself perfectly to computer calculations. This chapter also leads in to the calculation of the Khovanov homology of a knot.

We briefly cover movies as a way of visualising isotopies in Chapter 5 before looking at the Khovanov homology in Chapter 6. We review the basics of homological algebra and describe how the chain complexes and maps are assigned to each link to create an invariant. As I implemented the calculation of the Khovanov homology of braid closures, an example of how the calculation is performed is included.

Chapter 1

Knots and Links

This chapter introduces readers to some basic concepts used throughout this thesis. Mathematical knots are very similar to everyday knots. We can think of them as being made up of flexible, elastic strings that might take the form of a single, circular loop or be so tangled that we can't even tell if they are made up of just one string by looking. The main thing to remember is that mathematical knots are always closed loops. We must remember to fuse the two ends of our imagined strings so that for some knots there is no possibility of them unravelling.

1.1 Definitions

We'll begin by looking at the formal definitions knots, links, and isotopies.

Definition 1.1.1. A **knot** is a smooth embedding of S^1 in $\mathbb{R}^3$.

Definition 1.1.2. A **link** is a smooth embedding of a disjoint union of copies of S^1. Each of these copies of S^1 is itself a knot. We call each of these knots a **component** of the link.

Definition 1.1.3. An **oriented link** is a link along with an orientation on each of its components.

Ususally we are not interested in the particular embedding of S^1 into $\mathbb{R}^3$. Rather, we look at this embedding only up to an equivalence relation called 'isotopy'. Informally, links are isotopic if we can pull and stretch the various parts of one link, making sure that each strand never passes through itself, until it resembles the other link. Unfortunately, this is generally a long process — there are pairs of links whose planar projections require intermediate isotopies

via significantly more complicated projections before we can prove that they are isotopic [25]. Further, this method can't be used to prove inequivalence. Instead, we look for link invariants — qualities that isotopic links share.

Definition 1.1.4. An **isotopy** is a family of links $L_t : \sqcup S^1 \to \mathbb{R}^3,\ t \in [0,1]$ such that the associated map $M : \sqcup S^1 \times [0,1] \to \mathbb{R}^3$ given by $M(x,t) = L_t(x)$ is smooth.

Definition 1.1.5. Two links, L_1, L_2 are **isotopic** if there is an isotopy, M, such that $M(x,0) = L_1$ and $M(x,1) = L_2$.

Definition 1.1.6. The **isotopy group** of a link, $L : \sqcup S^1 \to \mathbb{R}^3$, is the set of all isotopies of L modulo higher order order isotopies. We will define these in §2.3.

Note that in this thesis we distinguish between isotopies and planar isotopies which will be defined later in this chapter.

Thus, a central question in knot theory is determining whether two links are equivalent or not; that is, are they isotopic? There are a variety of methods with which this has been attempted. Typically, we look for what are called link invariants. These are properties of a link that do not change under isotopy.

To do this, it is often convenient to write links in the form of knot diagrams.

1.2 Planar diagrams

Informally, a diagram of a link, L is the image of a projection of L onto a plane, along with the relative heights of strands at each crossing. A **regular projection** is a projection to a plane such that

- No more than two strands of L ever overlap at a single point in our diagram
- The tangents of the two strands at a crossing must not align
- No strand runs perpendicular to the plane of our projection

We call the points on this plane where two strands of L overlap *crossings* and the strands between crossings *arcs*. If the link has an orientation, its projection inherits this orientation in a natural way.

Definition 1.2.1. A diagram of a link, L, is a regular projection to a plane, along with the relative heights of the strands at each crossing.

The relative heights at each crossing are represented by drawing the overstrand as an unbroken line while there will be a gap between the understrand and the crossing point in the diagram. The information about the relative heights means we preserve the 3-dimensional structure of the link. In particular, each diagram can be interpreted (by lifting overcrossings out of the plane) as a 3-dimensional link and it is obvious that all links so constructed from the same diagram will be isotopic.

We often want to project a link onto a specific plane. This could be for reasons such as minimising the number of crossings or maintaining the same perspective when projecting a transforming link. Unfortunately, it is not guaranteed that this will result in a regular projection. Hence, when choosing a projection like this, we shift the offending arcs slightly with an isotopy of the original link to ensure we create a regular projection. Any projection of a knot with a finite number of crossings of a finite number of strands can be transformed into a regular projection by shifting any strands that violate the requirements. This is can be seen by performing induction on the edges [9]. Links with a regular planar projection are a dense subset of links in $\mathbb{R}^3$. Moving the strands like this means that the planar diagram depicts a different link. The two links are related by an isotopy. It is important to note here that we often do not distinguish between isotopic links as the link invariants we will be working with are isotopy invariants.

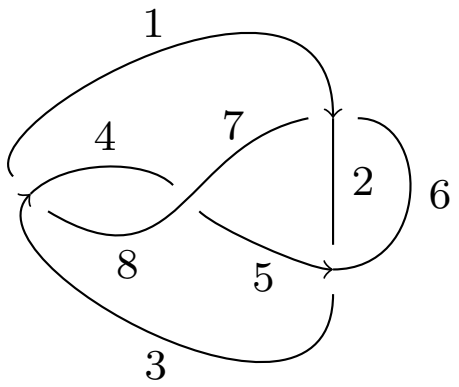
Definition 1.2.2. A **planar isotopy** is a deformation of the link within the plane of its planar diagram that leaves every crossing intact.

Two diagrams are isotopic if and only if we can transform one into the other via a planar isotopy. If they are isotopic, the projected links must also be isotopic. However, isotopic knots may not always have isotopic diagrams.

It is helpful to have a combinatorial description of a link diagram. This makes it possible to program computers to perform calculations. It also reduces the number of diagrams necessary in explanations and makes entering links into a computer much easier. One such description is the “planar diagram” or “PD” notation from the KnotTheory mathematica package [8]. We label each of the arcs in an oriented link diagram. Choose any arc to start and number from 1, incrementing at every crossing and following the direction of orientation. After making a circuit of the first component, start with the next number on another

until all arcs are labelled. We can then label each crossing by the four arcs that meet there. The arcs are given in an anticlockwise order, starting from the incoming understrand.

Example 1.2.1. The PD presentation of the knot below is $X_{8,4,1,3}X_{4,8,5,7}X_{6,1,7,2}X_{2,5,3,6}$



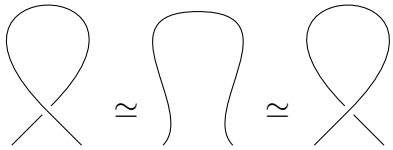
1.3 Equivalence of Links

In a planar diagram, both the path of each arc and the number of crossings in the diagram can differ between isotopic links and even between different projections of the same link. Two diagrams which differ by only the path of an arc between two crossings are clearly isotopic. This means that only the crossings and the endpoints of each path are necessary to determine the isotopy class of a link. If this information is identical for two diagrams, the corresponding links must be isotopic. However, the converse is not necessarily true. That is, two diagrams which are not planar isotopic may still represent isotopic links. It is still not clear how to tell if two diagrams with different crossings are isotopic. To more easily classify links, we need a better understanding of the action of isotopies on the projections of links and when two different diagrams represent the same knot.

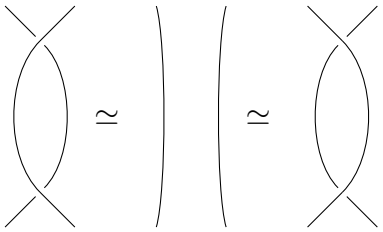
To this end, we introduce Reidemeister's Theorem. Reidemeister proved that we can express all isotopies between links with regular projections as combinations of planar isotopies and three 'generating' isotopies.

Theorem 1.3.1 (Reidemeister's Theorem)**.** [28] Two link diagrams are projections of links from the same isotopy class if and only if we can transform one into the other through a sequence of planar isotopies and Reidemeister moves. The Reidemeister moves are:

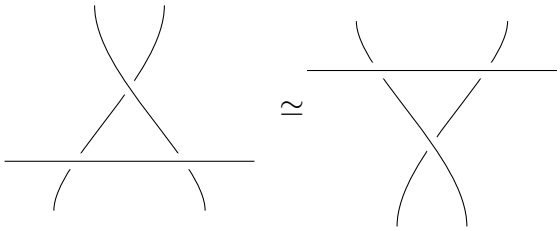
- Reidemeister 1



- Reidemeister 2



- Reidemeister 3



Murasugi describes a proof of this theorem in his book *Knot Theory and its Applications* [27].

Chapter 2

Braids

Braids have been studied since the 1920's when they were first described by Artin [3]. While he originally studied them as geometric objects, he also proved that the braid groups have an equivalent, purely algebraic definition. They appear in many areas of mathematics including cryptography [2], operator algebras [22] and robotics [17] and their study has enriched many branches of mathematics. We introduce them here because of the parallels between the geometric interpretation and links and the opportunity this provides us to study links from a more algebraic perspective.

In order to define a braid, we need to fix some notation. Take a cube in $\mathbb{R}^3$ e.g. $\{(x, y, z) \in \mathbb{R}^3 | x, y, z \in [0, 1]\}$, a set of n points, A_i, on the bottom face, at $(\frac{i}{n+1}, \frac{1}{2}, 0)$, and a set of n points, B_i, on the opposing face, at $(\frac{i}{n+1}, \frac{1}{2}, 1)$ for $i \in 1, ..., n$.

Definition 2.0.1. Given such a cube, an **n-stranded braid** is a collection of n smooth, non-intersecting curves such that one curve starts at each A_i and ends at some B_j. These curves, or strands, must have non-zero partial z derivative and remain within the cube.

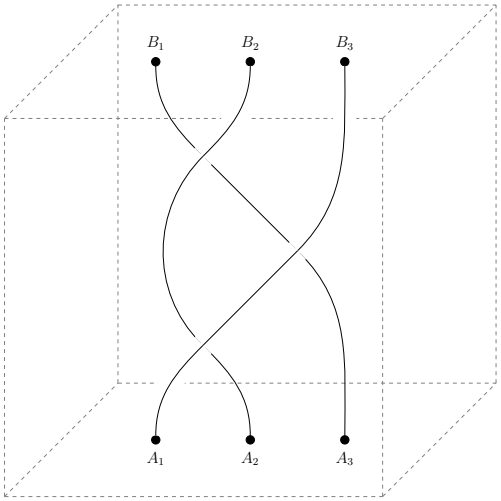


Figure 2.1: The braid $\sigma_1\sigma_2\sigma_1 \in B_3$

We say that two braids are equivalent if they are related by an isotopy that fixes the endpoints of each strand. Braids with a fixed number of strands form a group. The identity is the braid with strands travelling vertically from each A_i to B_i.

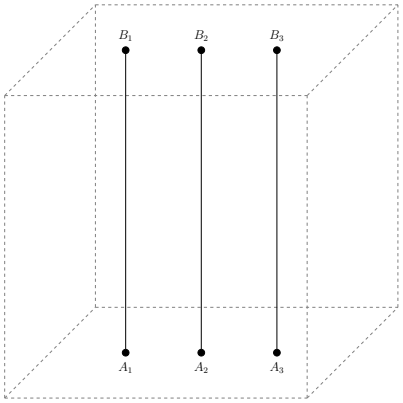


Figure 2.2: The identity on B_3

The group operation is stacking two braids on top of each other so that the ends of the strands line up this must then be dilated back into the cube.

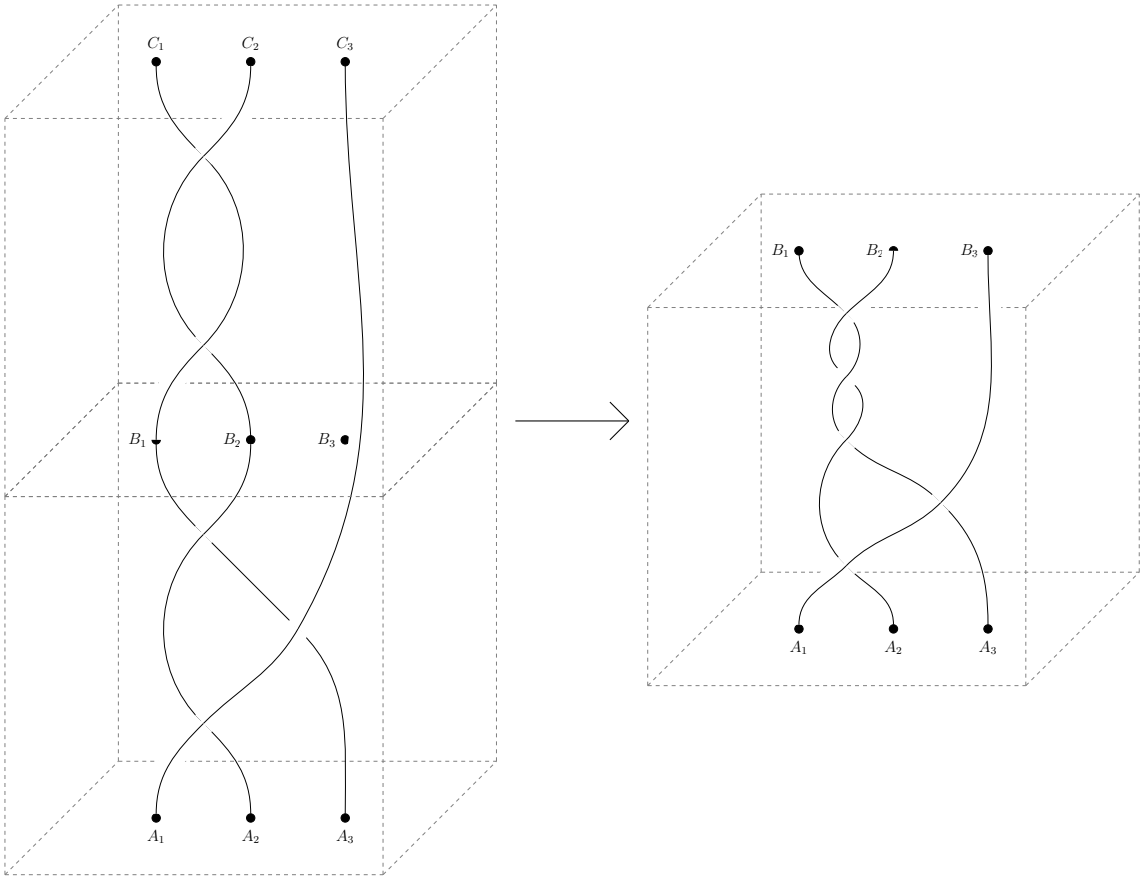


Figure 2.3: Composing braids $\sigma_1\sigma_2\sigma_1$ and $\sigma_1\sigma_1$

Definition 2.0.2. The **trace closure** of a braid, b, is the object formed when we connect each A_i with an arc in the plane $y = \frac{1}{2}$ to the corresponding B_i such that no two arcs cross and each lies outside the unit cube defined around b.

Example 2.0.2. The trace closure of $\sigma_1\sigma_2\sigma_1$ is the link depicted in Figure 2.4.

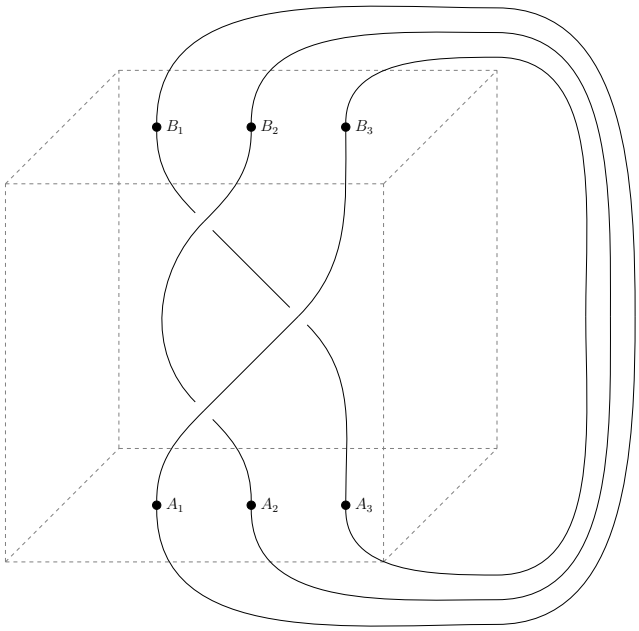


Figure 2.4: $Tr(\sigma_1\sigma_2\sigma_1)$

The braid groups can be represented algebraically as

$$B_n = \left\{ \sigma_1, ..., \sigma_{n-1} \middle| \begin{array}{ll} \sigma_i\sigma_j = \sigma_j\sigma_i & |i-j| > 1 \\ \sigma_i\sigma_j\sigma_i = \sigma_j\sigma_i\sigma_j & |i-j| = 1 \end{array} \right\}$$

where n is the number of strands in each braid [3]. The braid depicted in Definition 1.4.1 is written as the 'word' $\sigma_1\sigma_2\sigma_1$ and reads from bottom to top in the diagram.

Definition 2.0.3. A word in the braid group generators is called a **braid word**.

2.1 Markov's Theorem

We have seen earlier that we can obtain a link from any braid by taking its trace closure. The link obtained is unique up to isotopy. To confirm this, we need to ensure that the braid relations all correspond to isotopies. If every form of a braid is isotopic, the trace closure is unique.

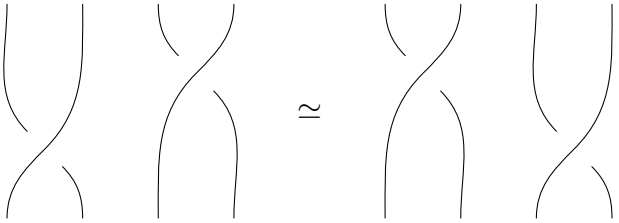
Theorem 2.1.1. If b_1 and b_2 are braid words which correspond to the same braid, there exists an isotopy between them.

Later, in §2.3, we show that this isotopy is unique.

Proof. The first,

$$\sigma_i\sigma_j = \sigma_j\sigma_i \quad |i-j| > 1$$

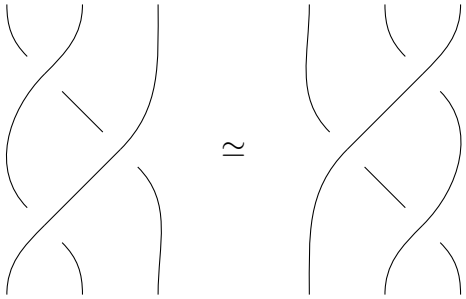
denotes a planar isotopy.



The second braid relation,

$$\sigma_i\sigma_j\sigma_i = \sigma_j\sigma_i\sigma_j \quad |i-j| = 1$$

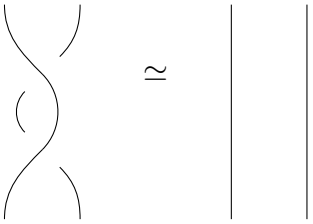
is equivalent to performing a Reidemeister 3 move on the braid.



Finally, we musn't forget the trivial relation,

$$\sigma_i\sigma_i^{-1} = Id$$

which is the equivalent of a Reidemeister 2 move on the braid.



All braid relations correspond to isotopies in the geometric interpretation. □

While the link obtained by taking the trace closure of a braid is unique, the reverse is not true. We show in the next chapter that every link has a braid

representative whose trace closure is isotopic to the link, however, this braid representative is not unique.

Consider the link depicted in Figure 2.4. Clearly, $\sigma_1\sigma_2\sigma_1$ is a braid representative of this link. However, we can reduce the number of crossings in this diagram by performing a Reidemeister 1 move on the second crossing, σ_2. The resulting link is isotopic to $Tr(\sigma_1\sigma_2\sigma_1)$ however, it is clearly also the trace closure of $\sigma_1\sigma_1$. This is called a **destabilisation**. Doing the opposite and adding a loop to the trace closure via a Reidemeister 1 move is known as a **stabilisation**.

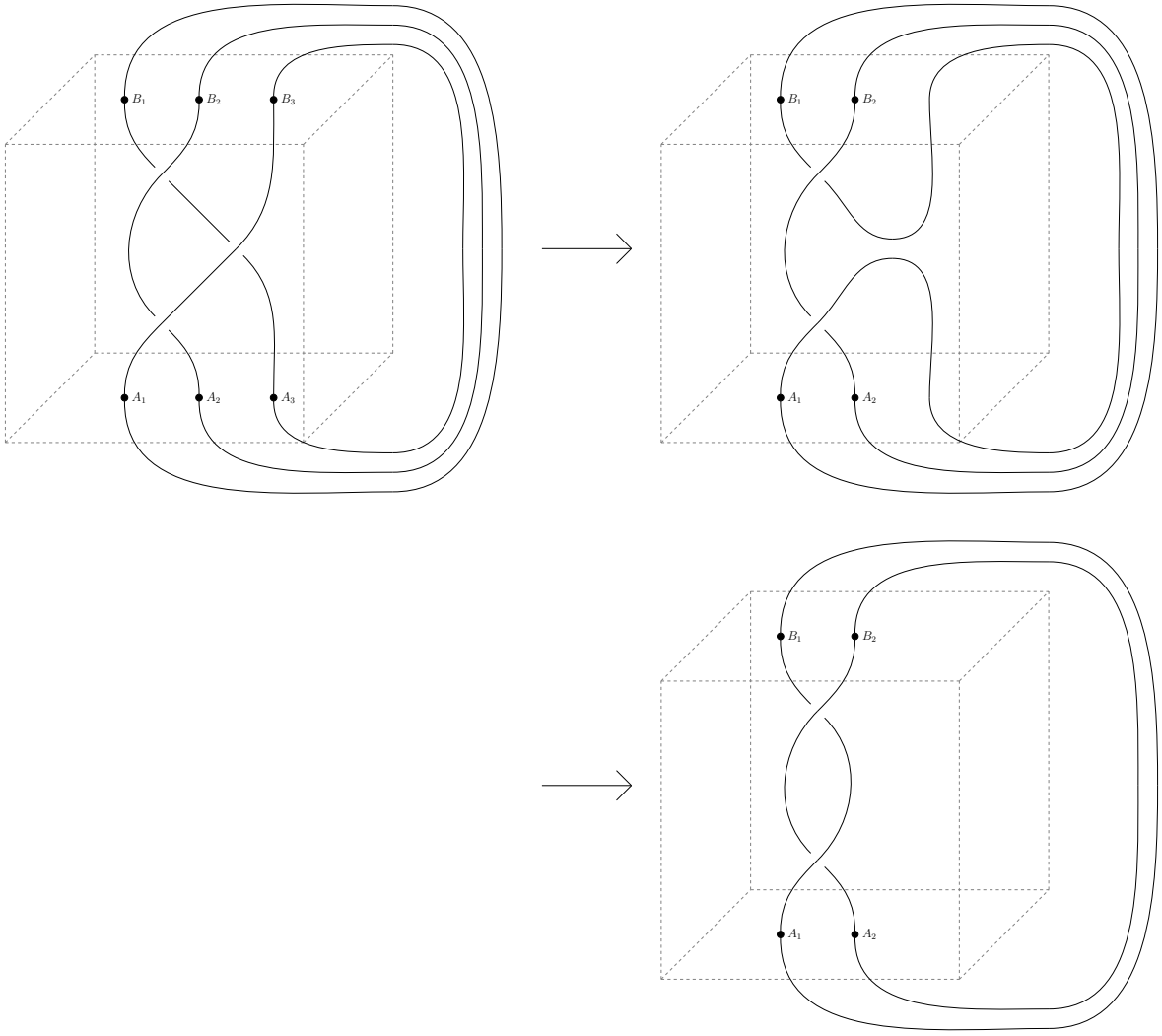


Figure 2.5: $Tr(\sigma_1\sigma_2\sigma_1) \simeq Tr(\sigma_1\sigma_1)$

Similarly, we can pull one of the crossings through the closure of the braid from one end to the other. This is a planar isotopy of the trace closure but causes a significant change in the braid word. It is equivalent to conjugating the braid by the shifted generator. Hence, we refer to it as a **conjugation**.

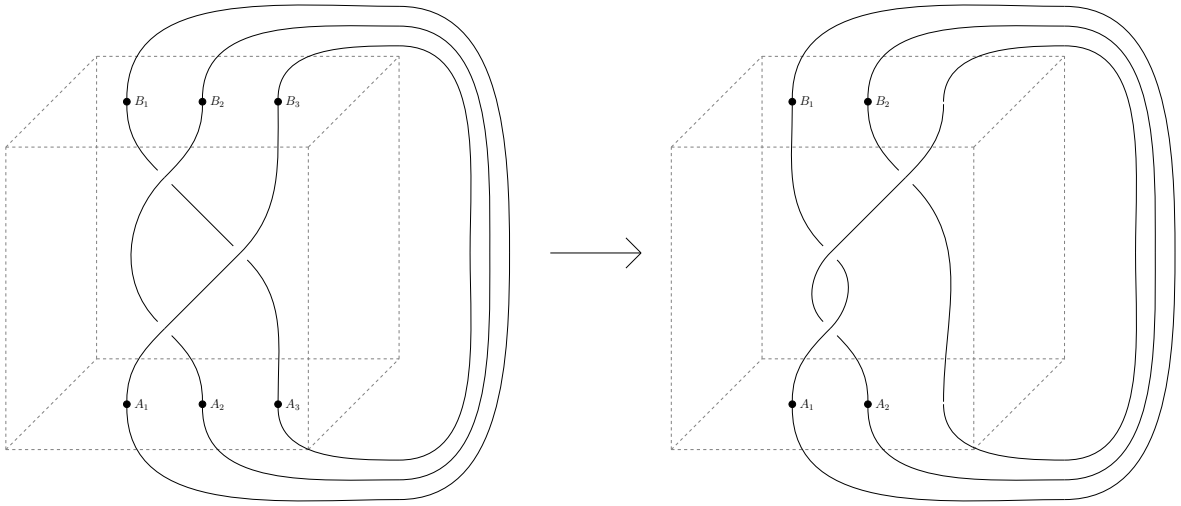


Figure 2.6: $Tr(\sigma_1\sigma_2\sigma_1) \simeq Tr(\sigma_1\sigma_1\sigma_2)$

In 1935, Markov [26] proved that these two operations, applied to a braid, generate all other braids with the same trace. The statement of the theorem is as follows:

Theorem 2.1.2. Given two braids b and b', $Tr(b) = Tr(b')$ if and only if we can transform from b to b' via a sequence of the following operations:

1. **Conjugation** with any other element of the braid group
   i.e. $b \sim cbc^{-1}\ \forall b, c \in B_n$
2. **Stabilisation/Destabilisation**
   i.e. $b \sim b\sigma_i^{\pm 1}$ for $i = n$ where B_n is the smallest braid group that contains b.

These are called the Markov moves.

2.2 Centralisers

The centraliser of a braid, b, in B_n is defined as

$$Z(b) = \{c \in B_n | cb = bc\}$$

It is the subgroup of all elements that commute with b. The braid itself and the full twist $\Delta \in B_n$ ($\delta \in B_3$ illustrated in Figure 2.7) are always members of the centraliser; however other generators are more difficult to find.

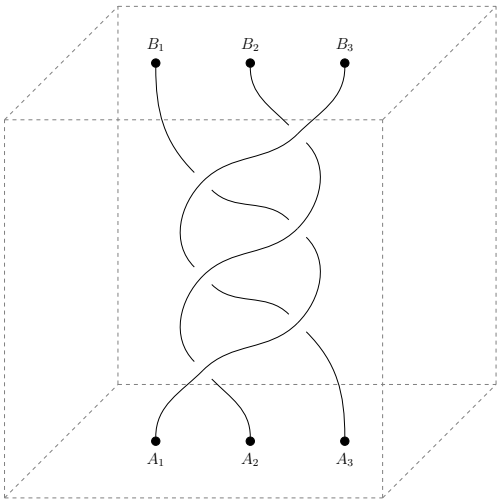


Figure 2.7: The full twist in B_3

Franco and González-Meneses describe an algorithmic method to calculate centralisers in the braid groups [15]. It has been implemented and used to compute centralisers in some of the smaller braid groups including the centraliser in the examples below. Their method works by constructing a graph associated to a braid, b, such that the fundamental group of the graph maps onto $Z(b)$. The generating set of the fundamental group will then map onto the generators of $Z(b)$.

Example 2.2.1.

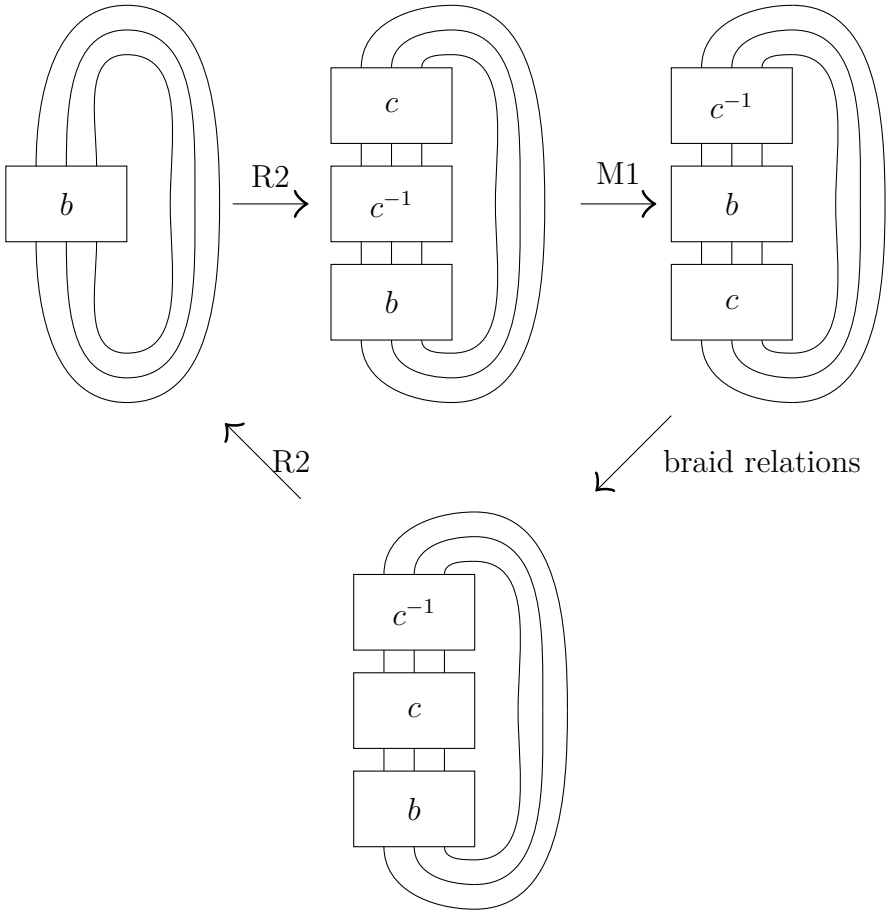
$$Z(\sigma_1^6 \in B_4) = \langle \sigma_1, \sigma_3, \sigma_2\sigma_1^2\sigma_2 \rangle$$

The full twist, $\sigma_1\sigma_2\sigma_3\sigma_1\sigma_2\sigma_1^2\sigma_2\sigma_3\sigma_1\sigma_2\sigma_1$, and σ_1^6 can both be generated by a composition of the above three generators.

We can use the elements of the centraliser to find an isotopy from $Tr(b)$ to itself.

Definition 2.2.1. Given a braid, b, and an element of its centraliser, c, the map $\zeta(c) : Z(b) \to Isotopy(Tr(b))$ is shown in the following diagram[1]:

[1]Note: The diagram shown is a *movie* of the isotopy. These are described in chapter 6



That is, we take the trace of the braid, b, and, through a sequence of Reidemeister 2 moves, we introduce c and its inverse so that we now have $Tr(cc^{-1}b)$. Pulling the centraliser around the braid through a Markov 1 move, we obtain $Tr(c^{-1}bc)$. The elements c and b commute so using the braid relations, we obtain $Tr(c^{-1}cb)$ which we can return to $Tr(b)$ through another sequence of Reidemeister 1 moves. In §2.3 we prove that there is a unique isotopy between bc and cb in the braid group so this map is well defined. The isotopy, ζ, is not necessarily isotopic to the identity. This will become important later on when we look at the Khovanov Homology.

Lemma 2.2.2. Applying this map to the full twist, $\zeta(\Delta)$, rotates the braid by 2π around the core of the braid closure.

Proof sketch. We can imagine the first part of the map, $Tr(b) \mapsto Tr(\Delta\Delta^{-1}b)$ as taking the strands just above b and twisting them in opposite directions to get $Tr(\Delta\Delta^{-1}b)$. To perform the Markov 1 move, we drag Δ around the closure of the braid. This equates to rotating every strand in the closure by 2π. The map $Tr(\Delta^{-1}b\Delta) \mapsto Tr(\Delta^{-1}\Delta b)$ is also just a rotation of b by 2π and then we rotate

the last remaining stretch of the trace closure to cancel out Δ^{-1} leaving us with just $Tr(b)$. Hence, we have rotated the whole link by 2π. □

In §6.3 we show that, when b is the identity, $\zeta(\Delta)$ is nontrivial.

2.3 Isotopies on braids

Isotopies of braids are defined in the same way as isotopies of links with the caveat that the end points remain fixed. We need to show that when two braid words, w_1 and w_2 are equal in the braid group, there is a unique (up to higher isotopy) isotopy between them. We relied on this for $w_1 = bc$ and $w_2 = cb$ in the previous section.

To investigate, we need to clarify what it means for two isotopies to not be distinct. That is, we need to define how two isotopies can be isotopic.

Definition 2.3.1. An **n-isotopy** is a family of isotopies $\varphi_u : \sqcup S^1 \times [0,1]^{n-1} \to \mathbb{R}^3,\ u \in [0,1]$ such that the associated map $M : \sqcup S^1 \times [0,1]^{n-1} \times [0,1] \to \mathbb{R}^3$ given by $M(x, t_1, ..., t_{n-1}, u) = \varphi_u(x, t_1, ..., t_{n-1})$ is smooth.

More specifically for our purposes:

Definition 2.3.2. Two isotopies $\varphi_0, \varphi_1 : \sqcup S^1 \times [0,1] \to \mathbb{R}^3$ are **2-isotopic** if there exists a 2-isotopy $\psi : \sqcup S^1 \times [0,1] \times [0,1] \to \mathbb{R}^3$ such that $\psi(x,t,0) = \varphi_0(x,t)$ and $\psi(x,t,1) = \varphi_1(x,t)$

An isotopy between two braids is unique if it is isotopic to every other isotopy between those braids.

Theorem 2.3.1. If two braids, b_1, b_2, are isotopic, then the isotopy between them is unique up to a 2nd order isotopy.

Before we get to the proof of this theorem, we need a closer look at the structure of the braid group and a little more background in topology.

Firstly, we introduce the term homotopy.

Definition 2.3.3. A homotopy is a family of maps $f_t : \sqcup X \to Y,\ t \in [0,1]$ such that the associated map $F : \sqcup X \times [0,1] \to Y$ given by $F(x,t) = f_t(x)$ is continuous.

The definition of a homotopy is very similar to an isotopy, the difference being that the associated map is continuous rather than smooth. Hence, isotopy is a stronger statement than homotopy.

Definition 2.3.4. A **covering space** of a space X is a space $\tilde{X}$ with a map $p : \tilde{X} \to X$ such that there is an open cover $\{U_\alpha\}$ of X and that, for every α, $p^{-1}(U_\alpha)$ is a disjoint union of open sets in $\tilde{X}$ and each of these open sets is mapped homeomorphically onto U_α by p. The map p is called a **covering map**.

We have two facts about covering spaces that we will soon need.

Lemma 2.3.2 (Homotopy lifting property)**.** Given a covering space, $p : \tilde{X} \to X$, a homotopy $f_t : Y \to X$ and a map $\tilde{f}_0 : Y \to \tilde{X}$ lifting f_0, we can find a unique homotopy $\tilde{f}_t : Y \to \tilde{X}$ of $\tilde{f}_0$ that lifts f_t.

Lemma 2.3.3. A covering map $p : (\tilde{X}, \tilde{x}_0) \to (X, x_0)$ induces isomorphisms $p_* : \pi_n(\tilde{X}, \tilde{x}_0) \to \pi_n(X, x_0)$ for all $n \geq 2$.

Proof sketch. Following the proof in Hatcher [20], we find that the surjectivity of p_* is given by the fact that every map $(S^n, s_0) \to (X, x_0)$ where $n \geq 2$ lifts to $(\tilde{X}, \tilde{x}_0)$ and that the injectivity is a consequence of the homotopy lifting property. □

Definition 2.3.5. A **fibration** is a map $p : E \to B$ with the homotopy lifting property with respect to all spaces X. This means that for every map $h : X \times [0, 1] \to B$ and lift $f_0 : X \to E$ such that $p(f_0(x)) = h(x, 0)$, there exists a lift of all of h to E denoted $\tilde{h} : X \times [0, 1] \to E$ where $p(\tilde{h}) = h$ and $\tilde{h}(-, 0) = f_0$.

Definition 2.3.6. A **fibre** of the space X given a map $f : X \to Y$ is a subspace $U \in X$ corresponding to the preimage of a point $y \in Y$.

Definition 2.3.7. Given a topological space X and a positive integer k, we define

$$F(X, k) = \{(x_1, ..., x_k) \in X^k : x_i \neq x_j \text{ when } i \neq j\}$$

to be the k**-configuration space** of X.

Each element of the k-configuration space of X is a set of k distinct, ordered points in X. The symmetric group on k letters, Σ_k acts freely on $F(X, k)$ by permuting the k points. This means that we can quotient $F(X, k)$ by Σ_k to get the unordered k-configuration space of X. That is

$$SF(X, k) = F(X, k)/\Sigma_k.$$

This quotient map, $p : F(X,k) \to SF(X,k)$ is a covering map. We can see this by setting $\{U_\alpha\}$ in our definition to be a set of open neighbourhoods around each of the k distinct, unordered points that make up each element of $SF(X,k)$.

Definition 2.3.8. Given a space X, the map

$$p_k : F(X,k) \to F(X,1)$$

is the projection onto the first point of configuration space.

The following theorem by Fadell and Neuwirth [13] is one of the fundamental theorems of k-configuration spaces.

Theorem 2.3.4. The projection $p : F(\mathbb{R}^2,k) \to F(\mathbb{R}^2,1)$ is a fibration with fibre $F(\mathbb{R}^2,k-1)$.

Definition 2.3.9. Let G be a discrete group and $n \geq 1$. A topological space X is an **Eilenberg-MacLane space**, $K(G,n)$, if all homotopy groups $\pi_k(X)$ are trivial except for $\pi_n(X)$ and $\pi_n(X)$ is isomorphic to G.

This leads us to the following theorem:

Theorem 2.3.5. The k-configuration space $F(\mathbb{R}^2,k)$ is a $K(G,1)$ space.

Cohen and Pakianathan give an inductive proof of this claim in [12]. Further, they prove that $F(\mathbb{R}^2,k)$ is actually a $K(PB_k,1)$ space where PB_k is the pure Âğbraid group — the group of braids that do not permute their endpoints so that, in the previous description of the braid group, the curve from each A_i terminates at B_i. In other words, $\pi_1(F(\mathbb{R}^2,k)) = PB_k$. There is a one-to-one correspondence between homotopy classes of paths in $F(\mathbb{R}^2,k)$ starting and ending at some fixed point $x = (x_1,...,x_k) \in F(\mathbb{R}^2,k)$ and pure braids based at x. (This means $(x_1,...,x_k) = (A_1,...,A_k)$). This makes 2-disks in $F(\mathbb{R}^2,k)$ the equivalent of isotopies between braids and 3-disks the 2-isotopies of braids.

Given that $F(\mathbb{R}^2,k)$ is a $K(PB_k,1)$ space and $p : F(X,k) \to SF(X,k)$ is a covering map, the homotopy groups $\pi_k(SF(\mathbb{R}^2,k))$ are trivial. This means that $SF(\mathbb{R}^2,k)$ is also a $K(G,1)$ space, possibly for a different G. More specifically, $p : F(X,k) \to SF(X,k)$ is a quotient map that removes the order of the points so in this case G is PB_k with the order on the endpoints removed. This gives us the braid group, B_k. Hence, $SF(\mathbb{R}^2,k)$ is a $K(B_k,1)$ space.

Proof sketch that $\pi_1(SF(\mathbb{R}^2, k))$ *is* B_k. $F(\mathbb{R}^2, k)$ is a covering space of $SF(\mathbb{R}^2, k)$. Hence, its fundamental group $\pi_1(F(\mathbb{R}^2, k))$ is a subgroup of $\pi_1(SF(\mathbb{R}^2, k))$. Fixing $x = (x_1, ..., x_k) \in F(\mathbb{R}^2, k)$, let us identify elements of $\pi_1(SF(\mathbb{R}^2, k))$ with homotopy classes of paths in $F(\mathbb{R}^2, k)$ which start at x. If we use the same correspondence as that between loops in $F(\mathbb{R}^2, k)$ and the pure braids, we find that these homotopy classes have a one-to-one correspondence with braids based at x. □

Proof of Theorem 2.3.1. Given that $SF(\mathbb{R}^2, k)$ is a $K(B_k, 1)$ space, there is a one-to-one correspondence between the elements of $\pi_1(SF(\mathbb{R}^2, k), x)$ and the braids based at x. Following from this, there is a on-to-one correspondence between the elements of $\pi_2(SF(\mathbb{R}^2, k), x)$ and the isotopies between braids based at x. Given that $\pi_2(SF(\mathbb{R}^2, k))$ is trivial, any two isotopies, ϕ_1, ϕ_2 between two braids b_1, b_2 must be 2-isotopic. Hence any isotopy between two braids is unique up to 2-isotopy. □

Chapter 3

Alexander's Theorem

Alexander's Theorem [1] tells us of the close relationship between knots and braids.

Theorem 3.0.6 (Alexander's theorem)**.** Every link is isotopic to the trace closure of a braid.

There are many ways of proving Alexander's Theorem. This chapter gives an algorithmic proof that particularly lends itself to computation and provides an explicit method of calculating a braid whose trace closure is the original knot or link. In 1987, Yamada published an alternative proof of Alexander's theorem. His motivation was to develop a method of finding the braid representative of a link that keeps both the writhe and the number of Seifert circles (described later in this chapter) invariant. This method was later refined and simplified by Vogel to make it easier to program into a computer.

Before we get into the proof, we first need to clarify a few terms.

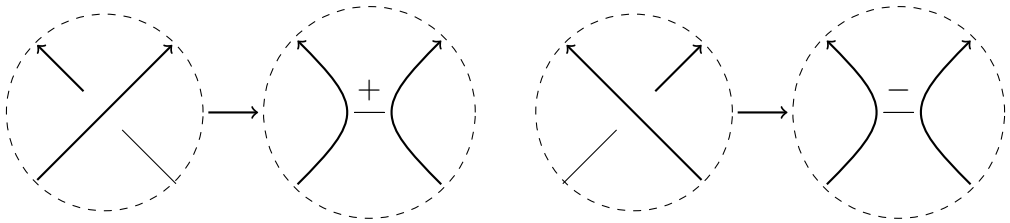
3.1 Seifert Surfaces

In the 1930's Pontrjagin and Frankl [16] devised the following theorem:

Theorem 3.1.1. Given an oriented link, L, in $\mathbb{R}^3$, there exists an orientable, connected surface, F, with boundary L. We call such a surface a **Seifert surface**.

Seifert's algorithm to find one of these surfaces is also a very nice proof of the theorem.

Proof. To find a Seifert surface for a link, L, we first need to find a link diagram, D. We replace every crossing with an oriented smoothing. This decomposes D into a collection of simple closed curves, **Seifert curves**, so that we now have a link diagram of one or more copies of the unknot. To avoid losing the crossing information, we place a band at every smoothing and label it with the type of crossing it is replacing.



We now have what is referred to as a **Seifert diagram**.

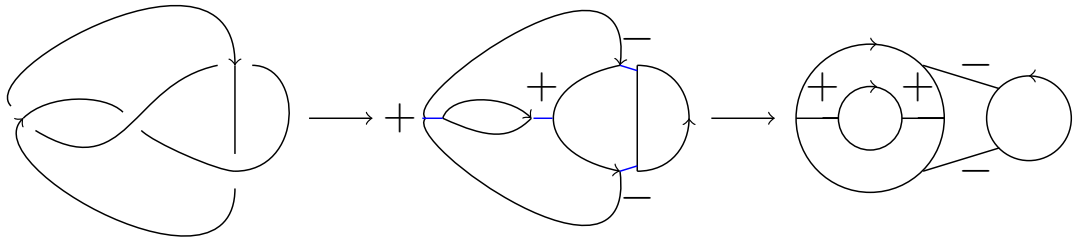
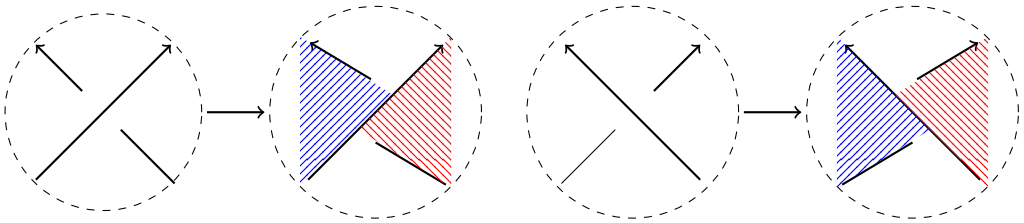


Figure 3.1: An example of applying the Seifert algorithm to the figure eight knot.

We construct the Seifert surface in several steps. First, some of the circles may be nested. If this is the case, we raise the circles in $\mathbb{R}^2 \times [0, 1]$ so that the disks they bound are entirely disjoint. Next, we replace each of the circles with these disks.

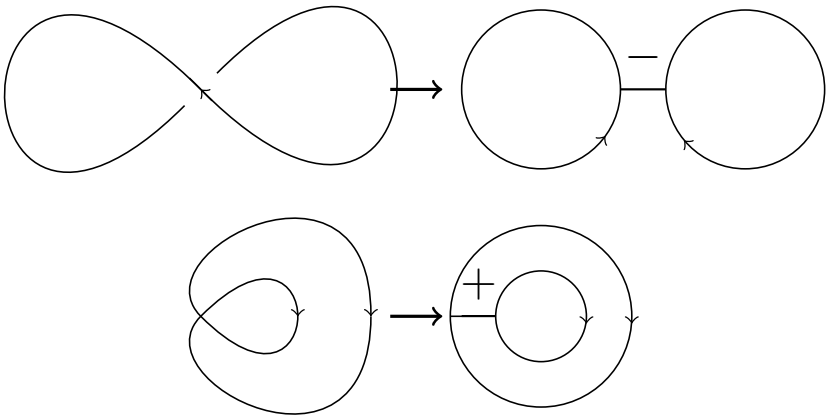
Moving on to the bands, we replace each with a twisted square. The orientation of the twist will depend on the type of crossing the band represents. A negative crossing will be replaced with a negative twist and a positive crossing with a positive one as depicted below.



These twisted squares attach to the disks at the points the bands intersect. The resulting surface is connected, orientable and has boundary isotopic to L. The orientation is induced by the orientation of L. □

It is important to note that there is not a unique Seifert surface for every link and an isotopy between links does not imply an isotopy exists between their Seifert surfaces. In fact, we do not even get a unique surface by following the above algorithm. Apart from the effect of the initial choice of link diagram, changing the relative heights of any nested circles can result in a different surface at the output. Additionally, we can change the genus of any Seifert surface without affecting its boundary. The minimum genus of a Seifert surface of a link is a link invariant. Methods of calculating this minimum genus for links are beyond the scope of this thesis but for more information, Murasugi's book [27] is a good reference.

Notice that since each band represents a crossing, any adjacent circles connected by a band will have opposite orientations while any nested circles connected by a band will have the same orientation.



3.2 The Yamada-Vogel Algorithm

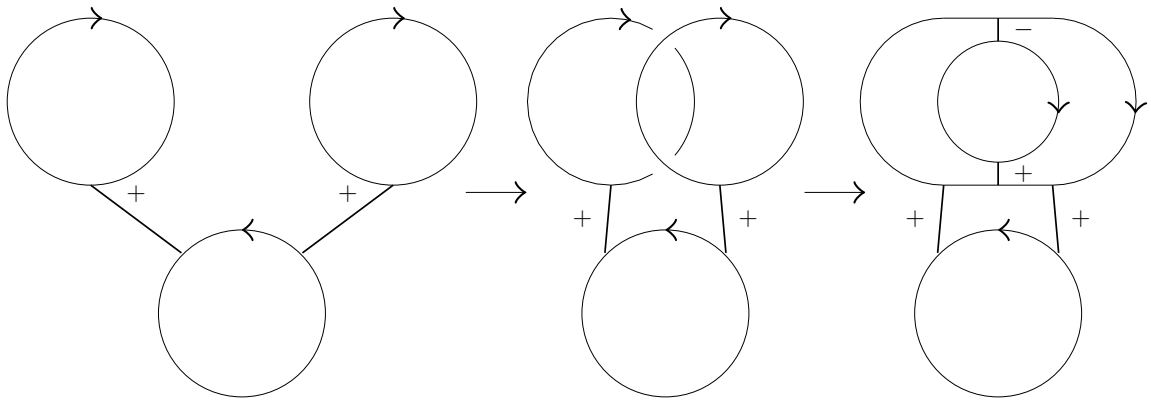
The following is the simpler, algorithmic proof of Alexander's Theorem developed by Yamada and Vogel [30, 29].

To find a braid for any knot or link, we take the planar diagram of a link and rewrite it as a Seifert diagram using Seifert's algorithm in S^2. We can then apply the Yamada-Vogel algorithm to the Seifert diagram to get the braid.

The Yamada-Vogel algorithm works by finding what are called reducing arcs between two circles of the same orientation and then combining these into one circle with a nested circle inside. We will call this a **reducing move**. Every time this is done, the number of 'incoherent circles' is reduced.

Definition 3.2.1. A **reducing arc** is an arc that connects two circles of the same orientation and does not intersect the diagram except at its end points.

Definition 3.2.2. A **reducing move** is an operation on a Seifert diagram that is equivalent to performing a Reidemeister 2 move on the corresponding link diagram. Two circles connected by a reducing arc are shifted so that they overlap each other. The Seifert algorithm is then applied to the two new crossings and two nested circles are created as in the following diagram.



Definition 3.2.3. A pair of Seifert circles are **incoherent** if they are unnested with respect to each other and have the same orientation or if one is nested within the other but they have different orientations.

Definition 3.2.4. Given a Seifert diagram, D, the **height**, $h(D)$, is the number of pairs of incoherent circles in the diagram.

Note that the Seifert diagram of the closure of a braid will always have height 0 as all Seifert circles will have the same orientation and will already be nested.

Lemma 3.2.1. Given a Seifert diagram, D, if $h(D) > 0$, we can perform a reducing move on it.

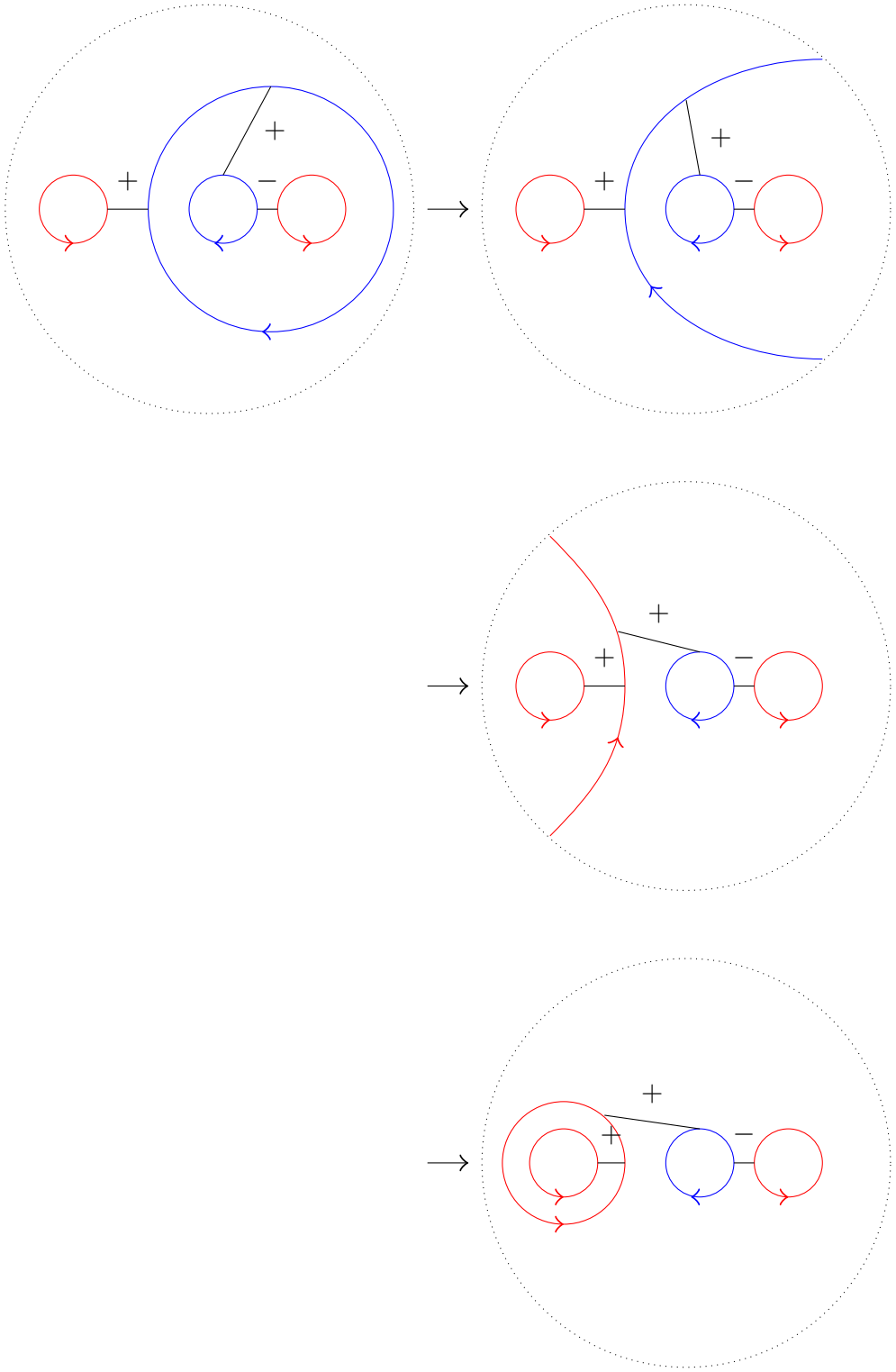
Proof. Given a diagram, D, in S^2, if $h(D) > 0$, there is at least one pair of incoherent circles in the diagram. Choosing one of these circles, c_1, there are two possibilities:

1. There is a circle, c_2, in the same nesting as c_1 that is incoherent to c_1. That is, c_1 and c_2 share the same orientation and are both unnested or nested in the same circle.

2. There is a circle, c_2, that is nested within c_1 but has a different orientation.

In the first case, we can find a reducing arc between c_1 and either c_2 or another circle of the same orientation. We can reach every circle in the same nesting as c_1 by finding a path along bands and around circles. The circle after every second band will have the same orientation as c_1. Hence, if we trace a path along a band, b_1, from c_1 to an intermediate circle, c_i, and then along a band adjacent to b_1 on c_i, we will reach a circle, c, with the same orientation as c_1. We can then perform a reducing move along the reducing arc that connects c_1 and c.

In the second case, we first ensure that there are no pairs of unnested incoherent circles. This means that there can only be, at most, two unnested circles in our diagram. We take the containing circle of the outermost incoherent pair and any circles it is nested in. Stretching these around the sphere, we can invert them so that the other stack of circle is now nested within them. Inverting the circles changes their orientation so that we now have an incoherent pair of unnested circles and we can reduce these as above.



□

Thus, we can reduce the height of any Seifert diagram to 0. If $h(D) = 0$, then we have either one or two stacks of nested circles. We can ensure that we are left with just one stack of nested circles using the method described in Case 2 above.

Reverting all the bands back to crossings, we have an oriented link whose strands orbit in the same direction around a single point. This means that we can cut the strands along some radial, stretch out the link and obtain a braid. In this manner, we can find a braid representative for any link.

3.3 Implementation

I have implemented this proof in Mathematica; the notebook is available at https://tqft.net/web/research/hilaryhunt. To use this implementation, you must have the KnotTheory‘ package, which is available at http://katlas.org/wiki/The_Mathematica_Package_KnotTheory%60, installed. Run all cells in the notebook. The program takes links in PD notation as input and returns a braid, again in the notation used at katlas.org.

Example 3.3.1. To find a braid representative of the second eight-crossing knot listed in the Rolfsen knot table (found at [8], we can enter an input such as

```
diagramToBraid[PD[X[1, 4, 2, 5], X[5, 12, 6, 13], X[3, 11,
4, 10], X[11, 3, 12, 2], X[7, 14, 8, 15], X[9, 16, 10, 1],
X[13, 6, 14, 7], X[15, 8, 16, 9]]]
```

or simply

```
diagramToBraid[PD[Knot["8 2"]]]
```

The program will then output

```
BR[3, {1, -2, 1, -2, -2, -2, -2, -2}]
```

Indicating that $\sigma_1\sigma_2^{-1}\sigma_1\sigma_2^{-1}\sigma_2^{-1}\sigma_2^{-1}\sigma_2^{-1}\sigma_2^{-1} \in B_3$ is a braid representative of the knot.

Chapter 4

The Jones Polynomial

One of the more successful link invariants is the Jones Polynomial. The Jones polynomial is a Laurent polynomial that can be computed from an oriented link. It was originally discovered by Jones in his study of von Neumann algebras [21].

Theorem 4.0.2 ([22])**.** The Jones polynomial, $V(L)$, is a Laurent polynomial valued invariant of oriented links which satisfies the following relation:

$$\frac{1}{t}V(L_+) - tV(L_-) = \left(\sqrt{t} - \frac{1}{\sqrt{t}}\right)V(L_0)$$

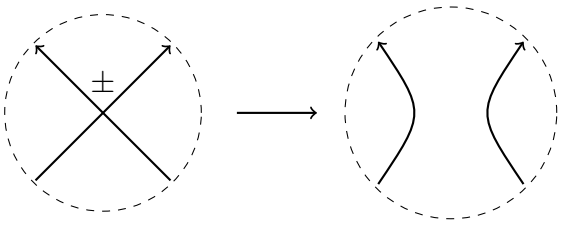
where apart from one crossing, L_+, L_- and L_0 are idential link diagrams. At this crossing, L_+ has a positive crossing, L_- has a negative crossing and L_0 has the oriented smoothing (see below) of the crossing. It is uniquely determined by

$$V(\bigcirc) = 1$$

$$V(L \cup \bigcirc) = -\left(\tfrac{1}{\sqrt{t}} + \sqrt{t}\right)V(L)$$

The uniqueness of the Jones polynomial and its invariance under isotopy are explored throughout this chapter.

Definition 4.0.1. The **oriented smoothing** of a crossing is depicted below:



To calculate the Jones polynomial of a link, we choose a crossing to label it and determine the other two new links by changing the orientation of the crossing. Rewriting the earlier equation, we get an equation of the Jones polynomial in terms of the Jones polynomial of two simpler links.

For example, the Jones polynomial of the figure eight knot can be calculated as follows:

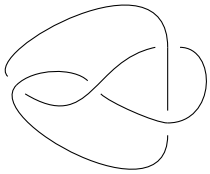
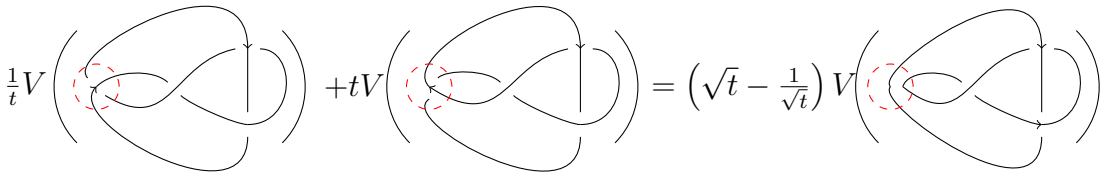
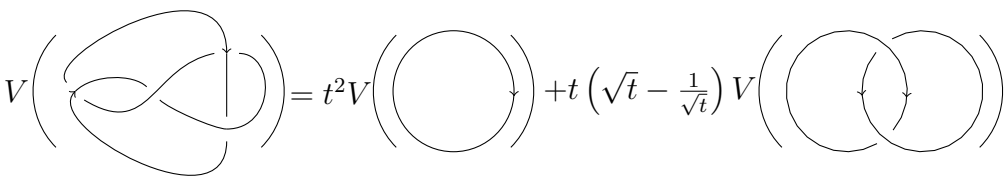
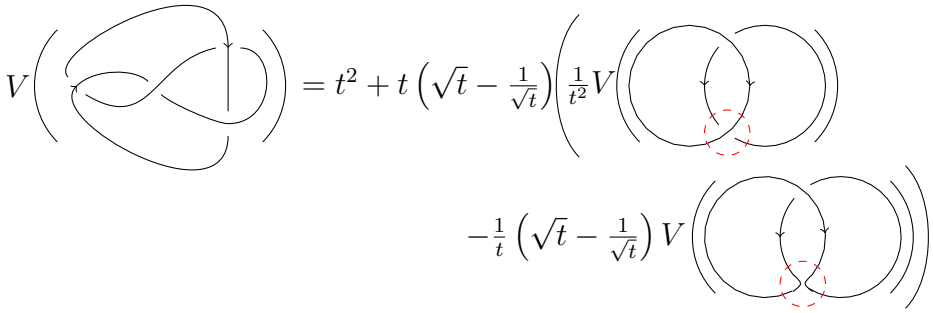


Figure 4.1: The figure eight knot



The Jones polynomial is invariant under all three Reidemeister moves. Using them, we can see that the second link is isotopic to the unknot. Similarly, the third link in the above equation is isotopic to the negative Hopf link. So we have





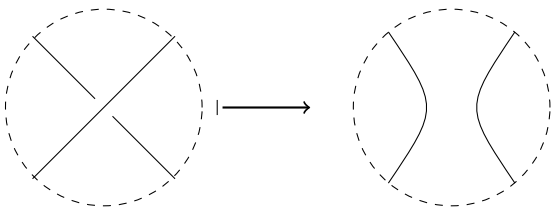
$$V(figure\ eight\ knot) = t^2 - \tfrac{1}{t}\left(\sqrt{t} - \tfrac{1}{\sqrt{t}}\right)\left(\sqrt{t} + \tfrac{1}{\sqrt{t}}\right) - \left(\sqrt{t} - \tfrac{1}{\sqrt{t}}\right)^2$$
$$= t^2 - t + 1 - \tfrac{1}{t} + \tfrac{1}{t^2}$$

While this method provides a quick way to calculate the Jones polynomial by hand, it is much harder for a computer to simplify diagrams and realise, for example, that just changing the first crossing of the figure eight knot above turns it into the unknot. Hence, when implementing a program to compute the Jones polynomial I used the algorithmic method developed by Kauffman instead [23]. This involves taking a state sum over all possible resolutions of a the link. This state sum is called the **Kauffman bracket**. The Kauffman bracket is much easier to implement and we will later be using similar methods to compute the Khovanov homology of links.

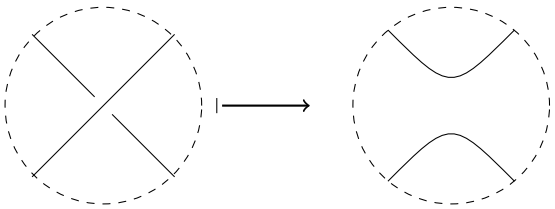
4.1 The Kauffman bracket

Soon after the discovery of the Jones polynomial, Kauffman introduced a state sum model. In doing so, he discovered another method to calculate the Jones Polynomial. It is calculated by assigning a specific weighting to each resolution of a link depending on how it was resolved.

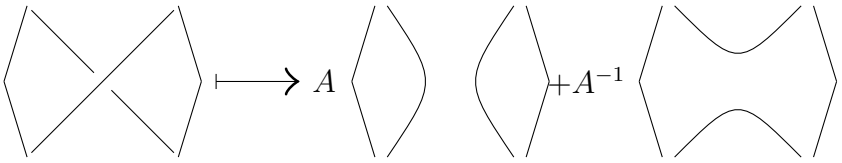
Definition 4.1.1. The **0-smoothing** of a crossing, is formed by joining the overstrand with the understrand on the left when heading towards the crossing.



Definition 4.1.2. The **1-smoothing** is the other resolution of the crossing.



Definition 4.1.3. Given an unoriented link diagram, D, the **Kauffman bracket**, $\langle D \rangle$, is a Laurent polynomial calculated using the following **skein relation** on the crossings:



The 0-smoothings are given the weighting A while 1-smoothings are given weighting A^{-1}.
It is uniquely determined by

$$\langle \bigcirc \rangle = 1$$

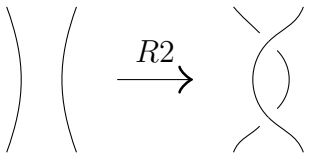
$$\langle D \cup \bigcirc \rangle = -\left(A^2 + A^{-2}\right) \langle D \rangle$$

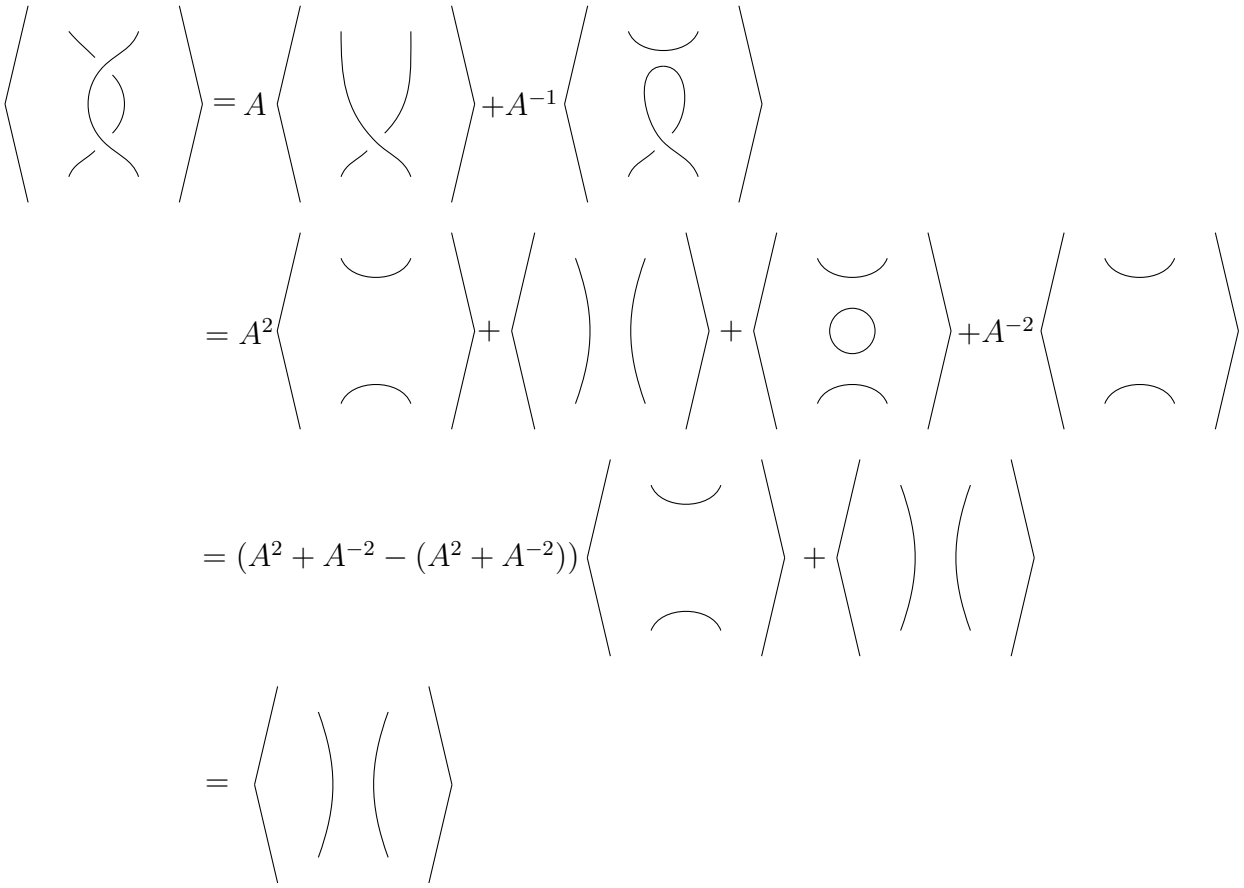
We can calculate the Kauffman bracket polynomial of a link diagram, D, by taking what is known as a **state sum** over all possible resolutions of D with the weightings given above. That is, for each resolution of D, we add $A^{2k-n}(-A^2 - A^{-2})^c$ to the polynomial where n is the number of crossings in D, k is the number of 0-smoothings and $c + 1$ is the total number of loops in the resolution. Note that since there are 2 possible resolutions for each crossing, there will be 2^n resolutions of D. This state sum constructs a unique polynomial for each link diagram. Hence, the Kauffman bracket is well defined.

Notice that the Kauffman bracket depends only on the crossings in the link diagram. Hence, it is an invariant of planar isotopies — isotopies that don't affect the crossings in a link diagram. To be a link invariant, it must also be invariant under all three Reidemeister moves.

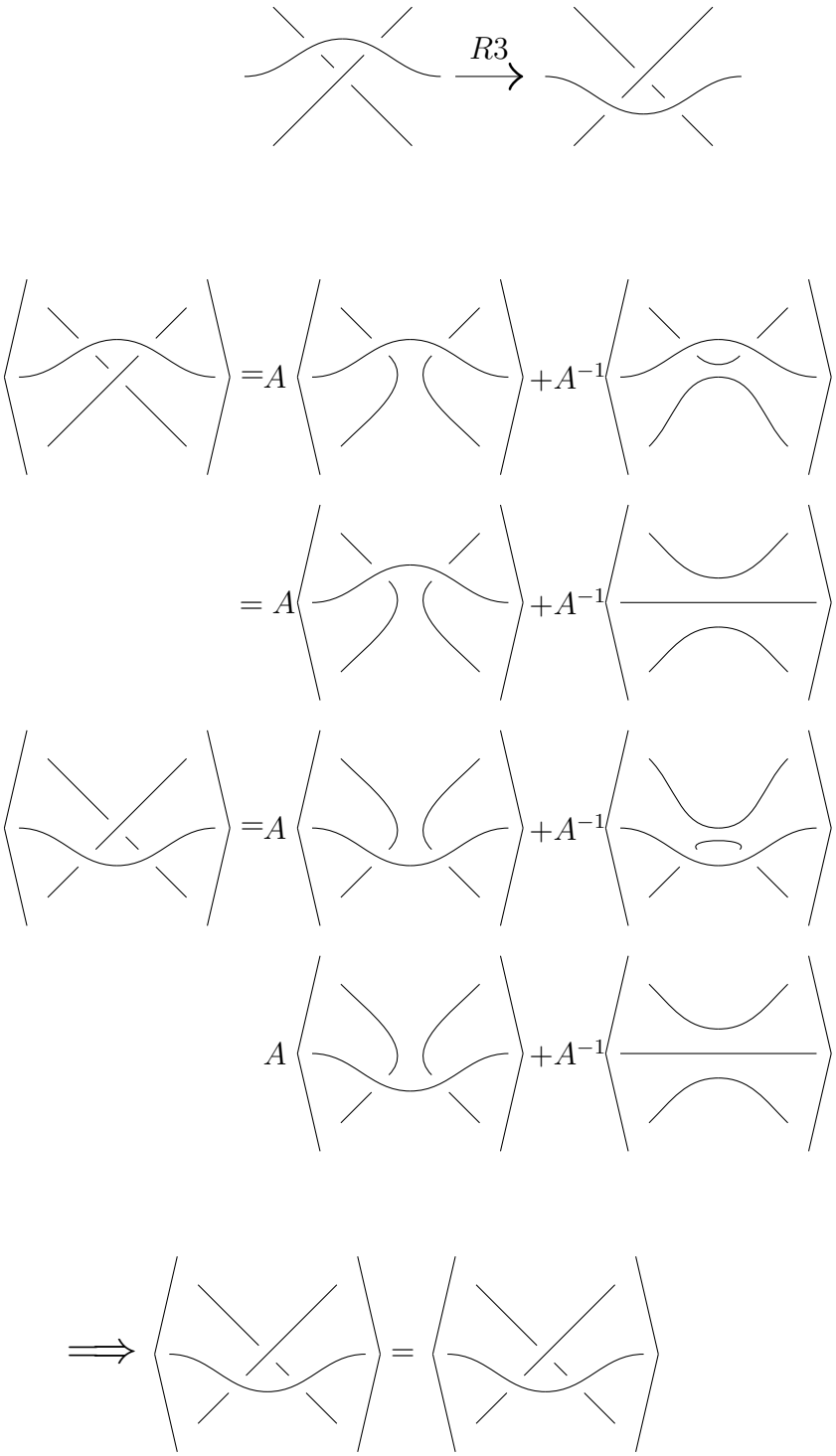
Lemma 4.1.1. The Kauffman bracket is invariant under Redemeister 2 and Reidemeister 3.

Proof. This can be seen with some short calculations:
Invariance under Reidemeister 2





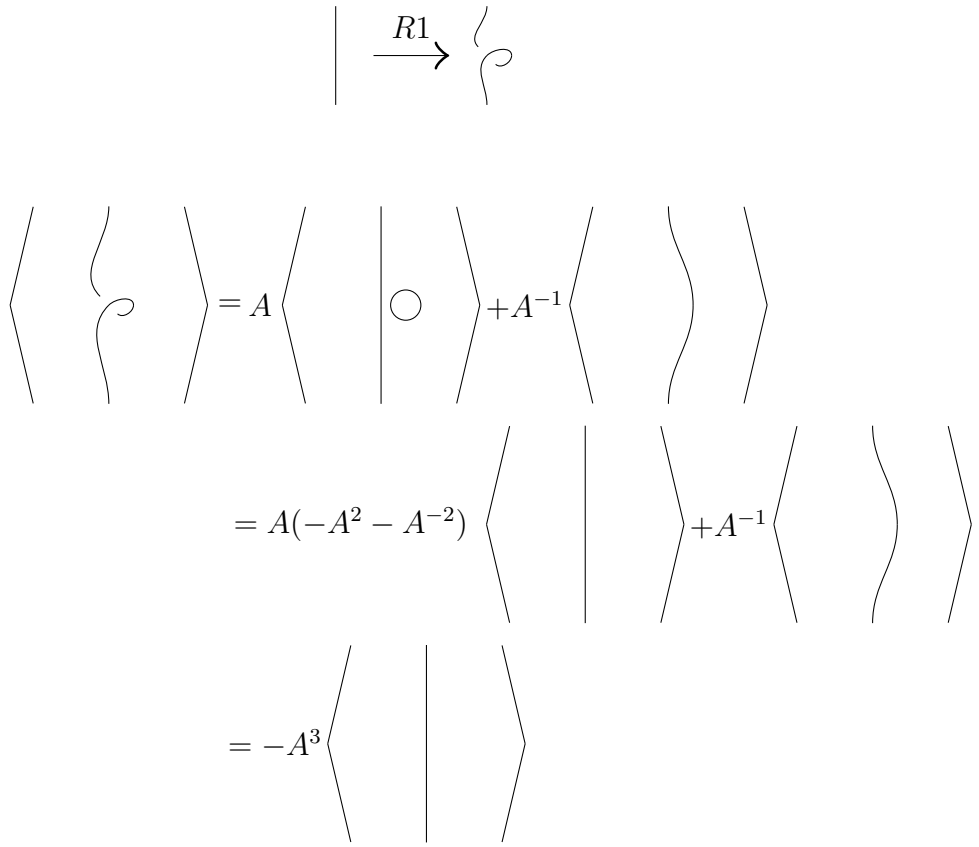
Invariance under Reidemeister 3



□

While it is invariant under Reidemeister 2 and 3, the Kauffman bracket is not invariant under Reidemeister 1. Every crossing introduced by a Reidemeister 1

move multiplies the Kauffman bracket by $-A^3$ or $-A^{-3}$ depending on the direction of the 'twist'. We can see this by applying the skein relation to the twist and removing the loop generated. An example is shown below.



4.2 From the Kauffman bracket to the Jones polynomial

To turn the Kauffman bracket into a link invariant, we need a normalisation to account for the variance under Reidemeister 1. The Kauffman bracket is not a true link invariant because it is not invariant under Reidemeister 1. To prevent this, we need to take into account what is known as the writhe of a link.

Definition 4.2.1. The **writhe** of a link diagram is the sum of the signs of each crossing.

Notice that the writhe either increases or decreases by 1 under Reidemeister 1; however, it is invariant under both Reidemeister 2 and 3. We can ensure that

the bracket polynomial is invariant under Reidemeister 1 by taking the crossing orientations into account. Hence, we have different rules for each type of crossing. It can be shown that (with a change of variable) this normalised Kauffman bracket polynomial is the Jones polynomial.

Proof sketch (We follow the proof in [19] very closely). When we increase the writhe of a link diagram, D, under Reidemeister 1, we multiply the Kauffman bracket by $-A^3$. Similarly, decreasing the writhe by 1 multiplies $\langle D \rangle$ by $-A^{-3}$. Hence, we can define a function

$$f(D) = (-A)^{-3*\text{writhe}(D)}\langle D \rangle$$

which is invariant under Reidemeister 1. As $\langle D \rangle$ is invariant under both Reidemeister 2 and 3, it follows, that $f(D)$ is invariant under all three Reidemeister moves.
Let $D!$ be the mirror image of D. Then we find that

$$f(D) = f(D!).$$

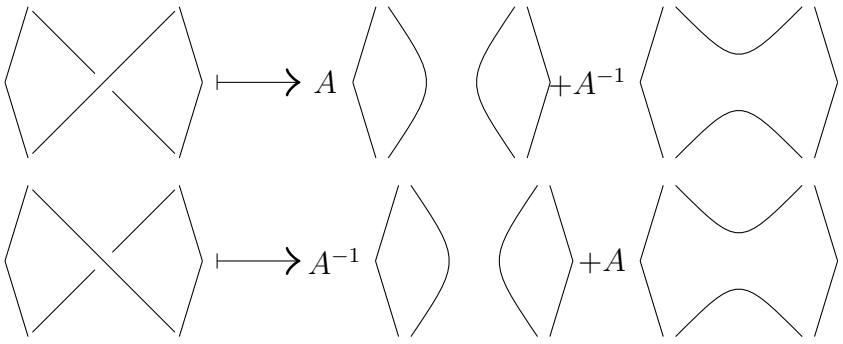
Recall that the equation of the Jones polynomial is given by

$$\frac{1}{t}V(L_+) - tV(L_-) = \left(\sqrt{t} - \frac{1}{\sqrt{t}}\right) V(L_0)$$

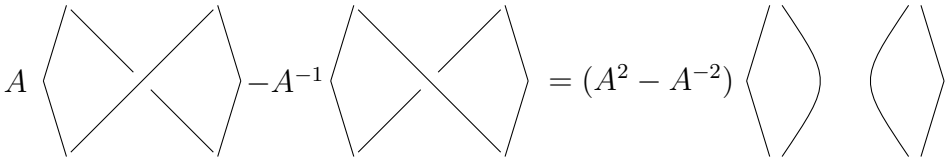
and

$$V(\bigcirc) = 1$$

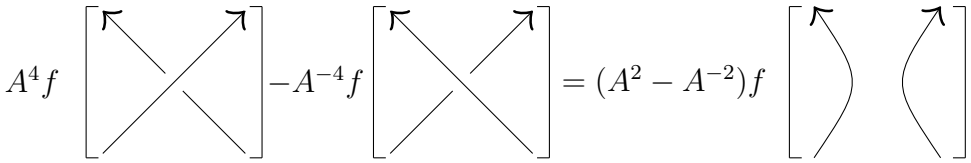
A positive crossing is the mirror image of a negative crossing and we have:



Hence, we find that:

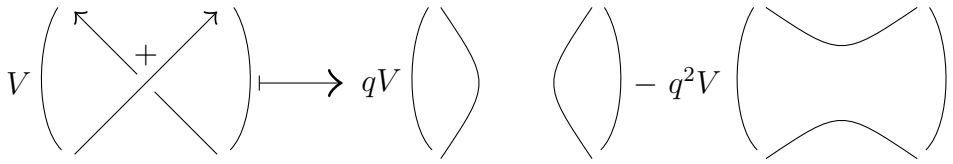


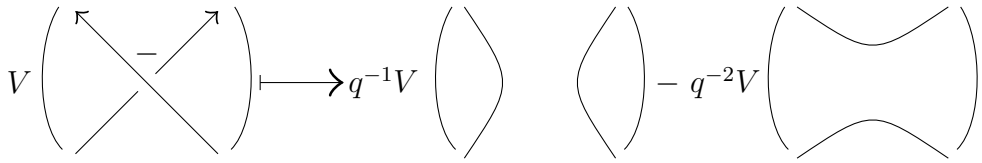
Orienting the crossings and normalising according to the writhes, we find:



With a change of variable, $A^{-4} = t$, this is the equation of the Jones polynomial. □

Definition 4.2.2. The Jones polynomial of a link can be calculated using the following skein relation on any of its link diagrams, D:





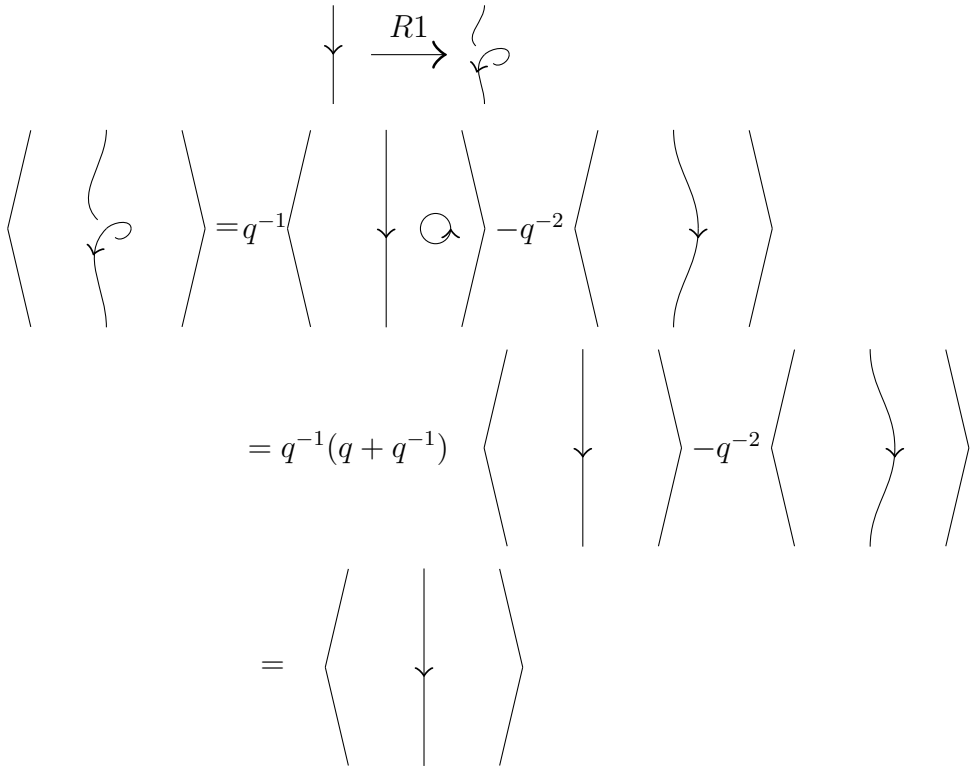
It is uniquely determined by:

$$V(\bigcirc) = 1$$

$$V(D \cup \bigcirc) = -(q + q^{-1})\, V(D)$$

In this definition, we have changed variables again both to distinguish between the Kauffman polynomial and this new formulation of the Jones polynomial and also as this is the form we will see in when we get to the Khovanov homology. For reference, $q = t^2$ where t was our original variable.

A few short calculations show that this formulation is invariant under Reidemeister 1. Below is an example when introducing a negative crossing:



As the Jones polynomial can be calculated by taking a state sum and is invariant under the Reidemeister moves, we can conclude that, up to isotopy, it assigns a unique polynomial to each link.

Chapter 5

Movie presentations of isotopies

5.1 Definitions

In order to get a better picture of the action of the isotopy of a link, we can draw the isotopy in stages; as a sequence of planar diagrams showing the gradual deformation of the link using the same projection. These stages, called **stills**, differ by a Reidemeister move or a planar isotopy. We call the maps between stills **elementary moves**.

Definition 5.1.1. The sequence of stills and elementary moves between them is called a **movie**.

Every movie represents an isotopy that is well-defined up to 2nd order isotopy. This isotopy is isotopic to the composition of elementary moves in the movie. We can use movies to show how isotopies between two different links might differ. We can also think of isotopies of links as surfaces in 4-space where the 4th dimension is time. Each of the stills in a movie is the projection onto $\mathbb{R}^2$ of a slice of this surface at a particular point in time. As with the planar projections of links, it is not always possible to project an isotopy so that each still is a regular projection of the link in each time slice. However, as with finding a regular projection, it is always possible to perturb the surface slightly so that we can depict a 2-isotopic isotopy in a movie. We have the following theorem:

Theorem 5.1.1. For every isotopy, M, between links, we can find a movie which represents M.

The proof of this theorem can be found in [11].

5.2 Carter-Saito Theorem

One question we might ask about isotopies is, given two different isotopies (with different movies), ϕ and ψ, between the same links, are ϕ and ψ themselves 2-isotopic? What is the difference if they are not? In 1993, Carter and Saito came up with the movie equivalent of Reidemeister moves. They called these **movie moves** and proved the following theorem.

Theorem 5.2.1. Two movies are isotopic if and only if they are related by a sequence of movie moves. These movie moves are listed in Figure 5.1.

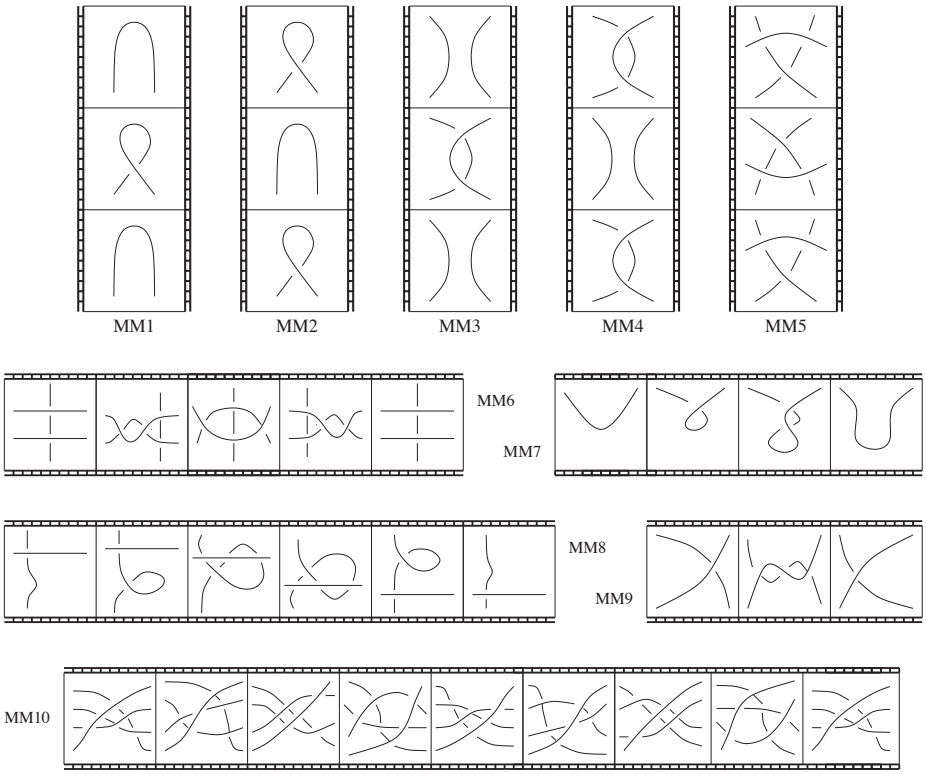


Figure 5.1: These diagrams are reproduced with permission from [6]

Finding an isotopy between movies is equivalent to finding an isotopy of isotopies. That is, we take two isotopies, $\phi_1 : \sqcup S^1 \times I \to \mathbb{R}^3$ and $\phi_2 : \sqcup S^1 \times I \to \mathbb{R}^3$, from the link $L_1 : \sqcup S^1 \to \mathbb{R}^3$ to $L_2 : \sqcup S^1 \to \mathbb{R}^3$ and find an isotopy $\psi : \sqcup S^1 \times I \times I \to \mathbb{R}^3$ from ϕ_1 to ϕ_2. [draw square picture]

5.3 Flying rings and distinct 2-isotopies

In light of Theorem 2.3.1, that isotopic braids are uniquely 2-isotopic up to 3-isotopy, one might wonder how to see that there are link isotopies which are not 2-isotopic. To do this, we will look at one of the simplest examples, the configuration space of n flying rings, otherwise known as the group of isotopies of the trivial link with n components.

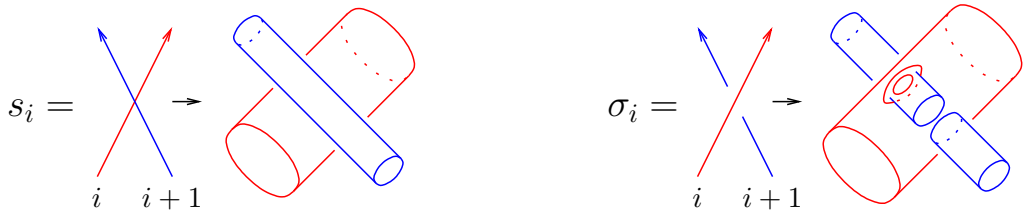
In their paper on the configuration spaces of rings and wickets [10], Brendle and Hatcher prove both that these two group have the same homotopy type and that their fundamental group is the welded braid group W_n defined by Fenn, Rimanyi and Rourke [14], also known as the loop braid group [4].

The welded braid group is well understood and its generators are distinct — non-isotopic. It is defined as follows

$$W_n = \left\{ \sigma_1, ..., \sigma_{n-1}, s_1, ..., s_{n-1} \;\middle|\; \begin{array}{ll} \sigma_i\sigma_j = \sigma_j\sigma_i & |i-j|>1 \\ \sigma_i\sigma_{i+1}\sigma_i = \sigma_{i+1}\sigma_i\sigma_{i+1} & \\ s_i^2 = 1 & \\ s_i s_j = s_j s_i & |i-j|>1 \\ s_i s_{i+1} s_i = s_{i+1} s_i s_{i+1} & \\ \sigma_i s_j = s_j \sigma_i & |i-j|>1 \\ s_i s_{i+1} \sigma_i = \sigma_{i+1} s_i s_{i+1} & \\ \sigma_i \sigma_{i+1} s_i = s_{i+1} \sigma_i \sigma_{i+1} & \end{array} \right\}$$

The isotopies of the link are generated by permuting the positions of the components. There are a few ways to do this. One method is to just move them around each other so that they do not meet at all. The others involve pulling one through the center of another in the process of swapping them. For every two adjacent components, x_i, x_{i+1}, we get three isotopies — one from the first method and two from the second where pulling x_i through x_{i+1} is distinct from pulling x_{i+1} through x_i.

To see this, we imagine the group of isotopies as braided tubes in 4-space with the fourth dimension being time. Passing the rings around each other without them interacting is equivalent to the welded crossings in W_n. Pulling one ring through the other, means one tube passes through the other and is equivalent to a positive or negative crossing.[1]



We can find a representation, $\rho : W_n \to U(1)$, of W_n given by

$$\begin{aligned} \rho(s_i) &= \pm 1 \\ \rho(\sigma_i) &= q \in U(1) \end{aligned}$$

As s_i, σ_i and σ_i^{-1}, the three different types of generators of W_n, are distinct in this representation, the three isotopies switching any two flying rings must also be distinct. Hence, we have an example of non-2-isotopic isotopies of a trivial link.

[1] Diagrams in this section are reproduced with permission from [7]

Chapter 6

The Khovanov Homology

6.1 General Outline

Before getting into the mechanics of Khovanov Homology, let us first take a look at the overall picture. Khovanov discovered that we can associate a particular vector space to the resolutions of a planar diagram, and choose the differentials between each resolution so that the resulting chain complex, considered up to homotopy equivalence, is a link invariant. The big theorem in Khovanov Homology can be paraphrased as follows:

Theorem 6.1.1 ([24, 5])**.** Given two planar diagrams L_1 and L_2 differing by a Reidemeister move ϕ, Khovanov homology associates a chain complex to each diagram and a chain map to the Reidemeister move such that

1. The chain map is a homotopy equivalence and so induces an isomorphism on homology
2. The chain maps associated to each side of each movie move are homotopic up to a sign.

This leads to the following corollaries.

Corollary 6.1.2. If two planar diagrams are isotopic, they have isomorphic Khovanov homologies.

Proof. From Reidemeister's theorem, we know that all isotopies are sequences of Reidemeister moves. If each Reidemeister move is associated to a chain map that induces an isomorphosm on homology then an isotopy is associated to a composition of these chain maps. Hence all isotopies must induce an isomorphism on homology. □

Corollary 6.1.3. There is a well defined isomorphism associated to any isotopy class of isotopies on the homology.

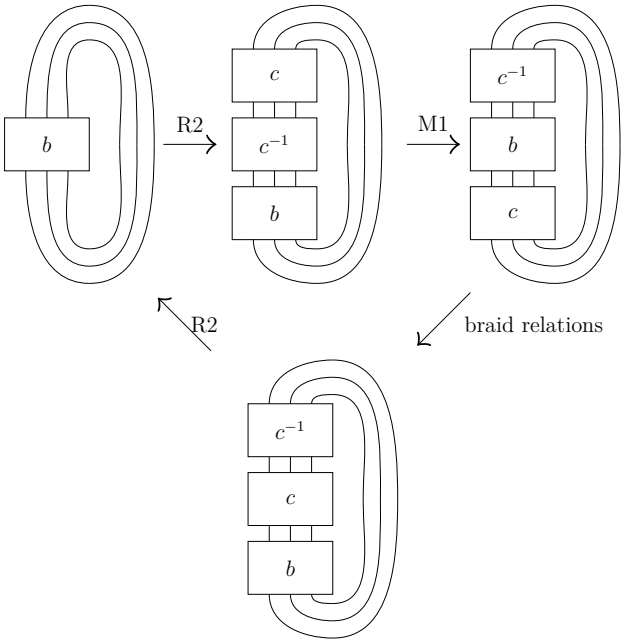
Proof. Isotopic isotopies are related by a sequence of movie moves and the chain maps associated to each side of a movie move are homotopic up to a sign. Hence, they give the same isomorphism on homology. □

Khovanov tells us how to find these isomorphisms explicitly [24].

6.2 Action of the centraliser of a braid on the Khovanov homology of its trace closure

Theorem 6.2.1. Given a braid, b, there is a representation of its centraliser, $Z(b)$, on its Khovanov homology, $Kh(Tr(b))$.

Proof. Recall the isotopy of $Tr(b)$, $\zeta(c) : Tr(b) \to Isotopy(Tr(b))$ defined in section 4.3 for an element of the centraliser, $c \in Z(b)$.



This isotopy is well-defined so the representation is given by $Kh \circ \zeta$. □

6.3 Chain Complexes and Homologies

Before we move on to how to the construction of Khovanov homology, we need to define a few more tools.

Definition 6.3.1. A **chain complex**, $\mathcal{C}$, is a sequence of homomorphisms (or **differentials**), $d_n : C_n \to C_{n-1}, d_{n-1} : C_{n-1} \to C_{n-2}, ..., d_1 : C_1 \to C_0$ between abelian groups $C_i \in \mathcal{C}$ where $i \in \mathbb{Z}$ and $d_i d_{i+1} = 0 \ \ \forall i$.

The last condition ensures that $\operatorname{im} d_{n+1} \subset \ker d_n$. For our purposes, it suffices to work with vector spaces rather than abelian groups; one can easily generalise the remarks of this section to any abelian category.

Definition 6.3.2. The nth **homology group** of a chain complex is

$$H_n(\mathcal{C}) := \frac{\ker d_n}{\operatorname{im} d_{n+1}}$$

Just as we have maps between vector spaces, we also have maps between chain complexes. These are called **chain maps**.

Definition 6.3.3. A chain map $f : V_\bullet \to W_\bullet$ consists of linear maps $f_n : V_n \to W_n$ for each n such that $df = fd$.

Lemma 6.3.1. A chain map, $f : V_\bullet \to W_\bullet$, induces a map on homology

$$\mathcal{H}(f) : H(V_\bullet) \to H(W_\bullet).$$

Proof. Let $x' \in ker(d^V)$ be a representative of $x \in H(V_\bullet)$. Using the fact that $fd = df$, we see that $f(x')$ must be in $\ker d^W$. Define $H(f)(x) := f(x') + (\operatorname{im} d^W) \in H(W_\bullet)$. If we choose a different representative of x, e.g. $x'' = x' + c$ where $c \in im\delta^V$,

$$\begin{aligned} f(x'') + (\operatorname{im} \delta^W) = &\ f(x' + c) + (\operatorname{im} \delta^W) \\ = &\ f(x') + (\operatorname{im} \delta^W) \end{aligned}$$

So $H(f)$ doesn't depend on the choice of representative and is well defined. □

Definition 6.3.4. Two chain maps, $f, g : V_\bullet \to W_\bullet$, are **homotopic** if $\exists h : V_{n+1} \to W_n$ such that $f - g = dh + hd$.

Lemma 6.3.2. If f and g are homotopic ($f \simeq g$), then $H(f)$ and $H(g)$ are equal.

Proof. Let the homotopy between f and g be $h : V_{n+1} \to W_n$ such that $f - g = dh + hd$. Let x' be a representative of $x \in H(f)$. Then $x' \in \ker d$ so $hd(x') = 0$. Clearly $dh(x') \in \operatorname{im} d^W$. Hence, we have that $(f - g)(x') = y$ where $y \in \operatorname{im} d^W$. However, we know that elements differing only by members of $\operatorname{im} d$ are representatives of the same element in the homology group. This means that $H(f)(x) = H(g)(x)$ so the two homology groups are equal. □

In another analogy to vector spaces, we can talk about the Euler characteristic of a chain complex just as we talk about the dimension of a vector space.

Definition 6.3.5. The **Euler characteristic** of a chain complex, $V_\bullet$, is

$$\chi(V_\bullet) := \sum_n (-1)^n \dim V_n$$

Note that this doesn't make sense unless we have a finite chain complex.

Lemma 6.3.3.

$$\chi(V_\bullet) = \chi(H_\bullet(V))$$

Proof. The dimension of each homology group, H_n is given by

$$\dim H_n = \dim \ker d_n - \dim \operatorname{im} d_{n-1}$$

Hence, the Euler characteristic of the homology is

$$\begin{aligned}
\chi(H(V_\bullet)) &= \textstyle\sum_n (-1)^n \dim H_n(V) \\
&= \textstyle\sum_n (-1)^n \dim H_n \\
&= \textstyle\sum_n (-1)^n (\dim \ker d_n - \dim \operatorname{im} d_{n-1}) \\
&= \textstyle\sum_n (-1)^n (\dim \ker d_n + \dim \operatorname{im} d_n) \\
&= \textstyle\sum_n (-1)^n V_n \ \text{(by the rank-nullity theorem)} \\
&= \chi(V_\bullet)
\end{aligned}$$

□

When computing Khovanov homology, we use what are known as **graded vector spaces**. A graded vector space, V, is a vector space which decomposes as a direct sum over $\mathbb{Z}$. i.e. $V = \bigoplus_{n \in \mathbb{Z}} V_n$.

An example of a graded vector space is the space of polynomials, $\mathbb{P}$. It can be broken down into a direct sum of P_n, the space of monomials of degree n. Hence, polynomials can be 'graded' by degree.

Definition 6.3.6. The **graded dimension** (or qdim) of a graded vector space is a Laurent series which is usually given in the variable q

$$\operatorname{qdim} V = \sum_n \in \mathbb{Z} q^n \dim V_n$$

Example 6.3.4. The graded dimension of the space of polynomials in x and y of degree at most two is

$$\begin{aligned} \operatorname{qdim} \mathbb{C}\{x, y, x^2, xy, y^2\} &= q^0 \dim \mathbb{C} + q^1 \dim \mathbb{C}\{x, y\} + q^2 \dim \mathbb{C}\{x^2, xy, y^2\} \\ &= 1 + 2q + 3q^2 \end{aligned}$$

Definition 6.3.7. The **graded Euler characteristic** of a chain complex, $V_\bullet$, is

$$\chi(V_\bullet) := \sum_n (-1)^n \operatorname{qdim} V_n$$

6.4 Construction

To define the Khovanov homology, we need to first build a chain complex, $KhC(L)$, from our knot diagram. Denote the number of crossings in the knot diagram as n. We start by resolving all n crossings of our link into either 0-smoothings or 1-smoothings (recall from §5.1).

As there are two options for each crossing, we end up with 2^n different possible resolutions. Drawing edges between resolutions where a 0-smoothing becomes a 1-smoothing and arranging these by the number of 1-smoothings, we end up with an n-dimensional cube where each edge connects the 0-smoothings and 1-smoothings of a single crossing. This is what we call the cube of resolutions.

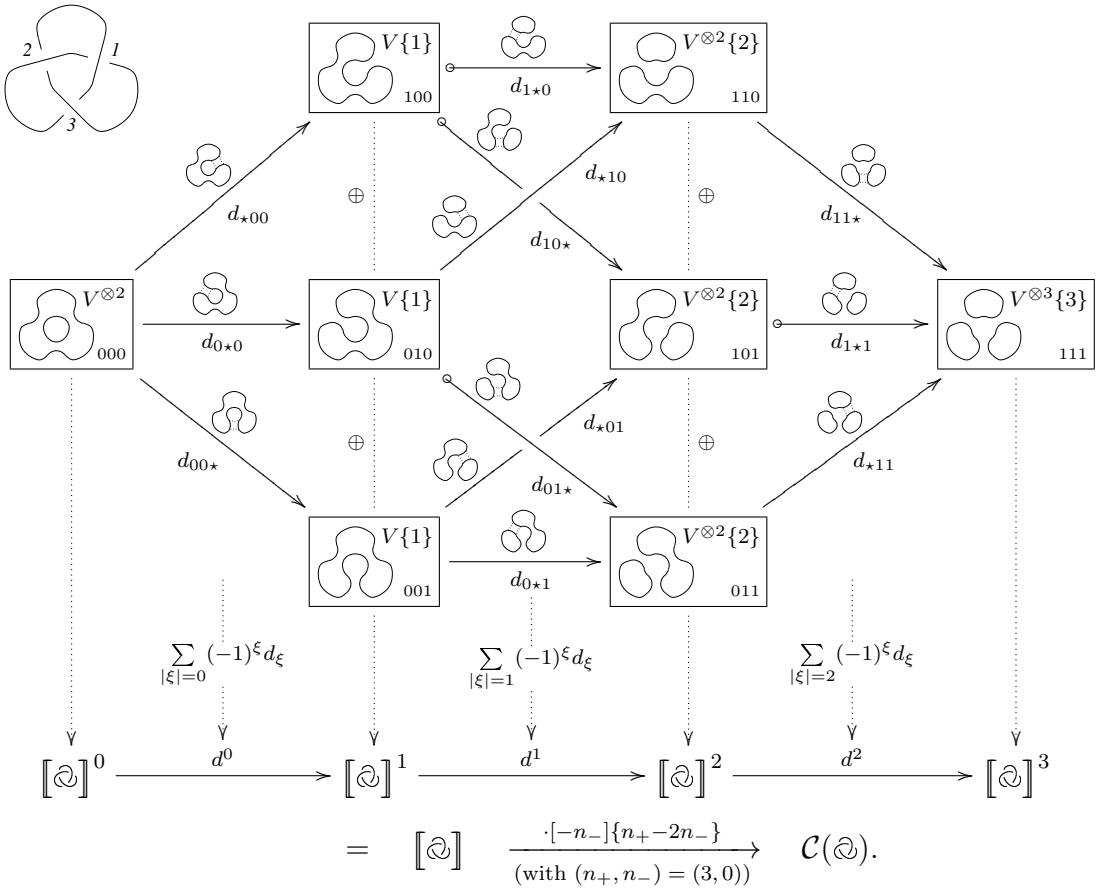


Figure 6.1: The cube of resolutions of the right-handed trefoil. Taken from [5]

Each resolution is the union of one or more disjoint unknots.

Lemma 6.4.1. If we assign each resolution of a link, L, a term of the form $(-q)^r(q+q^{-1})^k$ where r is the number of 1-smoothings in the resolution and k is the number of disjoint cycles in the smoothing, we can then sum all these terms to get the Kauffman bracket of L.

After normalisation, this is the Jones polynomial of our link.

Khovanov's idea was to categorify the Jones polynomial by replacing it with a chain complex of graded vector spaces with graded dimensions chosen so that the Euler characteristic would give the Jones polynomial. The homology of the chain complex could then be calculated and, if the differentials are chosen cleverly, this could be an invariant of the link. Khovanov found that this was indeed possible and we describe his recipe here. Let V be the vector space with basis elements v_+ and v_- whose degrees are ± 1 respectively. We assign the vector space, $V^{\otimes k}\{r\}$ to each resolution where k and r are as above. The number, r, in curly brackets

is the grading shift of the vector space. Thus $\text{qdim}(V\{r\}) = q^r\text{qdim}(V)$. Each 1-smoothing increases the grading of the vector space associated to the resolution by 1. The rth chain group, $KhC(L)$ is the direct sum of every resolution with r 1-smoothings.

If we follow any edge between two vertices of our cube, we find that either one of the loops in the tail resolution splits into two loops in the next resolution or two loops merge into one. To see this, imagine that we take a small disk just containing our smoothing (where the crossing used ot be). There are two arcs contained in this disk. Either these two arcs are part of the same cycle and so changing the smoothing splits this cycle into two or the arcs are part of different cycles and changing the smoothing merges them into one cycle. We need to define differentials from one resolution of L to another along these edges which a 0-smoothing into a 1-smoothing. To see what is happening to the vector spaces assigned to each resolution, we define the differentials on their basis vectors. These should be the identity on the tensor products associated with the unaffected cycles so we can look at just the affected loops.

In his paper [24], Khovanov defines these maps to be:

$$m : V \otimes V \to V, \quad m : \begin{cases} v_+ \otimes v_+ \mapsto v_+ \\ v_+ \otimes v_- \mapsto v_- \\ v_- \otimes v_+ \mapsto v_- \\ v_- \otimes v_- \mapsto 0 \end{cases}$$

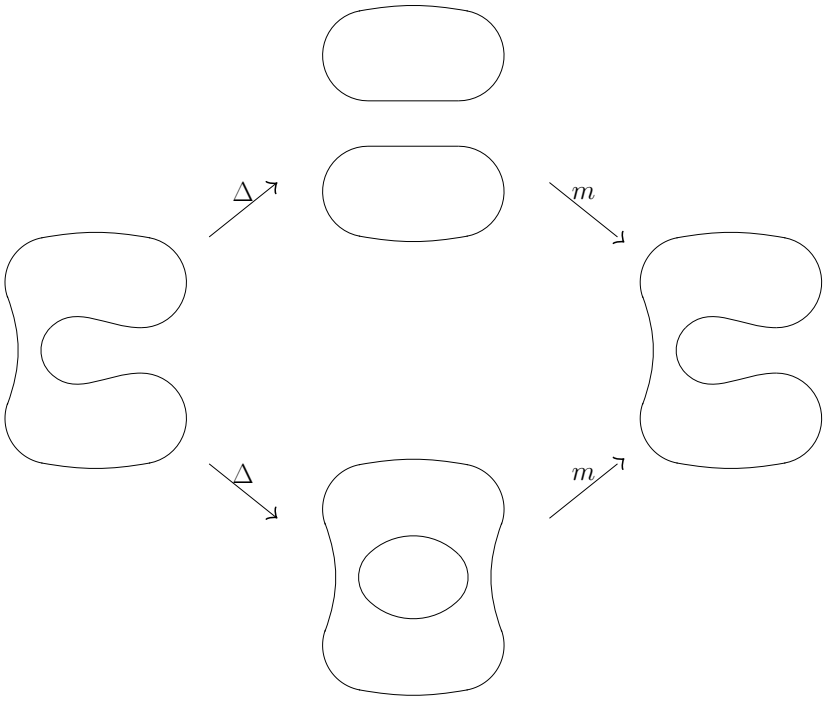
$$\Delta : V \to V \otimes V, \quad \Delta : \begin{cases} v_+ \mapsto v_+ \otimes v_- + v_+ \otimes v_- \\ v_- \mapsto v_- \otimes v_- \end{cases}$$

There are a number of factors taken into account in choosing these maps. Notice that the degree of both maps is -1. The degree of the vector space associated to each resolution is shifted up by 1 for each 1-smoothing. Hence, the degree of our differentials is 0. Additionally, there is no specific order on the loops in our resolutions so $m(v_+ \otimes v_-) = m(v_- \otimes v_+)$ and $v_+ \otimes v_-$ and $v_- \otimes v_+$ always have the same coefficients in the image of Δ. These restrictions determine the maps up to scalar factors.

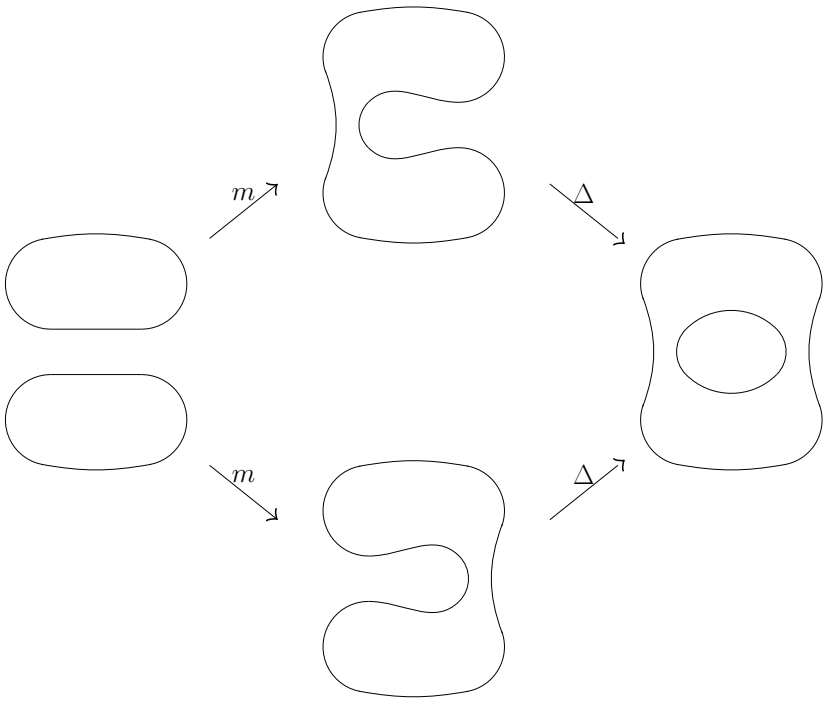
We have the additional constraints that $d \circ d = 0$ and that the differentials

chosen ensure that every face of the cube commutes. Focusing on the latter, there are several cases we must consider. If every map on a face is m or every map is Δ, showing that the face commutes is trivial. If half the maps are m and the other half Δ, we have one of the following scenarios.

- Both paths around the square give us Δm. While the order in which we change the resolution of each crossing changes, the same loops are involved in both paths so we get the same chain map. This means that the following diagram commutes.



- Both paths around the square give us $m\Delta = m\Delta$. This gives us the following diagram which also commutes.



- Lastly, we need to show that Δm and $(\mathbb{1}\otimes m)(\Delta\otimes\mathbb{1})$ give us the same result.

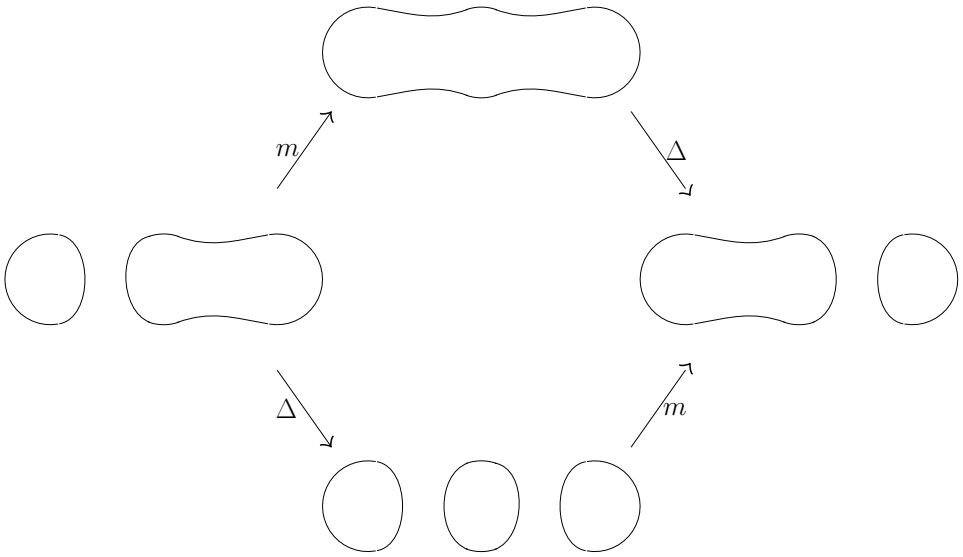
  The map Δm is given by:

$$\begin{array}{rcccc}
\Delta m : V\otimes V & \xrightarrow{m} & V & \xrightarrow{\Delta} & V\otimes V \\
v_+\otimes v_+ & \mapsto & v_+ & \mapsto & v_+\otimes v_- + v_-\otimes v_+ \\
v_+\otimes v_- & \mapsto & v_- & \mapsto & v_-\otimes v_- \\
v_-\otimes v_+ & \mapsto & v_- & \mapsto & v_-\otimes v_- \\
v_-\otimes v_- & \mapsto & 0 & \mapsto & 0
\end{array}$$

  The map $(\mathbb{1}\otimes m)(\Delta\otimes\mathbb{1})$ is given by:

$$\begin{array}{rcccc}
(\mathbb{1}\otimes m)(\Delta\otimes\mathbb{1}) : V\otimes V & \xrightarrow{\Delta} & V\otimes V\otimes V & \xrightarrow{m} & V\otimes V \\
v_+\otimes v_+ & \to & (v_+\otimes v_- + v_-\otimes v_+)\otimes v_+ & \to & v_+\otimes v_- + v_-\otimes v_+ \\
v_+\otimes v_- & \to & (v_+\otimes v_- + v_-\otimes v_+)\otimes v_- & \to & v_-\otimes v_- \\
v_-\otimes v_+ & \to & (v_-\otimes v_-)\otimes v_+ & \to & v_-\otimes v_- \\
v_-\otimes v_- & \to & v_-\otimes v_-\otimes v_- & \to & 0
\end{array}$$

  As we can see, $\Delta m = (\mathbb{1}\otimes m)(\Delta\otimes\mathbb{1})$. The relevant picture is:



The commutivity of the cube of resolutions ensures that the basis of the vector space attached to each resolution is independent of the order the 1-smoothings are introduced.

The differential, d, must satisfy $d \circ d = 0$. This will be achieved if the faces of our cube anti-commute. By choice of differential, we have ensured that all faces of the cube commute. By sprinkling in somes signs at the right points, we can force the faces to anticommute. There are various methods of calculating exactly where the 'right points' are.[[cite]] In this thesis we will stick to the method outlined in the following example.

6.5 An Example: The Trefoil

To illustrate the construction of Khoanov homology, let us look at the right-handed trefoil. We start by drawing out the cube of resolutions of the trefoil and labelling each resolution by the number of 0 and 1-smoothings. Label the edges similarly but with a $\star$ for the crossing that is being changed (See Figure 6.1). For example, we would label the edge between 001 and 101 with $\star 01$.

We assign a copy of V generated by $\{v_+, v_-\}$ to each circle in each resolution. Each resolution is assigned a graded vector space taken as the tensor product of each copy of V it contains. The homological grading of each vector space depends on which resolution it is attached to. Which grading it is in depends

on the number of 1-smoothings in its resolution. We take the direct sum of the vector spaces in each grading. This leaves us with the following vector spaces:

$$\{0\}V^{\otimes 2}$$
$$\{1\}V \oplus V \oplus V$$
$$\{2\}V^{\otimes 2} \oplus V^{\otimes 2} \oplus V^{\otimes 2}$$
$$\{3\}V^{\otimes 3}$$

Now to make a chain complex, all we need are the maps between them. To explicitly construct the differentials, we need to give an order to the cycles in each of our resolutions. We have defined the merging and splitting differentials above and we have the identity on all vectors assigned to uninvolved circles. This tells us exactly what the differentials need to be. Having calculated the dimensions of each of the vector spaces we can represent the differentials as $m \times n$ matrices where we are travelling from an n-dimensional vector space to an m-dimensional vector space.

Looking at the maps from the 0 grading to the 1 grading, both circles in the 0 grading are involved and they merge into one circle in the 1 grading. Hence, we have three copies of the merging differential. These can be written in matrix form as follows:

$$d_{\star 00} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \end{bmatrix} \quad d_{0\star 0} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \end{bmatrix} \quad d_{00\star} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \end{bmatrix}$$

With the circle order given in the diagram, think of the first column as the case where both circles are assigned the basis vector v_+, the second as the circles beign assigned the basis vectors v_+ and v_- respectively and so on. Similarly, the first row of the matrix is the case where the newly formed circle is assigned v_+ and the second row is where it is assigned v_-. As we are taking the direct sum of the three vector spaces, the resulting differential is:

$$d_0 = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \end{bmatrix}$$

Similarly, all of the edges between the 1 grading and the 2 grading are assigned the splitting differential. We assign $-$ signs to $d_{01\star}, d_{10\star}$ and $d_{1\star 0}$.

$$d_{0\star 1} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 0 \end{bmatrix} \quad d_{01\star} = \begin{bmatrix} -1 & 0 \\ 0 & -1 \\ 0 & -1 \\ 0 & 0 \end{bmatrix} \quad d_{10\star} = \begin{bmatrix} -1 & 0 \\ 0 & -1 \\ 0 & -1 \\ 0 & 0 \end{bmatrix}$$

$$d_{\star 01} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 0 \end{bmatrix} \quad d_{\star 10} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 0 \end{bmatrix} \quad d_{1\star 0} = \begin{bmatrix} -1 & 0 \\ 0 & -1 \\ 0 & -1 \\ 0 & 0 \end{bmatrix}$$

Putting all of these together is slightly trickier as we must keep in mind the order and insert 0 blocks where there is no map.

$$d_1 = \begin{bmatrix} 1 & 0 & -1 & 0 & 0 & 0 \\ 0 & 1 & 0 & -1 & 0 & 0 \\ 0 & 1 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & -1 & 0 \\ 0 & 1 & 0 & 0 & 0 & -1 \\ 0 & 1 & 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & -1 & 0 \\ 0 & 0 & 0 & 1 & 0 & -1 \\ 0 & 0 & 0 & 1 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Determining the maps between the 2 grading and the 3 grading, we need to be aware of which circle is splitting and which circles are then formed. Note especially that in $d_{11\star}$, the first circle in grading 2 splits into the first and the

third circle in grading 3.

$$d_{\star 11} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad d_{1\star 1} = \begin{bmatrix} -1 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 \\ 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad d_{11\star} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The resulting differential is:

$$d_2 = \begin{bmatrix} 1 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & -1 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Lastly, we have the map d_3 which sends everything to 0.

Finally, after determing the chain complex associated to the link, we must calculate its homology groups. While finding the image and kernel of each matrix is feasible for the trefoil and other links with only a small number of crossings, doing so and then finding the homology becomes increasingly unwieldy as the number of crossings scales up. Instead, we look at each grading individually. We have already discussed which vector spaces lie in which homological (t) grading. However, the chain complex we have built is bigraded. As mentioned above, we assign each v_+ a q-grading of 1 and each v_- a q-grading of -1. The link has 3 positive crossings but no negative crossings so we increase the q-grading of every vector space by 3. Hence, we can also break the differential matrices down into matrices for each q-grading. Let $d_{t,q}$ be the map from homological grading t and q-grading q. Then we have:

$$d_{0,1} = [0] \qquad d_{0,3} = \begin{bmatrix} 1 & 1 \\ 1 & 1 \\ 1 & 1 \end{bmatrix} \qquad d_{0,5} = \begin{bmatrix} 1 \\ 1 \\ 1 \end{bmatrix}$$

$$\ker d_{0,1} = \{(1)\} \quad \ker d_{0,3} = \left\{ \begin{pmatrix} 1 \\ -1 \end{pmatrix} \right\} \qquad \ker d_{0,1} = 0$$

$$\operatorname{im} d_{0,1} = 0 \qquad \operatorname{im} d_{0,3} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1- \end{pmatrix} \right\} \quad \operatorname{im} d_{0,1} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \end{pmatrix} \right\}$$

$$d_{1,3} = \begin{bmatrix} 1 & -1 & 0 \\ 1 & 0 & -1 \\ 0 & 1 & -1 \end{bmatrix} \qquad d_{1,5} = \begin{bmatrix} 1 & -1 & 0 \\ 1 & -1 & 0 \\ 1 & 0 & -1 \\ 1 & 0 & -1 \\ 0 & 1 & -1 \\ 0 & 1 & -1 \end{bmatrix}$$

$$\ker d_{1,3} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \end{pmatrix} \right\} \qquad \ker d_{1,5} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \end{pmatrix} \right\}$$

$$\operatorname{im} d_{1,3} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 \\ 0 \\ -1 \end{pmatrix} \right\} \quad \operatorname{im} d_{1,5} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} -1 \\ -1 \\ 0 \\ 0 \\ 1 \\ 1 \end{pmatrix} \right\}$$

$$d_{2,3} = \begin{bmatrix} 1 & -1 & 1 \end{bmatrix} \qquad d_{2,5} = \begin{bmatrix} 0 & 1 & -1 & 0 & 1 & 0 \\ 1 & 0 & -1 & 0 & 0 & 1 \\ 0 & 1 & 0 & -1 & 0 & 1 \end{bmatrix}$$

$$\ker d_{2,3} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 \\ 0 \\ -1 \end{pmatrix} \right\} \quad \ker d_{2,5} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} -2 \\ -1 \\ -1 \\ 0 \\ 0 \\ 1 \end{pmatrix}, \begin{pmatrix} 1 \\ 0 \\ 1 \\ 0 \\ 1 \\ 0 \end{pmatrix} \right\}$$

$$\operatorname{im} d_{2,3} = \{(1)\} \qquad \operatorname{im} d_{2,5} = \left\{ \begin{pmatrix} 0 \\ 1 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 \\ 0 \\ 1 \end{pmatrix}, \begin{pmatrix} -1 \\ -1 \\ 0 \end{pmatrix} \right\}$$

$$d_{2,7} = \begin{bmatrix} 1 & 0 & 1 \\ 0 & -1 & 1 \\ 1 & -1 & 0 \end{bmatrix}$$

$$\ker d_{2,7} = 0$$

$$\operatorname{im} d_{2,7} = \left\{ \begin{pmatrix} 1 \\ 0 \\ 1 \end{pmatrix}, \begin{pmatrix} 0 \\ -1 \\ -1 \end{pmatrix}, \begin{pmatrix} 1 \\ 1 \\ 0 \end{pmatrix} \right\}$$

Of course, everything is in the kernel of d_3 and its image is 0.

After finding the image and kernel of each differential, we get the homology groups:

$$\begin{aligned} H_0 &= \mathbb{C}\{\ker d_{0,1} \cup \ker d_{0,3} \cup \ker d_{0,5}\} \\ &= \mathbb{C}\left\{(v_- \otimes v_-), \begin{pmatrix} v_+ \otimes v_- \\ -v_- \otimes v_+ \end{pmatrix}\right\} \\ \operatorname{qdim}(H_0) &= q + q^3 \end{aligned}$$

$$\begin{aligned} H_1 &= \mathbb{C}\{(\ker d_{1,2}/\operatorname{im} d_{0,3}) \cup (\ker d_{1,4}/\operatorname{im} d_{0,5})\} \\ &= 0 \end{aligned}$$

$$\begin{aligned} H_2 &= \mathbb{C}\{(\ker d_{2,1}/\operatorname{im} d_{1,2}) \cup (\ker d_{2,3}/\operatorname{im} d_{1,4}) \cup \ker d_{2,5}\} \\ &= \mathbb{C}\left\{0 \cup \begin{pmatrix} v_- \otimes v_+ \\ v_- \otimes v_+ \\ v_- \otimes v_+ \end{pmatrix} \cup 0\right\} \\ &= \mathbb{C}\left\{\begin{pmatrix} v_- \otimes v_+ \\ v_- \otimes v_+ \\ v_- \otimes v_+ \end{pmatrix}\right\} \\ \operatorname{qdim}(H_2) &= q^5 \end{aligned}$$

$$\begin{aligned} H_3 &= \mathbb{C}\{\ker d_3/(\operatorname{im} d_{2,3} \cup \operatorname{im} d_{2,5} \cup \operatorname{im} d_{2,7}) \\ &= \mathbb{C}\{(v_+ \otimes v_+ \otimes v_+)\} \\ \operatorname{qdim}(H_3) &= q^9 \end{aligned}$$

Now that we have all the homology groups, we can construct what is known as the **Khovanov polynomial**

Definition 6.5.1. The Khovanov polynomial, $K(q,t)$, is a two variable Laurent polynomial invariant of links calculated from the Khovanov homology using the

following equation:

$$K(q,t) = \sum_k t^k \operatorname{qdim}(H_k)$$

The Khovanov homology of a link is often represented by its Khovanov polynomial. The polynomial contains slightly less information as it only conveys the isomorphism classes of the homology groups rather than the groups themselves but it is more concise.

The Khovanov polynomial of the right-handed trefoil is

$$q + q^3 + t^2q^5 + t^3q^9.$$

Notice that, if we set $t = -1$, the Khovanov polynomial becomes the graded Euler characteristic of the homology.

$$\begin{aligned} K_{trefoil}(q,-1) &= q + q^3 + q^5 - q^9 \\ &= (q+q^{-1})(q^2 + q^6 - q^8) \end{aligned}$$

This is the Jones polynomial of the trefoil with the change of variable described in §4.2 multiplied by $(q + q^{-1})$.

In fact, since, to find the Khovanov polynomial, we give the same weighting to each smoothing and assign a vector space with q-grading $(q+q^{-1})$ to each loop in each resolution, the graded Euler characacteristic of the Khovanov homology is the Jones polynomial with the value of the unknot being:

$$V(\bigcirc) = q + q^{-1}$$

6.6 Implementation

Together with Scott Morrison, I have implemented a program to calculate the Khovanov homology of a braid closure in Mathematica; the notebook is available at https://tqft.net/web/research/hilaryhunt. To use this implementation, you must have the KnotTheory‘ package, which is available at http://katlas.org/wiki/The_Mathematica_Package_KnotTheory%60, installed. Run all cells in the notebook. The program takes braids as input and returns the Khovanov polynomial of their trace closure.

Example 6.6.1. To find the Khovanov polynomial of knot 5_2 from the Rolfsen knot table (found at [8]) which has braid representative $\sigma_1\sigma_1\sigma_1\sigma_2\sigma_1^{-1}\sigma_2 \in B_3$, we enter

```
Kh[BR[3,{1,1,1,2,-1,2}]]
```

The program will then output the Khovanov polynomial:

$$q + q^3 + q^3t + q^5t^2 + q^7t^2 + q^9t^3 + q^9t^4 + q^{13}t^5$$

In order to calculate the isomorphisms corresponding to self-isotopies of a link, I have been working on implementing a function to calculate them for each Reidemeister move. This function currently calculates the isomorphisms for Reidemeister 2 moves.

Hannah Keese, Anthony Licata, Scott Morrison and I have adapted this program to calculate the Annular Khovanov homology of links. While Annular Khovanov homology will not be covered in this thesis, we refer you to [18].

Chapter 7

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