Homfly polynomials of braids with a full twist

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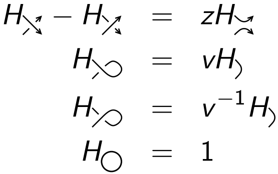
The Fourth East Asian School of Knots and Related Topics

January 22, 2008

Our conventions

Let D be an oriented link diagram. The *framed Homfly polynomial* $H_D(v,z)$ is defined by



The *Homfly polynomial* itself is

$$P_D(v,z) = v^w H_D(v,z),$$

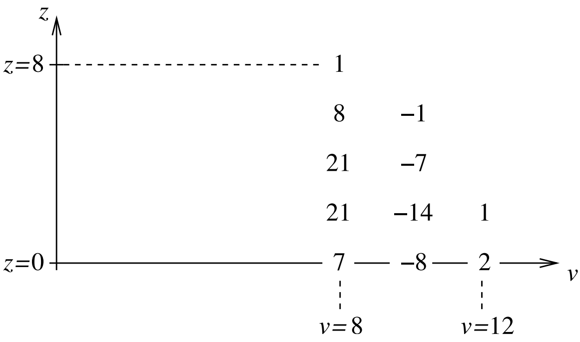
where w is the writhe of D.

Newton polygon

We record Homfly coefficients on the vz–plane.
Example: The Homfly polynomial of the torus knot $T(3,5)$ is

$$P_{T(3,5)}(v,z) = z^8v^8 + 8z^6v^8 - z^6v^{10} + 21z^4v^8 - 7z^4v^{10} \\ + 21z^2v^8 - 14z^2v^{10} + z^2v^{12} + 7v^8 - 8v^{10} + 2v^{12},$$

and we will write it as



Morton–Franks-Williams (MFW) inequalities

The famous inequality is

braid index $\geq$ number of non-zero columns in P.

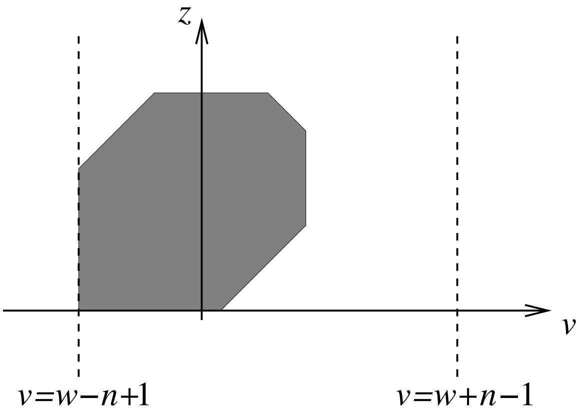
This follows from the following pair of inequalities. Let β be a braid word on

n strands, with exponent sum w.

Let $P_{\widehat{\beta}}(v, z)$ be the Homfly polynomial of the closure of β. Then,

lower MFW estimate: $w - n + 1 \leq$ lowest v–degree of $P_{\widehat{\beta}}$
upper MFW estimate: highest v–degree of $P_{\widehat{\beta}} \leq w + n - 1$.

MFW on our pictures



(The gray shaded region is the Newton polygon of $P_{\widehat{\beta}}$.)

An example

If we represent $T(3,5)$ with the braid word

$$\beta = (\sigma_1\sigma_2)^5 =$$

,

then

$$\begin{aligned} n &= 3, \\ w &= 10, \\ w - n + 1 &= 8, \\ w + n - 1 &= 12, \end{aligned}$$

and we see that both the lower and the upper MFW estimates are sharp for this braid. Indeed, the Homfly polynomial has $3(= n)$ columns.

The extreme columns

Lower MFW is sharp for a braid if and only if the leftmost column of P corresponds to $v = w - n + 1$. Similiarly for upper MFW and the rightmost column.

An indication that *actual coefficients* in these columns may be interesting: If we re-normalize by requiring

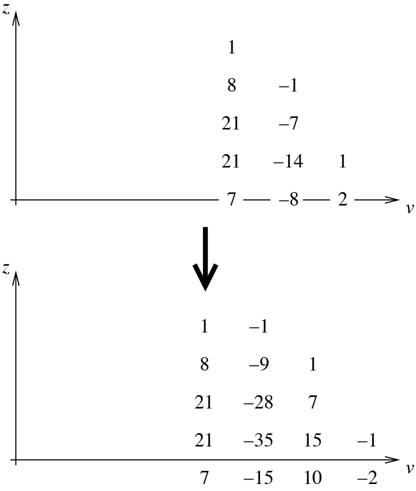
$$H'_{\bigcirc} = \frac{v^{-1} - v}{z} \text{ instead of } H_{\bigcirc} = 1,$$

then the extreme columns, up to sign, do not change.

The numbers (up to sign) also persist if we use $a = v^{-1}$, $l = -\sqrt{-1} \cdot v^{-1}$, $m = \sqrt{-1} \cdot z$ etc.

Versions of Homfly

Example: Re-normalization changes $P_{T(3,5)}$ into $P'_{T(3,5)}$ as follows:



Digression: Rulings

However there is a much better reason to look at the extreme columns.

Rutherford (2005): If the knot type K contains Legendrian representatives with sufficiently high Thurston–Bennequin number, then the coefficients in the left column of the Homfly polynomial $P_K(v,z)$ represent numbers of so-called 2–graded rulings (of various genera) of these Legendrian knots.

Similarly, the right column may speak of 2–graded rulings of the mirror of K.

Adding a full twist

We will denote the Garside braid (positive half twist) on n strands by Δ_n or simply by Δ. Then Δ^2 represents a positive full twist. The braid Δ^2 contains $n(n-1)$ crossings.

Example: $\Delta_3 =$ , $\Delta_3^2 =$ .

If β has n strands and exponent sum w, then $\beta\Delta^2$ still has

$$n \text{ strands but exponent sum } w + n(n-1).$$

Thus the upper MFW bound for $\beta\Delta^2$ is

$$w + n(n-1) + n - 1 = w + n^2 - 1.$$

The realization about extreme columns and full twists is...

Theorem

For any braid β, the lower MFW estimate is sharp if and only if the upper MFW estimate is sharp for the braid $\beta\Delta^2$. If this is the case, then

$$\text{left column of } P_{\widehat{\beta}} = (-1)^{n-1} \text{ right column of } P_{\widehat{\beta\Delta^2}}. \qquad (1)$$

Remark

Actually, we can claim the following for an arbitrary braid β:

$$\begin{aligned} &\text{the coefficient of } v^{w-n+1} \text{ in } P_{\widehat{\beta}} \\ &\qquad = (-1)^{n-1} \text{ the coefficient of } v^{w+n^2-1} \text{ in } P_{\widehat{\beta\Delta^2}}. \qquad (2) \end{aligned}$$

This either says that $0 = 0$, or the more meaningful formula (1), depending on whether the sharpness condition is met.

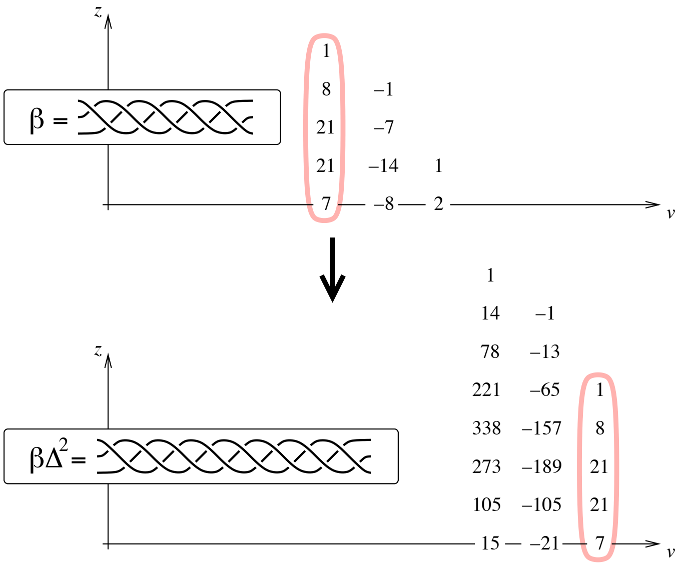
Positive and non-positive braids

For positive braids β, the two equivalent sharpness requirements are both known to hold, so our claim (2) is always 'meaningful.'

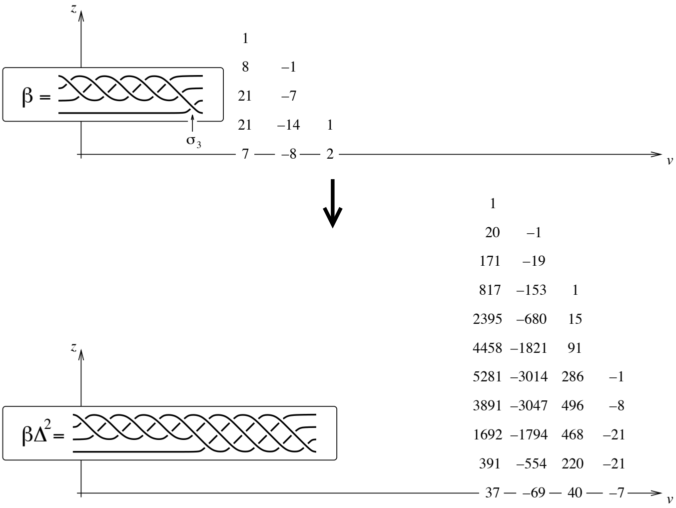
But the Morton–Franks-Williams inequalities are sharp for many other knots, too. Up to 10 crossings, there are only five knots that do *not* possess braid representations with a sharp (lower) MFW estimate.

Thus, (2) is informative for many non-positive braids, too.

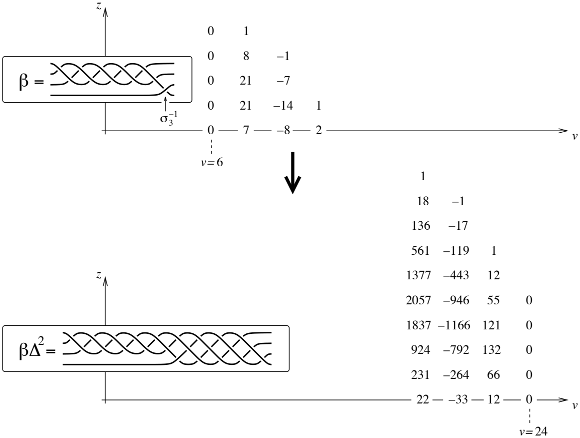
In our main example:



A related example (positive Markov stabilization):



A ‘failure’ (negative Markov stabilization):

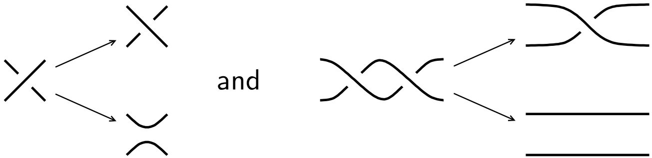


Here, the lower MFW bound (for β) is $(10-1)-4+1=6$ and the upper one (for $\beta\Delta^2$) is $(10-1)+4^2-1=24$. (In fact, $\widehat{\beta\Delta^2}$ is the torus knot $T(3,10)$.)

Computation trees

For any braid, a *computation tree* can be built (and used to determine the Homfly polynomial) using the following 4 types of steps.

- Isotopy (braid group relations)
- Conjugation: $\beta_1\beta_2 \mapsto \beta_2\beta_1$
- Positive Markov destabilization: $\alpha\sigma_i \in B_{i+1}$ becomes $\alpha \in B_i$
- Two types of Conway splits:



The *terminal nodes* of the computation tree are labeled with trivial (crossingless) braids (on various numbers of strands).

Plan of the proof

It is possible to avoid the Hecke algebra and prove our theorem using skein theory.

Let Γ be a computation tree for β.

Idea: Build a computation tree $\widetilde{\Gamma}$ for $\beta\Delta^2$ that imitates Γ.

Namely, we 'tack on' a full twist and see how much of Γ can be preserved. (We need to analyze the 4 moves.)

Answer: Γ survives as a subtree of $\widetilde{\Gamma}$. (Understanding the specifics makes it possible to read off our formula.)

3 cases are easy...

Isotopy and Conway splits: No problem! These moves are completely local.

Conjugation: Recall that Δ^2 is in the center of the braid group. Thus, the conjugation move

$$\beta_1\beta_2 \mapsto \beta_2\beta_1 \quad \text{in } \Gamma$$

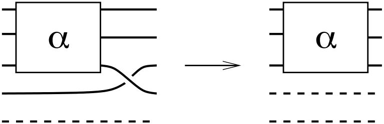
can be replaced by an isotopy followed by a conjugation

$$\beta_1\beta_2\Delta^2 \mapsto \beta_1\Delta^2\beta_2 \mapsto \beta_2\beta_1\Delta^2 \quad \text{in } \widetilde{\Gamma}.$$

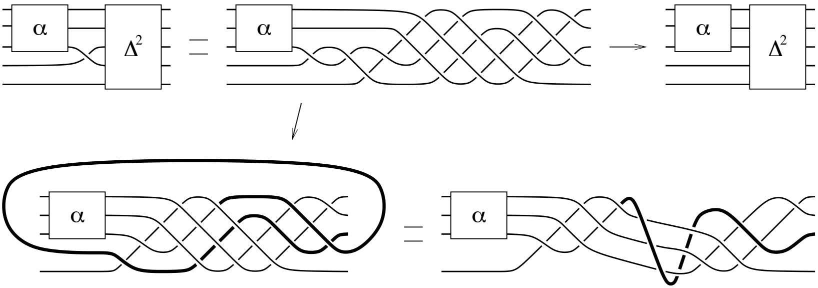
...and one is a bit harder

To imitate a Markov destabilization in Γ, we need a Conway split in $\widetilde{\Gamma}$.

If in Γ, we see this:



Then in $\widetilde{\Gamma}$, we can do this:



This starts a new, 'unnecessary' branch in $\widetilde{\Gamma}$...

But the braid at the beginning of that branch is on at most $n - 1$ strands. (More precisely, isotopies, conjugations, and a Markov destabilization can be applied so that the number of strands is reduced by 1.) Luckily, this implies that the new branch does not contribute to the relevant part of $P_{\widehat{\beta \Delta^2}}$.

Conclusion of the proof

So far, $\widetilde{\Gamma}$ contains a copy of Γ with extra branches that do not matter.

However at the terminal nodes of $\widetilde{\Gamma}$, where the trivial braids used to be, now there are copies of Δ^2.

But $P_{\widehat{\Delta^2}}(v, z)$ (or a computation tree for Δ^2) is well understood. In particular, the rightmost column contains a single 1. This allows us to read off the formula.

Open questions

- Any applications?
- Are there generalizations to Khovanov homology or Khovanov-Rozansky homology?