TWO OF JABŁONOWSKI'S CANDIDATE INEQUALITIES HOLD FOR ALL PRIME KNOTS WITH AT MOST 18 CROSSINGS

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Abstract. Jabłonowski proposed nine candidate inequalities between integer knot invariants and proved structural special cases. Two of them compare the concordance invariants of Ozsváth–Szabó and Rasmussen with the z-degree of the HOMFLY polynomial: $2|\tau(K)| \le \deg_z P(K)$ and $|s(K)| \le \deg_z P(K)$. We show by an exact computation that both hold for every prime knot with at most 18 crossings, and hence for every connected sum of such knots. The genus and τ come from knot Floer homology (Szabó's program in SnapPy), s (where it is needed) from Schütz's KnotJob, and $\deg_z P$ from Regina, cross-checked with SageMath wherever it decides the outcome. By Jabłonowski's results and the argument of his Proposition 5.19, only the non-alternating knots with $\deg_z P < 2g$ need τ and s; there are none up to 14 crossings and 34,974 with 15 to 18 crossings. On 2,331 of them the inequalities are sharp; at least 2,254 of these lie outside both proof mechanisms of his paper. On 152 sharp knots a short chain of genus-one moves, together with τ, determines the four-ball genus, $g_4 = \deg_z P/2 < g$.

1. Introduction

In [Jab] Jabłonowski combines forty-seven established inequalities among thirty-three integer knot invariants with the knot tables up to thirteen crossings, and formulates nine candidate comparisons that are not implied by the network [Jab, §5]. Two of them are

$$\text{(c8)}\quad 2|\tau(K)| \le \deg_z P(K), \qquad\qquad \text{(c9)}\quad |s(K)| \le \deg_z P(K),$$

where τ is the Ozsváth–Szabó invariant [OS] with $\tau(T_{2,3}) = 1$ for the right-handed trefoil $T_{2,3}$, s is Rasmussen's invariant over $\mathbb{Q}$ [Ras] with $s(T_{2,3}) = 2$, and $\deg_z P$ is the maximal z-degree of the HOMFLY polynomial $P(a, z)$. The signature σ is normalised by $\sigma(T_{2,3}) = -2$. On his database of the

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12,965 prime knots with at most thirteen crossings both candidates are certified on all rows, with 741 exact equalities each [Jab, table in §5] (with the source-bound qualification he attaches to his numerical statements [Jab, §4]). He proves (c8) and (c9) for positive knots (with equality), for every knot with $\deg_z P = 2g$, in particular for homogeneous knots, and for simultaneously signature-thin knots, in particular for quasi-alternating and alternating knots [Jab, Prop. 5.17, Prop. 5.19, Prop. 5.23, Cor. 5.24].

Theorem 1. *Every prime knot K with crossing number $c(K) \leq 18$ satisfies $2|\tau(K)| \leq \deg_z P(K)$ and $|s(K)| \leq \deg_z P(K)$.*

The proof is a computation on the complete tables, described in Sections 2 and 3. All three quantities are additive under connected sum: τ and s are concordance homomorphisms, and P is multiplicative, so the top z-coefficients multiply and, being non-zero elements of the domain $\mathbb{Z}[a^{\pm 1}]$, have a non-zero product. With $|\tau(K_1) + \tau(K_2)| \leq |\tau(K_1)| + |\tau(K_2)|$, and likewise for s, the inequalities pass to sums:

Corollary 2. *(c8) and (c9) hold for every knot whose prime summands all have crossing number at most* 18*.*

The computation also shows where the candidates are tight. The knots that need τ and s at all, those with $\deg_z P < 2g$, occur in the tables from fifteen crossings on. Among them we find 2,331 knots on which (c8) and (c9) hold with equality; none of them is homogeneous, and 2,254 of them are not simultaneously signature-thin, so that neither of the two mechanisms in [Jab] applies to these 2,254 (Section 4).

2. Reduction to the genus-gap knots

Write g for the Seifert genus and g_4 for the smooth four-ball genus. The following is the argument of [Jab, Prop. 5.19], stated with an inequality in place of the equality.

Lemma 3. *If $\deg_z P(K) \geq 2g(K)$, then K satisfies (c8) and (c9).*

Proof. By the slice-genus bounds of Ozsváth–Szabó and Rasmussen [OS, Ras], $2|\tau(K)| \leq 2g_4(K) \leq 2g(K) \leq \deg_z P(K)$ and $|s(K)| \leq 2g_4(K) \leq 2g(K) \leq \deg_z P(K)$. □

Alternating knots are homogeneous [Cro], so they have $\deg_z P = 2g$ [Jab, Lemma 5.7] and satisfy (c8) and (c9) by Lemma 3; they are also covered by [Jab, Cor. 5.24]. So for Theorem 1 it suffices to check, for every prime non-alternating knot with at most 18 crossings, whether $\deg_z P \geq 2g$, and to compute τ and s exactly on the knots where this fails. For $c \leq 13$ we did not use this shortcut: there we computed all quantities on all 12,965 prime knots, including the alternating ones, to calibrate the code (Section 3).

We call a knot with $\deg_z P < 2g$ a *genus-gap knot*. Morton's inequality bounds $\deg_z P$ from above by twice the canonical genus [Mor]; it gives no

lower bound in terms of g. Jabłonowski states that knots with $\deg_z P < 2g$ are known [Jab, §5]. On all prime knots with at most thirteen crossings we find $\deg_z P - 2g \in \{0, 2, 4\}$, never negative; in the tables the smallest crossing number of a genus-gap knot is 15, for instance 15nh_001609 with $g = 4$ and $\deg_z P = 6$.

3. The computation

Knots. For $c \leq 13$ we used the 12,965 prime knots of KnotInfo [KI]; for $c = 14$ the 27,436 non-alternating knots of Hoste–Thistlethwaite–Weeks [HTW]; for $15 \leq c \leq 18$ the non-alternating knots of Burton's census [Bur]: 168,030, 1,008,906, 6,283,414 and 39,866,181 knots, including the satellite knots (86 at $c = 18$). There is no torus knot with crossing number 18. All invariants involved are unchanged under mirroring, up to the signs of τ, s and σ, so it does not matter that the tables list knots up to mirror image; in particular, torus knots are positive up to mirroring and covered by [Jab, Prop. 5.17] in any case. For the census knots, signed values of τ, s and σ below refer to the diagram that Regina decodes from the census entry `knot_sig`; this code does not distinguish a knot from its mirror image.

Invariants. From a planar diagram of each knot we computed:

- the knot Floer homology, with coefficients in $\mathbb{F}_2$, with Zoltán Szabó's knot Floer homology calculator as included in SnapPy [SnapPy], giving the Seifert genus g and τ. Knot Floer homology detects the genus [OSg]; for $\mathbb{F}_2$ coefficients this follows from Juhász [Ju, Theorems 1.4 and 1.5], since the top group contains $\mathbb{Z}$ as a direct summand. The invariant τ computed over $\mathbb{F}_2$ is the one of KnotInfo and of [Hom], and the bound $|\tau| \leq g_4$ of Lemma 3 holds for it [Hom, Theorem 3.1];
- the HOMFLY polynomial with Regina [Regina], giving $\deg_z P$. This value decides whether a knot is a genus-gap knot, so the proof relies on it exactly where $\deg_z P \geq 2g$ does not already follow from the Alexander polynomial: the Conway polynomial is a specialisation of P in the variable a, which cannot raise the z-degree, and its z-degree is the span of Δ, so $\deg_z P \geq \operatorname{span} \Delta$, and $\operatorname{span} \Delta = 2g$ forces $\deg_z P \geq 2g$ whatever the HOMFLY code returns. On every other knot, that is on all 34,974 genus-gap knots and on the 2,327,811 knots with $\deg_z P \geq 2g > \operatorname{span} \Delta$, the polynomial was also computed with the independent implementation in SageMath 10.9 [Sage] (libhomfly); the z-degree agreed in every case;
- the signature σ with SnapPy;
- on the genus-gap knots, Rasmussen's s over $\mathbb{Q}$ with Schütz's program KnotJob [KJ]. Schütz computed s over $\mathbb{Z}$ for every prime knot with at most 18 crossings with KnotJob [Sch, §6.1]; we did not compare our values with his.

As a per-knot consistency gate, the Alexander polynomial read off the knot Floer homology was compared with the one computed by Regina; it agreed

on every knot of every table. This gate tests the Alexander polynomial only. The genus and τ come from the one knot Floer program above, σ from SnapPy alone and s from KnotJob alone; only the Alexander polynomial (this gate) and $\deg_z P$ were computed with two independent programs. The runs of Table 1 had no computation errors.

Calibration. Before the runs the code was compared, one convention at a time, with KnotInfo on all 12,965 prime knots up to thirteen crossings: $|\tau|$, $|\sigma|$, g, $\deg_z P$ and $|s|$ agree on all of them, and on every knot with $\tau \neq 0$ our s and 2τ have the same sign on the same diagram; on the same diagrams $s = -\sigma$ on all 6,729 alternating knots, as it must be by [Jab, Lemma 5.22 and the proof of Corollary 5.24], which fixes the relative sign of σ against s and τ used in Section 4. Up to thirteen crossings we count 741 exact equalities in (c8) and in (c9), the number given in [Jab]. An artificial record violating both candidates was reported as a violation by the evaluation code.

A second diagram. On every genus-gap knot τ, g, σ and s were recomputed on a second diagram obtained by random Reidemeister moves and simplification. For $c = 18$ the second diagram differed from the first (as measured by Regina's signature of the diagram, `knotSig`, a text code for the diagram unrelated to the invariant σ) for 15,226 knots; for the other 16,498 a third diagram with a different diagram signature was drawn. On all 31,724 genus-gap knots with 18 crossings, τ, g, σ and s agree with sign on a genuinely different diagram. For $c \leq 17$ the second diagram is genuinely different for 1,454 of the 3,250 genus-gap knots and equal to the first for the others; there the recomputation only repeats the code. This check concerns the implementation; the proof does not depend on it.

	knots	errors	equality in (c8)	genus gap	sharp in gap
$c \leq 13$ (all)	12,965	0	741	0	–
$c = 14$ (non-alt.)	27,436	0	1,059	0	–
$c = 15$ (non-alt.)	168,030	0	3,429	46	5
$c = 16$ (non-alt.)	1,008,906	0	17,279	402	46
$c = 17$ (non-alt.)	6,283,414	0	73,911	2,802	192
$c = 18$ (non-alt.)	39,866,181	0	347,732	31,724	2,088

TABLE 1. No violation of (c8) or (c9) occurs in any row. Inequality (c8) was checked on every knot listed in the table; (c9) was checked for $c \leq 13$ on every knot and, from $c = 14$ on, on every genus-gap knot, the other knots being covered by Lemma 3. "Sharp in gap": genus-gap knots with $2|\tau| = |s| = \deg_z P$.

Proof of Theorem 1. Alternating knots are covered by Lemma 3 as explained in Section 2. By the enumerations of [KI, HTW, Bur], every non-alternating

prime knot with at most eighteen crossings occurs in one of the tables above; the theorem is computer-assisted and rests on these enumerations. On the knots with $\deg_z P \geq 2g$ the inequalities follow from Lemma 3; on the 34,974 genus-gap knots they were checked with the exact values of τ, s and $\deg_z P$. No violation occurred (Table 1). □

4. The genus-gap knots

Where they are. Up to 14 crossings there is no genus-gap knot (for the alternating knots because they are homogeneous). At 15 and 16 crossings all 448 have $(g, \deg_z P) = (4, 6)$. At 17 crossings 1,896 have $(4, 6)$ and 906 have $(5, 8)$. At 18 crossings 7,784 have $(4, 6)$, 23,923 have $(5, 8)$, and 17 have $(5, 6)$: in the tables, 18 is the smallest crossing number with $\deg_z P = 2g-4$.

Sharpness outside the proved classes. On 5, 46, 192 and 2,088 genus-gap knots with 15, 16, 17 and 18 crossings both inequalities hold with equality, $2|\tau| = |s| = \deg_z P < 2g$. Such a knot is not homogeneous, because homogeneous knots have $\deg_z P = 2g$ [Jab, Lemma 5.7]. A simultaneously signature-thin knot has $s = -\sigma$ [Jab, Lemma 5.22]; this fails on all 51 sharp knots with 15 and 16 crossings, which all have $(g, \deg_z P, \tau, s, \sigma) = (4, 6, 3, 6, -4)$ on the diagram decoded from `knot_sig`, on 181 of the 192 with 17 crossings and on 2,022 of the 2,088 with 18 crossings. These 2,254 knots lie outside both mechanisms of [Jab] and still satisfy (c8) and (c9) with no room to spare. We checked that all 2,254 also meet the necessary conditions for a counterexample in [Jab, Prop. 5.26(v)], $2|\tau| > |\sigma|$ and $|s| > |\sigma|$, and miss a counterexample to (c8) by one unit of $|\tau|$. On the remaining 77 we have $s = -\sigma$ and $2\tau = -\sigma$, so $2|\tau| = |s| = |\sigma| = \deg_z P$; we did not decide whether they are simultaneously signature-thin.

Four-ball genus. Let e and E be the minimal and maximal degree of P in the variable a; the quantity $\max(e, -E)$ does not change when a is replaced by $\pm a^{-1}$ or by $\pm ia$, so it does not depend on which of the usual normalisations of P (all with $P = 1$ on the unknot) is used. Every knot satisfies $\deg_z P \geq \max(e, -E)$: in the normalisation of [IS], $P = \sum c_{ij} v^i z^j$ satisfies $P(v, v^{-1} - v) = 1$ [IS, (7.1)], and since $v^i(v^{-1} - v)^j$ only has v-exponents between $i-j$ and $i+j$, some $c_{ij} \neq 0$ has $j \geq |i|$; if $\max(e, -E) \geq 0$ then $e \geq 0$ or $E \leq 0$, so $|i| \geq \max(e, -E)$, and $\deg_z P \geq j \geq |i| \geq \max(e, -E)$ (compare [Sh]); if $\max(e, -E) < 0$ there is nothing to prove, since $\deg_z P \geq 0$. Our certificate program asserts this inequality on every sharp knot. On 2,179 sharp knots, $2|\tau| \leq \max(e, -E)$, which gives (c8) a second time but uses the computed τ. On the other 152 (11 with 17 and 141 with 18 crossings) we looked for an upper bound on g_4 independent of τ and s, and found one on each: a chain of one to three crossing changes or pairs of saddle moves leads to a knot K' with $k + g(K') \leq \deg_z P/2$, where k is the number of moves, a pair of saddle moves counting as one move. Each saddle is the oriented smoothing of a crossing; a pair of them leads from the knot to a two-component link

and back to a knot, so, like a crossing change, it gives a connected orientable cobordism of genus one in $S^3 \times [0,1]$, and $g_4(K) \le k + g_4(K') \le k + g(K')$. Each chain was re-verified move by move on the diagrams. The starting diagram of a chain was compared with the census diagram, each diagram produced by a move other than the last with the simplified diagram stored for it, and each stored diagram with the one it replaces. Where two of these differ as planar diagram codes they were identified by equal HOMFLY polynomials and equal isometry signatures of their complements, computed with interval arithmetic (SnapPy's verified canonical retriangulation in SageMath; by Gordon–Luecke [GL] this identifies a knot up to mirroring, which does not change the genus): 231 such identifications, while 153 further pairs are equal as diagrams. At the last move $g(K')$ was computed by knot Floer homology directly on the diagram produced by the move, so no identification is needed there. Hence $g_4 \le \deg_z P/2$, and together with $2|\tau| = \deg_z P$ this gives $g_4 = |\tau| = \deg_z P/2 < g$ on these knots. This certificate uses neither the computed τ nor s for the upper bound.

s versus 2τ. On all but four genus-gap knots, $s = 2\tau$. The exceptions are 17nh_0053727 with $\tau = -1$, $s = 0$, and 18nh_00171672, 18nh_00700714, 18nh_01554086 with $\tau = 1$, $s = 0$ (names from [Bur]). Each value was confirmed on six pairwise different diagrams, the first being the diagram of the main run: τ and g by knot Floer homology, s over $\mathbb{Q}$, $\mathbb{F}_2$ and $\mathbb{F}_3$ on all six. That s and 2τ can differ is known since Hedden and Ording [HO]; we mention the four knots only because they are genus-gap knots.

Tool use

This work was prepared with substantial use of Claude Code (Anthropic), an agentic AI system based on large language models, working together with the author.

- *Mathematics.* The candidate inequalities of [Jab] were among the open questions found in a literature search carried out with Claude Code; the author chose them. The reduction, the computation and the certificates of Section 4 were worked out by Claude Code under the author's direction.
- *Writing and typesetting.* The text and the LaTeX source were written by Claude Code, in English; no translation tools were used. The paper contains one table and no figures.
- *References.* Literature was searched and sourced with Claude Code. Quotations and numbered statements from [Jab] were checked against the text of its version 5; bibliographic data were checked against Crossref or against the sources themselves.
- *Code.* The computations of Section 3 were written and run by Claude Code in Python, using SnapPy 3.3.2 with Szabó's knot Floer homology calculator, Regina 7.4, SageMath 10.9 (also for the verified isometry signatures) and KnotJob. The deposited scripts (see Data) are

English versions of the working scripts, together with scripts written for the later checks, all prepared by Claude Code; the deposit lists the exact software versions.

- *Checking.* Drafts were read in seventeen rounds by separate instances of Claude Code, without access to the discussion in which the arguments were developed; their findings were checked and incorporated where they held.

The author takes full responsibility for all contents.

Data

The per-knot values (g, $\deg_z P$, τ, s, σ, a planar diagram) for all 34,974 genus-gap knots, the values of τ, s and $\deg_z P$ for the 12,965 prime knots with at most thirteen crossings, the two z-degrees for the 2,327,811 knots of Section 3, the values on further diagrams for the four knots with $s \neq 2\tau$, the output of the evaluation code on the artificial record, the certificates of Section 4 and the scripts are deposited at doi:10.5281/zenodo.23566264 (all versions).

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