THE SMOOTH 4-GENUS OF (THE REST OF) THE PRIME KNOTS THROUGH 12 CROSSINGS

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Abstract. We compute the smooth 4-genera of the prime knots with 12 crossings whose values, as reported on the KnotInfo website, were unknown. This completes the calculation of the smooth 4-genus for all prime knots with 12 or fewer crossings.

1. Introduction

The genus (or 3-genus) $g(K)$ of a knot $K$ in the 3-sphere $S^3$ is the minimum genus of an orientable spanning surface (or Seifert surface) $F$ with $\partial F = K$ embedded in $S^3$. This is one of the most basic measures of the complexity of a knot, and following the development of knot Floer homology ([16],[20]) and the efforts of many researchers ([8],[10],[17]), determination of the 3-genus for a given knot can now be viewed as a ‘routine’ computation, in particular since the ability to compute knot Floer homology was recently added to the computer program SnapPy [24].

On the other hand, the smooth 4-genus $g_4(K)$ (which we will refer to as the 4-genus throughout this paper), which is the minimum genus of a smooth, orientable, properly embedded surface $\Sigma$ in the standard smooth 4-ball $B^4$ with $K = \Sigma \cap \partial B^4$, currently enjoys no such advantage. There are several computable lower bounds, both classical and modern, including the inequality

$$g_4(K) \geq |\sigma(K)|/2,$$

where $\sigma(K)$ is the knot signature [15]. Rasmussen’s $s$-invariant [21] and Ozsváth-Szabó’s $\nu$-invariant [18] also provide lower bounds on the 4-genus. The classical invariants 3-genus $g(K)$ and unknotting number $u(K)$ give upper bounds for the 4-genus, but $g_4(K) = g(K)$ is relatively rare (only 277 of the 2977 prime knots through 12 crossings have this equality), and the inequality $g_4(K) \leq u(K)$ is more often used to help determine unknotting number from a known value of $g_4(K)$, rather than the other way around. In practice, useful upper bounds on $g_4(K)$, in the end, typically come from direct construction of a smooth orientable spanning surface $\Sigma$.

Despite these seeming limitations, among the 2977 prime knots with 12 or fewer crossings, the smooth 4-genus is known for all but 3 of them (listed in Theorem 1.1(a) below) at the time of this writing, according the KnotInfo website [13]. In this paper in Theorem 1.1(a) we determine the value of $g_4(K)$ for these 3 remaining knots, completing the computation of the 4-genus for all prime knots with crossing number at most 12.

For 2205 of the 2977 prime knots with crossing number at most 12, upper bounds have been computed to show that (combined with Equation (1)) the 4-genus satisfies

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the equality \( g_4(K) = |\sigma(K)|/2 \). In 2015 Lewark and McCoy utilized genus one concordances (see Section 2 for definitions and background) to compute upper bounds for smooth 4-genera, and used algebraic methods (discussed more in Section 5 below) to find lower bounds on 4-genera. They determined the (previously unknown) smooth 4-genus of 639 knots and, as a result, there remained at the time only 22 knots of up to 12 crossings whose smooth 4-genera were still unknown. In the years since then, the 4-genus of the Conway knot \( K_{11n34} \) was determined in the spectacular result of Piccirillo that the Conway knot is not smoothly slice, and more recently (during the course of our work on this problem) Karageorghis and Swenton announced the computation of the values of \( g_4(K) \) for 18 of the remaining 21 knots (listed in Theorem 1.1(b) below). Their approach involved the calculation of the double slice genus \( g_{ds}(K) \) of these knots (the minimum genus of an unknotted surface \( \Sigma \) in \( S^4 \) with \( \Sigma \cap S^3 = K \), where \( S^3 \) is the equatorial 3-sphere); for these 18 knots they find that \( g_{ds}(K) = 2 \) or 3, implying that \( g_4(K) \leq 1 \).

Our approach is motivated by the work of Lewark and McCoy in [11]. For the three remaining knots for which the 4-genus was unknown, we use a combination of algebraic methods together with extended methods for a computer search for genus one concordances in order to determine the necessary lower bounds on the 4-genus. We also expand on the techniques of [11] for finding upper bounds on 4-genera through genus one concordances in order to directly construct a genus one spanning surface for the 18 knots for which the 4-genus was determined by Karageorghis and Swenton, giving an alternate proof of that result. In all of our work, we restrict our view to four specific operations for constructing genus one concordances: crossing change, switching a pair of oppositely signed crossings, or resolving or de-resolving a pair of crossings (see Section 2 for more details).

**Theorem 1.1.** (a) Each of the 3 knots \( K_{12a153}, K_{12n239} \) and \( K_{12n512} \) is genus one concordant, via de-resolution of a pair of crossings, to a knot with 4-genus 3, and hence each has smooth 4-genus equal to 2.

(b) Each of the 18 knots \( K_{11n80}, K_{12a187}, K_{12a230}, K_{12a317}, K_{12a450}, K_{12a570}, K_{12a624}, K_{12a636}, K_{12a905}, K_{12a1189}, K_{12a1208}, K_{12n52}, K_{12n63}, K_{12n225}, K_{12n555}, K_{12n558}, K_{12n665} \) and \( K_{12n886} \) is genus one concordant, via crossing resolution or switching two crossings, to one of the slice knots \( 6_1, 8_8, 8_{20}, 10_{75}, 10_{87}, 10_{137}, K_{11n74}, \) or \( K_{12n256} \), and hence each of the 18 knots has smooth 4-genus equal to 1.

We note that our computation of \( g_4(K) = 2 \) for the three knots \( K \) in Theorem 1.1(a), together with Karageorghis and Swenton’s work [9] which shows that \( g_{ds}(K) \leq 4 \), also determines that the double slice genus satisfies \( g_{ds}(K) = 4 \) for the knots \( K \) in the list \( K_{12a153}, K_{12n239} \) and \( K_{12n512} \).

## 2. Genus one concordances

A key tool in this paper is what should properly be thought of as the 4-genus version of a crossing change. A genus one concordance between two knots \( K_0, K_1 \) is a twice-punctured torus \( \Sigma \cong T^2 \setminus \int(D_2^2 \sqcup D_2^2) \) properly and smoothly embedded in \( S^3 \times [0,1] \) such that \( \Sigma \cap (S^3 \times \{0\}) = K_0 \) and \( \Sigma \cap (S^3 \times \{1\}) = K_1 \). Gluing \( \Sigma \subseteq S^3 \times [0,1] \) to any \( g_4 \)-minimizing surface in \( B^4 \) bounding \( K_1 \) yields a smooth
surface in $B^4$ of genus $g_4(K_1) + 1$ with boundary $K_0$, and so $g_4(K_0) \leq g_4(K_1) + 1$. Switching roles of $K_0$ and $K_1$ and using the same genus one concordance shows that $g_4(K_1) \leq g_4(K_0) + 1$, and so

\begin{equation}
(2) \quad g_4(K_1) - 1 \leq g_4(K_0) \leq g_4(K_1) + 1
\end{equation}

when $K_0$ and $K_1$ are genus one concordant.

Our goal is to use these inequalities to determine $g_4(K_0)$. We will do this in two ways. The first is to find a genus one concordance to a knot $K_1$ for which it is known that $g_4(K_0) \geq g_4(K_1) + 1$ (in our applications, $g_4(K_1) = 0$), and so (with Equation (2))

$g_4(K_0) = g_4(K_1) + 1$. In this case we say that the genus one concordance pulls the 4-genus of $K_0$ down to $g_4(K_1) + 1$. The second is to find a genus one concordance to a knot $K_1$ for which it is known that $g_4(K_0) \leq g_4(K_1) - 1$ (in our applications, $g_4(K_1) = 3$), and so $g_4(K_0) = g_4(K_1) - 1$. In this case we say that the genus one concordance pulls the 4-genus of $K_0$ up to $g_4(K_1) - 1$. In particular, since all of the 21 knots that we wish to consider here have 4-genus either 1 or 2 (from KnotInfo [13]), we seek a genus one concordance to a knot $K_1$ with $g_4(K_1) = 0$ (i.e., a smoothly slice knot), ‘pulling down’ to establish $g_4(K_0) = 1$, or to a knot $K_1$ with $g_4(K_1) = 3$, ‘pulling up’ to establish $g_4(K_0) = 2$.

We employ four standard operations for building genus one concordances from a knot $K$ in the process of making most of our 4-genus determinations. Each of these operations can be carried out on the level of knot diagrams, and they are especially amenable to implementation in software when $K$ is given as a closed braid. All of the genus one concordance operations are described by attaching two oriented bands to the knot $K$, or rather to $K \times I = a$ neighborhood of $K$ in an orientable spanning surface for $K$; see Figure 1. If the attaching regions of the bands represent linked pairs of points around $K$, the result of the two band attachments is a twice punctured torus that represents a genus one concordance between $K$ and another knot.

![Figure 1. A genus one concordance: schematic](image)

The first of these genus one concordance operations is crossing change; that is, if $K_1$ can be obtained from $K_0$ by a crossing change, then there is a genus one concordance between the two knots. This is because a crossing change can be achieved by attaching two oriented bands to $K_0$ (see Figure 2). The second operation, which we refer to as
switching two crossings, consists of simultaneously switching a positive and a negative crossing. This gives rise to genus one concordance since this again can be achieved by attaching a pair of oriented bands (Figure 3). The third is resolving two crossings in a diagram for $K_0$; that is, removing the crossings so that an orientation on $K_0$ is preserved. This again can be achieved by attaching two bands, and hence, so long as the resulting link is again a knot $K_1$, there is a genus one concordance between the two knots (Figure 4). The reverse of the resolving process, de-resolving two crossings (in which two crossings are inserted), can similarly be achieved by attaching two bands by running the process in Figure 4 in reverse; this is the fourth of the genus one concordance operations we employed in our computational search.

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{crossing_change}
\caption{Bands for a crossing change}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{switching_crossings}
\caption{Bands for switching positive and negative crossings}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{resolving_crossings}
\caption{Bands for resolving two crossings}
\end{figure}

3. First step: A braid representation data set and braid operations

For a knot $K_0$ given as the closure of a braid, the four genus one concordance operations in Section 2 can be carried out directly from the braid word representation
of the knot. Denoting the standard generators for a braid on $n$ strands by $\sigma_1, \ldots, \sigma_{n-1}$, where $\sigma_i$ represents a crossing of the $i$-th strand over the $(i+1)$-st strand (reading upward), we use a common shorthand that $i$ stands for $\sigma_i$ and $-i$ stands for $\sigma_i^{-1}$. With this notation, a crossing change is effected by changing $i$ to $-i$, and simultaneously switching a positive and a negative crossing is effected by changing a positive entry to its negative and a negative entry to its positive in the braid word. Resolving two crossings is effected by deleting two generators (or their inverses) from the braid word, and the reverse, or de-resolution, is effected by inserting two generators or their inverses into the braid word. Note that in a knot diagram for $K_0$ that is the closure of a braid, all of the strands in the braid can be oriented in the same direction (e.g., upward in the braid), and inserting or deleting any two braid generators preserves the orientation. All four of these braid word operations therefore performs one of the genus one concordance operations in Section 2 and changes the 4-genus of the underlying knot by at most one.

The first step in our process for determining 4-genus, and for determining genus one concordances with knots of known 4-genus via the four crossing operations, is to generate a database of representations of the 21 knots $K_0$ listed in Theorem 1.1 as closures of braids. In fact, braid representatives of these 21 knots were found using a larger database of randomly-generated braids which we had built for an ongoing project with a goal of determining the unknotting number of some of the (as of this writing) 668 knots which the KnotInfo site reports have unknown unknotting number; this database was also used in our disproof of the Bernhard-Jablan Conjecture [2].

The construction of this larger database starts with a procedure for generating random braids on 4 to 12 strands, using random braid words of length between 20 and 60. A python script is used to check that the closure of the braid is a knot, and if so, the braid is added to the database along with the volume of the knot computed using SnapPy [24]. For each of the 21 knots $K_0$ in Theorem 1.1 and for each of the closed braid diagrams for knots $K_1$ in this larger database whose volume matched the volume of $K_0$ to within several decimal places, we used SnapPy (in particular the command “M0.is_isometric_to(M1)” for the knot exteriors M0 and M1 of $K_0$ and $K_1$) to check directly whether the knots were equal; if so, the braid closure representation was added to the database for that knot $K_0$. This gave us our initial collection of braid representatives for the 21 knots.

### 4. Pulling 4-genus down

Using the braids in the database for the 21 knots $K_0$ discussed in Section 3, we carried out all possible instances of the three braid word operations corresponding to the first three genus one concordance operations (crossing change, switching two crossings, and crossing resolution), namely changing the sign of a single letter, simultaneously changing a positive entry to its negative and a negative entry to its positive, and deleting two letters (or their inverses), in the braid word. For each braid we considered from the database, we also carried out 800 random de-resolutions, by randomly generated insertions of two letters.

For each resulting braid, we then check whether the knot $K_1$ obtained by taking the closure of the braid satisfies $g_4(K_1) = 0$ by using SnapPy to identify the knot $K_1$ and then checking whether that knot is in the list from KnotInfo of knots (up to 12
crossings) that are smoothly slice. We note that this part of the project was done
before the announcement on the arXiv (in April 2021) of the results of Karageorghis
and Swenton determining the 4-genera of the 18 knots in Theorem 1.1(b), and
at that time it was known, from the KnotInfo database, that all 21 of the knots \( K_0 \)
have smooth 4-genus either 1 or 2. Thus a genus one concordance with a smoothly
slice knot ‘pulled the 4-genus down’, to determine that \( g_4(K_0) = 1 \). For the 18 knots
in Theorem 1.1(b), our efforts succeeded. In particular, for 17 of these 18 knots, we
have a genus one concordance to a smoothly slice knot constructed by switching two
crossings.

In full detail, for each of the 18 knots we list a braid representative for it, the slice
knot (and the transformed braid representative) that is genus one concordant to it,
and the type of genus one concordance which yields the 4-genus determination. For
every knot, there are, in the end, many braids and genus one concordances to choose
from; we have selected from among the shortest braid representatives found.

\[
\begin{align*}
K_{11n80} & \quad [5, 3, -4, 2, -4, 6, -1, 2, -3, -1, -1, 4, 2, 1, 6, 5, 6, -5, 2, 3, -6, 5, 4, -2] \\
6_1 & \quad [5, -4, 2, -4, 6, -1, 2, -3, -1, -1, 4, 1, 6, 5, 6, -5, 2, 3, -6, 5, 4, -2] \\
& \text{(resolve two crossings)}
\end{align*}
\]

\[
\begin{align*}
K_{12a187} & \quad [2, -3, 4, 6, 5, 5, -2, -6, -1, 4, -3, -6, 4, 2, 2, 5, 3, 4, -3, 4, -3, -5] \\
6_1 & \quad [2, -3, 4, 6, 5, 5, -2, -6, -1, -3, -6, 4, 2, 2, 5, 3, -3, 4, -3, -5] \\
& \text{(resolve two crossings)}
\end{align*}
\]

\[
\begin{align*}
K_{12a230} & \quad [-4, 3, -2, 1, 2, -3, 4, 4, -5, 6, -5, 3, 6, 4, 2, 3, 2, -1, 4, -5, -3, -3] \\
8_20 & \quad [-4, -2, 1, 2, -3, 4, 4, -5, -5, 3, 6, 4, 2, 3, 2, -1, 4, -5, -3, -3] \\
& \text{(resolve two crossings)}
\end{align*}
\]

\[
\begin{align*}
K_{12a317} & \quad [4, 5, 5, -3, -2, -3, 4, 4, 3, 5, -4, 3, -2, 3, -5, 1, 2, 2, -3] \\
6_1 & \quad [4, 5, -3, -2, -3, 4, 4, 3, 5, -4, 3, -2, -5, 1, 2, 2, -3] \\
& \text{(resolve two crossings)}
\end{align*}
\]

\[
\begin{align*}
K_{12a450} & \quad [1, -4, -3, 1, 2, -6, 4, -3, 4, -6, 2, 3, 5, -4, 5, -1, -3, 2, 6, 4] \\
6_1 & \quad [1, -4, -3, 1, 2, -6, 4, -3, -6, 2, 3, 5, -4, 5, -1, -3, 6, 4] \\
& \text{(resolve two crossings)}
\end{align*}
\]

\[
\begin{align*}
K_{12a570} & \quad [-4, 6, 6, -4, 3, 5, 4, 2, -1, -1, -2, 5, -6, -4, 5, 3, -2, 3, 5, 2, 1, 2, 4, -5] \\
6_1 & \quad [-4, 6, -4, 3, 5, 4, -1, -1, -2, 5, -6, -4, 5, 3, -2, 3, 5, 2, 1, 2, 4, -5] \\
& \text{(resolve two crossings)}
\end{align*}
\]

\[
\begin{align*}
K_{12a624} & \quad [3, -2, 6, -5, -6, -4, -3, 5, 5, -5, -6, 1, 5, 2, 4, 6, 3, -5, 4, 5, 2, 2] \\
6_1 & \quad [3, -2, 6, -5, -6, -4, -3, 5, 5, -5, -5, -6, 1, 5, 4, 6, 3, -5, 4, 5, 2, 2] \\
& \text{(resolve two crossings)}
\end{align*}
\]
\[ K_{12a636} \] \([-3, -6, 2, -1, -2, -5, 4, 5, -3, 3, 6, 6, 5, 4, -2, 3, -2, 6, 1, -5, 3, 4]\]
6\(_1\) \([\text{resolve two crossings}]\)

\[ K_{12a905} \] \([1, 2, 2, -3, 2, -3, -3, -4, -2, 3, 4, 4, -3, -2, 1, 3, 2, -2, 3, -2]\]
10\(_{87}\) \([\text{switch two crossings, marked with underlining}]\)

\[ K_{12a1189} \] \([2, 2, -4, 3, 3, -2, 4, 1, 2, 1, -3, -4, 2, -1, 2, -3, -2, 1, -4, 3]\]
10\(_{137}\) \([\text{resolve two crossings}]\)

\[ K_{12a1208} \] \([-2, 4, 1, -3, 4, -3, 2, -4, 3, 3, -2, 2, 1, 1, 4, -2, 3, 3, -1, 4, -3]\]
10\(_{137}\) \([\text{resolve two crossings}]\)

\[ K_{12n52} \] \([3, -1, 6, 4, -1, -5, 4, 6, -3, 2, -5, 2, 1, 3, 5, -5, -5, 4, 5, 3, -4, 2]\]
10\(_{75}\) \([\text{resolve two crossings}]\)

\[ K_{12n63} \] \([-5, -5, 3, -2, 3, 3, 2, 6, 2, -1, -3, 2, 4, -1, 5, 6, 6, 3, 2, -3, -1, -3, 4, 1]\]
6\(_1\) \([\text{resolve two crossings}]\)

\[ K_{12n225} \] \([-2, 5, 1, -3, -6, -6, 4, 6, -6, 1, -2, 4, 4, -5, -3, 2, -6, 2, -4, 1, -2, 5, 4, 4]\]
K\(_{11n74}\) \([\text{resolve two crossings}]\)

\[ K_{12n555} \] \([5, -3, -6, 5, 7, 4, 6, 1, 5, -3, 4, -2, 3, 5, 4, -6, -3, -6, -3, 4, 7]\]
6\(_1\) \([\text{resolve two crossings}]\)

\[ K_{12n558} \] \([3, -4, -1, -1, 3, -1, 4, -2, 3, 1, -4, 3, 1, 4, -3, 2, 3, 2]\]
8\(_8\) \([\text{resolve two crossings}]\)

\[ K_{12n665} \] \([1, 6, 4, 5, -5, -1, 4, -3, 5, 2, -3, -1, 2, 4, -5, 3, 3, -2, -5, 3, 2, 1, -2, 3, -2, 3]\]
K\(_{12n256}\) \([\text{resolve two crossings}]\)

\[ K_{12n886} \] \([4, 2, -3, 1, -5, 4, -3, -2, 3, 4, 3, 5, 2, 2, 4, 4, -3, -3, -1, -1, -2, -5, -3, 2, 3]\]
6\(_1\) \([\text{resolve two crossings}]\)
This completes the proof of Theorem 1.1(b). As illustrated by the above list, the genus one concordance operation of resolving two crossings has been by far the most successful strategy.

5. Pulling 4-genus up

For the remaining three knots $K_0$ with unknown smooth 4-genus, $K12a153$, $K12n239$, and $K12n512$, the procedure in Section 4 failed to find a slice knot that is genus one concordant with $K_0$ after running on 1800, 20000, and 3500 closed braid diagrams of the knot, respectively (and after running for several months, not including the time for creating the database). On the other hand, that procedure succeeded in finding the genus one concordances for the 18 knots discussed in Section 4 after running on 1 - 500 diagrams for each knot, and on less than 10 for most of them (and within a few days). This naturally led to the conclusion that, since all three knots are known to have 4-genus either 1 or 2, they most likely have smooth 4-genus equal to 2.

In the same computer search described in Section 4, in which the four braid word operations were performed on braid representations in our database for the three knots $K12a153$, $K12n239$, and $K12n512$, for each resulting braid we also checked whether the knot $K_1$ obtained by taking the closure of the braid satisfies $g_4(K_1) = 3$. As above this process uses SnapPy to identify the knot $K_1$ and then checks whether that knot is in the “target list” consisting of the set of knots from KnotInfo that have smooth 4-genus equal to 3. This attempt to pull the 4-genus up also did not succeed. However, in this case the situation is complicated by the fact that all three of the knots $K12a153$, $K12n239$, and $K12n512$ have topological 4-genus equal to 1, according to the KnotInfo site. In analogy with Equation (2), the topological 4-genera of knots that are genus one concordant differ by at most 1 (by an identical argument to the one in Section 2 for smooth 4-genus), and so any knot sharing a genus one concordance with one of the three knots must have topological 4-genus at most 2. There are only 24 knots with 12 or fewer crossings which have smooth 4-genus equal to 3 and also topological 4-genus at most 2 (again from the KnotInfo site), and thus effectively the number of potential knots in the “target list” was limited to only 24.

As a consequence, we created a second procedure for pulling up the 4-genus for the remaining three knots, with modifications both to increase the number of diagrams considered for each of the three knots and to increase the number of knots in the target list.

We describe the method of increasing the target list first. In order to construct a larger list of knots with smooth 4-genus (at least) 3 we adopt another result from the work of Lewark and McCoy, which is an application of Donaldson’s Diagonalization Theorem 5.1. We restate their result here.

**Theorem 5.1.** Let $K$ be a knot with a positive-definite $m \times m$ Goeritz matrix $G$. If $\sigma(K) \leq 0$ and $2g_4(K) = -\sigma(K)$, then there is an $(m - \sigma(K)) \times m$ integer matrix $M$, such that $G = M^T M$.

Lewark and McCoy use the contrapositive of this result to show that twelve 11- and 12-crossing knots $K$ with previously unknown smooth 4-genus and with $\sigma(K) = -2$ satisfy $g_4(K) \geq 2$ (and hence $g_4(K) = 2$). We also apply the contrapositive of Theorem 5.1 to build our larger target list of knots with 4-genus at least 3, as follows.
Using SnapPy’s census of knots with crossing number 13 through 16, contained in the “AlternatingKnotExteriors” and “NonalternatingKnotExteriors” databases, as our source data, we used SnapPy to find the knots $K$ with signature equal to -4. We note that some care needs to be taken in implementing this step, since one can find different (contradictory) conventions on the sign of the signature of a knot, and negative signature plays a very important role in Lewark and McCoy’s result. In particular, SnapPy [24], prior to version 3.0, implemented the ‘opposite’ sign convention for the signature; this was changed, however, in April 2021 with version 3.0. Among the knots with signature -4, we then used SnapPy in Sage [22] to carry out matrix factorization computations, via Sage’s built-in implementation of GAP [7], in order to find the knots $K$ for which the Goeritz matrix does not admit the decomposition in Theorem 5.1 and hence for which $g_4(K) \geq 3$.

Our implementation of this search found no knots $K$ with 14 or fewer crossings, with $\sigma(K) = -4$, for which Theorem 5.1 could conclude that $g_4(K) \geq 3$. We did, however, find three 15-crossing alternating knots and 27 16-crossing alternating knots for which we could conclude that $g_4(K) \geq 3$.

We also searched for target knots among the 1,769,978 hyperbolic 17-crossing alternating knots, using the DT codes contained in the tables of knots provided with the software package Regina [1]. This yielded 332 alternating 17-crossing knots with signature equal to $-4$ which we could show have smooth 4-genus at least 3. Using the 6,283,385 hyperbolic non-alternating 17-crossing knots gave a further 49 examples. This list of $24 + 3 + 27 + 332 + 49 = 435$ knots of crossing number up to 17 and 4-genus at least 3 is the target list of our second procedure.

In our second procedure we employed two methods to build a larger data set of diagrams for $K_0 \in \{K_{12n153}, K_{12n239}, K_{12n512}\}$, and of diagrams for knots $K_1$ that are genus one concordant to $K_0$.

The first method starts with a minimal crossing diagram for $K_0$, uses the “backtrack” function in SnapPy to randomly generate another diagram for $K_0$ with more crossings, and then applies the “braid_word” function in SnapPy to output a representation of $K_0$ as a closure of a braid. Then as before, this method generates diagrams for knots $K_1$ genus one concordant to $K_0$ by carrying out all possible instances of the braid word operations corresponding to crossing change, switching two crossings, and crossing resolution, along with 800 randomly generated insertions of two letters corresponding to de-resolutions.

The second method also starts with a minimal crossing diagram for $K_0$ and uses “backtrack” to randomly generate a new diagram for $K_0$ with more crossings, and then uses SnapPy’s “PD_code” to construct a planar diagram (PD) code for that diagram. We have written a separate algorithm in Python that carries out operations on PD codes corresponding to crossing change, switching two crossings, and resolving two crossings (although not de-resolution), and this is carried out for all possible operations on the PD code of the diagram for $K_0$ to create diagrams for knots $K_1$ genus one concordant to $K_0$.

The last step of the second procedure checks whether a knot $K_1$ in our data set, that is genus one concordant to $K_0$, is equal to one of the 435 knots in our target list of knots with 4-genus at least 3. Unlike our first procedure in Section 4, the diagrams involved here have more crossings. In this case, the procedure uses SnapPy
to compute the volume of the complement of $K_1$ and then to check whether that complement is isometric to the complements of any of the 435 target knots whose volume matches that of $S^3 \setminus K_1$ to several decimal places.

For the knots $K_{12a153}$ and $K_{12n239}$, both the planar diagram and the braid closure approaches succeeded. The planar diagram approach found smaller diagrams in general, and in particular, after further simplification (via Reidemeister moves), Figures 5 and 6 illustrate 17-crossing and 18-crossing diagrams for the knots $K_{12a153}$ and $K_{12n239}$ together with de-resolutions of two crossings yielding the knots $17\text{ah}_0168368$ (from Regina’s database) and $16a328556$ (from SnapPy’s database), respectively. A computation shows that the knots $17\text{ah}_0168368$ and $16a328556$ meet the conditions of the contrapositive of Theorem 5.1; their Goeritz matrices can be found in an appendix at the end of the paper. These knots therefore have 4-genera at least 3, and hence (from Equation 2 and the fact that the 4-genus is either 1 or 2 from KnotInfo) the knots $K_{12a153}$ and $K_{12n239}$ both have 4-genus equal to 2.

![Figure 5. A (de-)resolution for K12a153](image)

![Figure 6. A (de-)resolution for K12n239](image)

DT codes for these knot diagrams (starting from the indicated points) are:

$K_{12a153}$:

$[26, -30, -24, -18, -2, -28, -32, -34, -8, -6, -22, -20, -16, -10, -12, -4, -14]$

$17\text{ah}_0168368$:

$[28, -32, -36, -18, -2, -30, -24, -26, -8, -6, -34, -4, -14, -38, -10, -12, -22, -20, -16]$

$K_{12n239}$:
On the other hand, the knot $K_{12n512}$ proved more difficult to capture by these methods. In particular, after several months of searching, none of the 435 ‘target’ knots with 4-genus at least 3 that we had identified using Theorem 5.1 managed to turn up in our data of knots genus one concordant to $K_{12n512}$. We then expanded our target list of knots $K$ with $g_4(K) \geq 3$, by searching through the 8,400,285 alternating hyperbolic 18-crossing knots from the Regina database and again using Theorem 5.1 yielding 3544 further examples for our target list. (Out of 1,958,354 knots with signature $\pm 4$, this was a 0.18% ‘success’ rate). Running searches on the knots genus one concordant to the knot $K_{12n512}$, built from roughly 200,000 diagrams for $K_{12n512}$, succeeded using the braid closure approach, using the operation of de-resolution of two crossings. In particular, our procedure yielded the 11-strand braid

$$[4, 6, 3, -5, 2, -4, 1, 3, 7, 4, -6, 7, -6, -8, -6, 9, 5, -10, -6, 9, -5, 7, -4, -3, 8, 2, -7, -6, -5, 4, 3, 5, 7, 4, -6, 5, -7, -8, -7, -9, -6, 10, -7, -8, 7, 6, -5, -4, -3, -2, -1, -2, -3, -4, 5, 6, -7, 8, -9, 8, -7, -6, -5, -7]$$

for the knot $K_{12n512}$, and the braid

$$[4, 6, 3, -5, 2, -4, 1, 3, 7, 4, -6, 7, -6, -8, -6, 9, 5, -10, -6, 9, -5, 7, -4, -3, 8, 2, -7, -6, -5, 4, 3, 5, 7, 4, -6, 5, -7, -8, -7, -9, -6, 10, -7, -8, 7, 6, -5, -4, -3, -2, -1, -2, -3, -4, 5, 6, -7, 8, -9, 8, -7, -6, -5, -7, -8, -1]$$

for the knot $K_1 = 18ah_{2335674}$ (from the Regina database), which has $g_4(K_1) \geq 3$. The Goeritz matrix for the latter knot can also be found in the appendix. The knot 18ah_{2335674} is obtained from $K_{12n512}$ by inserting the last two entries of the braid word for 18ah_{2335674}, representing the de-resolution of the two crossings. Consequently, $K_{12n512}$ has smooth 4-genus at least 2, and so (with the information that the genus is at most 2 from KnotInfo) we have $g_4(K_{12n512}) = 2$.

With this result, the proof of Theorem 1.1 is complete; the knots $K_{12a153}, K_{12n239}$ and $K_{12n512}$ all have smooth 4-genus equal to 2. This finishes the computation of smooth 4-genus for all prime knots through 12 crossings.

6. Where to go from here?

Although the smooth 4-genus of every prime knot with 12 or fewer crossings is now known, this still does not allow us to immediately compute the 4-genus of the non-prime knots in the same crossing range. The 3-genus is well-known to be additive under connected sum [23], but it is equally well-known that the 4-genus is not; for example, the connected sum $K\sharp(-K)$ of a knot with its mirror image is (ribbon, and hence) a slice knot, so has smooth 4-genus zero. The computation of $g_4(K)$ for connected sums of knots is a challenging problem, and is closely related to the idea of cobordism distance [3], [9]. There are several interesting results on this problem, especially for connected sums of torus knots [14], [5], but it is far from complete.

Turning to topological 4-genus, there still remain, according to KnotInfo, 7 prime knots through 12 crossings whose topological 4-genus is unknown, namely $K_{12a244}$, $K_{12a810}$, $K_{12a905}$, $K_{12a1142}$, $K_{12n549}$, $K_{12n555}$, and $K_{12n642}$. All have $g_4^{\text{top}}(K)$ equal to 1 or 2. It is possible that techniques like the ones carried out here could shed
light on these remaining cases, as well; this is something that we plan to explore in the future.

The notion of a concordance (of genus zero) - that is, a (smooth) annulus in $S^3 \times I$ between knots $K_0$ and $K_1$ - is at the heart of still another knot invariant which essentially sits between $g_4(K)$ and $g_3(K)$: the concordance genus $g_c(K)$ is the minimum 3-genus of a knot concordant to $K$ [12]. Its value is known for every prime knot through 10 crossings, but its value is unknown (at present) for 208 prime knots through 12 crossings. It would be interesting to see if techniques similar to those employed here could make progress on shrinking this list.

7. Appendix: Matrix Computations

Here we provide Goeritz matrices for the three knots listed in Section 5 found to have $g_4(K) \geq 3$ and used to pull the smooth 4-genera of the knots $K_{12a153}$, $K_{12n239}$ and $K_{12n512}$ up to 2.

17ah_0168368 : DT code = [18, 20, 30, 28, 24, 4, 8, 26, 10, 2, 32, 34, 16, 14, 6, 12, 22]

Goeritz matrix =

$$
\begin{pmatrix}
5 & -3 & -1 & -1 & 0 & 0 & 0 & 0 \\
-3 & 6 & 0 & 0 & -3 & 0 & 0 & 0 \\
-1 & 0 & 3 & 0 & -1 & -1 & 0 & 0 \\
-1 & 0 & 0 & 3 & -1 & 0 & -1 & 0 \\
0 & -3 & -1 & -1 & 6 & 0 & 0 & -1 \\
0 & 0 & -1 & 0 & 2 & 0 & 0 & -1 \\
0 & 0 & 0 & -1 & 0 & 2 & 0 & 0 \\
0 & 0 & 0 & 0 & -1 & 0 & 3 & -1 \\
0 & 0 & 0 & 0 & 0 & -1 & 0 & -1 & 2
\end{pmatrix}
$$

K16a328556 : DT code = [6, 14, 26, 16, 20, 22, 4, 24, 32, 30, 28, 12, 2, 10, 8, 18]

Goeritz matrix =

$$
\begin{pmatrix}
3 & -1 & -1 & -1 & 0 & 0 & 0 & 0 \\
-1 & 3 & 0 & 0 & -1 & -1 & 0 & 0 \\
-1 & 0 & 3 & 0 & 0 & -1 & -1 & 0 \\
-1 & 0 & 0 & 5 & 0 & -2 & -1 & -1 \\
0 & -1 & 0 & 0 & 2 & 0 & 0 & -1 \\
0 & -1 & -1 & -2 & 0 & 6 & 0 & -1 \\
0 & 0 & -1 & -1 & 0 & 0 & 2 & 0 \\
0 & 0 & 0 & -1 & 0 & -1 & 0 & 3 \\
0 & 0 & 0 & 0 & -1 & 0 & 0 & 2
\end{pmatrix}
$$

18ah_2335674 : DT code = [32, 14, 30, 28, 24, 22, 36, 4, 6, 26, 12, 10, 34, 18, 16, 2, 20, 8]
Goeritz matrix =
\[
\begin{pmatrix}
2 & -1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
-1 & 4 & 0 & -1 & -1 & -1 & 0 & 0 & 0 & 0 \\
-1 & 0 & 4 & -2 & 0 & 0 & -1 & 0 & 0 & 0 \\
0 & -1 & -2 & 6 & 0 & -1 & -1 & -1 & 0 & 0 \\
0 & -1 & 0 & 0 & 2 & 0 & 0 & 0 & 0 & -1 \\
0 & -1 & 0 & 0 & 0 & 3 & 0 & 0 & -1 & 0 \\
0 & 0 & -1 & -1 & 0 & 0 & 3 & -1 & 0 & 0 \\
0 & 0 & 0 & -1 & 0 & 0 & -1 & 3 & 0 & 0 \\
0 & 0 & 0 & -1 & 0 & -1 & 0 & 0 & 3 & 0 \\
0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 2 & 0 \\
0 & 0 & 0 & 0 & 0 & -1 & 0 & -1 & 0 & 2
\end{pmatrix}
\]

In addition, files containing the names and DT codes of all of the knots that we identified using Theorem 5.1 to have 4-genus at least 3 and signature $-4$ can be found on the authors’ website, at

https://www.math.unl.edu/~mbrittenham2/knot_data/4genus/

along with the python code used to find the knots.

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