

# Simple Greedy 2-Approximation Algorithm for the Maximum Genus of a Graph

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## Abstract

The maximum genus  $\gamma_M(G)$  of a graph  $G$  is the largest genus of an orientable surface into which  $G$  has a cellular embedding. Combinatorially, it coincides with the maximum number of disjoint pairs of adjacent edges of  $G$  whose removal results in a connected spanning subgraph of  $G$ . In this paper we describe a greedy 2-approximation algorithm for maximum genus by proving that removing pairs of adjacent edges from  $G$  arbitrarily while retaining connectedness leads to at least  $\gamma_M(G)/2$  pairs of edges removed. As a consequence of our approach we also obtain a 2-approximate counterpart of Xuong's combinatorial characterisation of maximum genus.

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## 1 Introduction

One of the paradigms in topological graph theory is the study of all surface embeddings of a given graph. The *maximum genus*  $\gamma_M(G)$  parameter of a graph  $G$  is then the maximum integer  $g$  such that  $G$  has a cellular embedding in the orientable surface of genus  $g$ . A result of Duke [12] implies that a graph  $G$  has a cellular embedding in the orientable surface of genus  $g$  if and only if  $\gamma(G) \leq g \leq \gamma_M(G)$  where  $\gamma(G)$  denotes the (minimum) genus of  $G$ . The basic problem of the area, namely the determination of the set of genera of orientable surfaces upon which  $G$  can be embedded, thus reduces to calculation of  $\gamma(G)$  and  $\gamma_M(G)$ . Minimum genus, similarly to virtually all nonplanar topological graph invariants, is notoriously difficult. Its complexity remained open for more than 10 years after being included as one of the most prominent 12 open problems in the first edition of Garey and Johnson's book [15]. Eventually, Thomassen proved that it is NP-hard [48], even in the class of cubic graphs [50], but the problem is very difficult in practice [4]. For a related problem of Euler genus, a recent breakthrough by Kawarabayashi and Sidiropoulos [27] provided a  $O(g^{256} \log^{189} n)$  approximation. Many other algorithms for topological invariants

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are complex, error-prone, and very difficult to implement, see the discussion in [36] and [37]. On the other hand, maximum genus is considered rather well-understood mainly due to min-max characterisations [29, 52, 28, 38] the existence of polynomial-time algorithms [17, 13], and the fact that the problem is easy for 4-edge-connected graphs. However, the algorithm in [13] for the general case is essentially a reduction to optimum matching forest [16], another one of Garey and Johnson’s 12 open problems. Optimum matching forest problem itself is a special case of linear matroid parity, the problem used in the original reduction in [13] and a common generalisation of matroid intersection and matching in general graphs. While linear matroid parity is polynomial [32], similarly to existing algorithms in topological graph theory, the algorithms for matroid parity are quite involved, not providing the desired intuition, insight, and ease of implementation. Consequently, there is a gap between the actual situation and the perceived status of maximum genus.

In this paper we show that classical edge-addition techniques – ideas dating back to Norhaus et al. [39] and Ringeisen [42] – can be used to efficiently approximate maximum genus, essentially reducing the problem to repeated connectivity testing. The resulting algorithm differs from most other algorithms for nonplanar topological invariants by combining favourable approximation ratio, conceptual simplicity, ease of implementation, and running time guarantees.

## Related work

Maximum genus is a well-established [49, 45, 6, 7, 9, 5, 43, 24] and generalised problem [19, 21, 46, 47, 44, 1, 18, 20]. It is known that every 4-edge-connected graph has two edge-disjoint spanning trees [30] and Xuong’s theorem ([52], Theorem 3 below) implies that it has an embedding with one or two faces, depending on the parity of the cycle rank. This determines the maximum genus exactly, rendering the problem trivial for 4-edge-connected graphs. However, this fact does not make the determination of maximum genus much easier for graphs that are not 4-edge-connected and even bounding the maximum genus remains relatively complicated, see for example [45, 6, 24, 2].

Building on characterisations of maximum genus, Furst et al. [13] and Glukhov [17] independently devised polynomial-time algorithms for determining the maximum genus of an arbitrary graph. The algorithm of [13] uses Xuong’s characterisation of maximum genus and exploits a reduction to the cographic matroid parity on an auxiliary graph; its running time is bounded by  $O(mn\Delta \log^6 m)$ , where  $n$ ,  $m$ , and  $\Delta$  are the number of vertices, edges, and the maximum degree of the graph, respectively. As observed by Mohar and Thomassen [35], a reduction to a slightly less general problem of optimum matching forest is sufficient. However, optimum matching forest is a common generalisation of branching in directed graphs and matching in general graphs. While polynomial, the primal-dual algorithm solving optimum matching forest uses both the algorithms for optimum branchings and matchings in general graphs as subroutines [16]. For the linear matroid parity problem, itself rather difficult, Lovász [32, 34, 33] proved a min-max formula and derived a polynomial-time algorithm. To-date, the two fastest deterministic algorithms for the cographic [14], respectively linear [41], case of matroid parity are both (different) generalisations of the Edmonds’ graph matching algorithm, and no significantly simpler algorithm is known. While the area is still active [31, 10, 25], it seems unlikely that the present level of sophistication can be avoided.

A matroidal structure is also in the background of the second algorithm for maximum genus derived in [17], albeit in a different way. Starting with any spanning tree  $T$  of  $G$ , the algorithm greedily finds a sequence of graphs  $F_i$  such that  $T = F_0 \subseteq \dots \subseteq F_n \subseteq G$ ,  $|E(F_{i+1}) - E(F_i)| = 2$ , and  $\gamma_M(F_i) = i$  for all  $i$ , and  $\gamma_M(F_n) = \gamma_M(G)$ . However, the

extension from  $F_i$  to  $F_{i+1}$  is nontrivial; the underlying ideas of frame decompositions and recombinations can be seen in a slightly more general context of signed graphs in [44]. Consequently, it seems fair to say that the result is quite involved and inaccessible. The running time of this algorithm is bounded by  $O(m^6)$ .

A clever greedy approximation algorithm for the maximum genus of a graph was developed by Chen [5]. The algorithm has two main phases. First, it modifies a given graph  $G$  into a 3-regular graph  $H$  by vertex splitting, chooses an arbitrary spanning tree  $T$  of  $H$ , and finds a set  $P$  of disjoint pairs of adjacent edges in  $H - E(T)$  with the maximum possible size. Second, it constructs a single-face embedding of  $T \cup P$  and then inserts the remaining edges into the embedding while trying to raise the genus as much as possible. A doubly-linked face list data structure is maintained to support attempted edge insertions and to keep track of the embedding constructed. After all the edges had been inserted, a high-genus embedding of  $G$  in the same surface is constructed by contracting the edges created by vertex splitting. The algorithm constructs an embedding of  $G$  with genus at least  $\gamma_M(G)/4$  and its running time  $O(m \log n)$  is dominated by the second phase, that is, by operations on an embedded spanning subgraph of  $H$ . The disadvantages of the algorithm as presented in [5] are the need to actually work with the embedding, and the limited insight it provides into the relationship between the combinatorial structure of the decomposition and the genus of the resulting embedding. The first of these problems can be rectified and the whole process somewhat simplified by focusing on the value of the approximate maximum genus, as opposed to an embedding with such genus. The resulting algorithm then still requires vertex splitting into a 3-regular graph, constructing an optimal adjacency matching in a cotree, and examining the remaining components, and again yields only partial information about which edges of the graph eventually lead to an increase in the genus.

Several recent works deal with practical aspects of computations in topological graph theory [36, 4, 23, 37]. The common theme seems to be that from the practical perspective non-planar topological graph invariants are difficult to compute – for many problems there is either no suitable algorithm or the algorithms are hard to implement [36, 37]. For example, the project of determining all forbidden minors for torus is progressing very slowly due to the existing tools being insufficient, see [37]. In particular, the algorithm presented and used to find forbidden minors in [37] is conceptually simpler and faster in practice than the previous approaches, but has exponential running time. Even in the cases where there is a feasible approach, the inherent difficulty of the problem [4], or the size of the problem space [23] present significant obstacles. For example, it is not uncommon for a single graph on 10–20 vertices to require computation with length in days, although sparse graphs can be usually tackled reasonably well [23, 37].

Our terminology in the rest of the paper is standard and consistent with [35], in particular,  $E(G)$  denotes the set of edges of a graph  $G$ , and the cycle rank  $\beta(G)$  of a connected graph with  $n$  vertices and  $m$  edges is  $\beta(G) = m - n + 1$ . Additionally, we use  $\cup$  for set union and  $G + e$  for the addition of an edge  $e$  to a graph  $G$ . For more details on embeddings we refer the reader to [22] or [35]; a recent survey of maximum genus can be found in [3, Chapter 2].

## 2 Edge-addition techniques and maximum genus

One of the earliest results on embeddings of graphs is the following observation, which is sometimes called Ringeisen’s edge-addition lemma. Although it is implicit in [40], Ringeisen [42] was perhaps the first to draw an explicit attention to it.

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► **Lemma 1.** *Let  $\Pi$  be an embedding of a connected graph  $G$  and let  $e$  be an edge not contained in  $G$ , but incident with vertices in  $G$ .*

- (i) *If both ends of  $e$  are inserted into the same face of  $\Pi$ , then this face splits into two faces of the extended embedding of  $G + e$  and the genus does not change.*
- (ii) *If the ends of  $e$  are inserted into two distinct faces of  $\Pi$ , then in the extended embedding of  $G + e$  these faces are merged into one and the genus raises by one.*

The next lemma, independently obtained in [29], [26], and [52], constitutes the cornerstone of proofs of Xuong's theorem. It follows easily from Lemma 1.

► **Lemma 2.** *Let  $G$  be a connected graph and  $\{e, f\}$  a pair of adjacent edges not contained in  $G$ , but incident with vertices in  $G$ . If  $G$  has an embedding with a single face, then so does  $G \cup \{e, f\}$ .*

For a spanning tree  $T$  of  $G$ , let  $\xi(G, T)$  denote the number of components of  $G - E(T)$  with an odd number of edges.

► **Theorem 3 (Xuong's Theorem).** *Let  $G$  be a connected graph. Then*

$$\gamma_M(G) = (\beta(G) - \min_T \xi(G, T))/2$$

where the minimum is taken over all spanning trees of  $G$ .

It is not difficult to see that every cotree component with an even number of edges can be partitioned into pairs of adjacent edges, and that every cotree component with an odd number of edges can be partitioned into pairs of adjacent edges and one unpaired edge. Therefore, any spanning tree  $S$  minimising  $\xi(G, S)$  maximises the number of pairs in the above partition of the cotree. The proof strategy of Xuong's theorem can now be summarised as follows. First, embed  $S$  in the 2-sphere arbitrarily. Then repeatedly apply Lemma 2 to pairs obtained from the partition of the components of  $G - E(S)$ , each time raising the genus by one. Finally, add the remaining edges. Lemma 1 guarantees that the addition of the remaining edges cannot lower the genus. The result of this process is an embedding of  $G$  with genus at least  $(\beta(G) - \min_T \xi(G, T))/2$ .

The fact that a spanning tree minimising  $\xi(G, T)$  maximises the number of pairs of adjacent edges in the cotree suggests a slightly different, yet essentially equivalent combinatorial characterisation of maximum genus. It is due to Khomenko et al. [29] and in fact is older than Xuong's theorem itself.

► **Theorem 4.** *The maximum genus of a connected graph equals the maximum number of disjoint pairs of adjacent edges whose removal leaves a connected graph.*

The following useful lemma, found for example in [8], is an extension of Lemma 2 to embeddings with more than one face. It can either be proved directly by using Ringelsen's edge-adding technique or can be derived from Xuong's theorem. The lemma was used in [8] to devise an algorithm that constructs an embedding of genus  $\gamma_M(G) - 1$  whenever such an embedding exists (cf. Lemma 4.3 of [5]).

► **Lemma 5.** *Let  $G$  be a connected graph and  $\{e, f\}$  a pair of adjacent edges not contained in  $G$ , but incident with vertices in  $G$ . Then  $\gamma_M(G \cup \{e, f\}) \geq \gamma_M(G) + 1$ .*

Our algorithm is based on the rather obvious, but never fully exploited fact that Lemma 5 can be applied to sets of pairs of adjacent edges which do not necessarily have the maximum possible size. Indeed, if we find any  $k$  pairs of adjacent edges  $(e_i, f_i)_{i=1}^k$  in a graph  $G$  such

that  $G - \bigcup_{i=1}^k \{e_i, f_i\}$  is connected, then by Lemma 5 we can assert that the maximum genus of  $G$  is at least  $k$ . This suggests that identifying a large number of pairs of adjacent edges whose removal leaves a connected subgraph can be utilised to obtain a simple approximation algorithm for the maximum genus. Indeed, in the following section we show that choosing the pairs of adjacent edges arbitrarily yields a 2-approximation of maximum genus.

### 3 The Algorithm

In this section we present a greedy algorithm for finding at least  $\gamma_M(G)/2$  pairs of adjacent edges while the rest of the graph remains connected. The idea is simple: if the removal of a pair of adjacent edges does not disconnect the graph, then we remove it.

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**Algorithm 1:** Greedy-Max-Genus

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**Input** : Connected graph  $G$

**Output** : Set  $P$  of pairwise disjoint pairs of adjacent edges of  $G$  such that  $G - P$  is a connected spanning subgraph of  $G$

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1   $H \leftarrow G$ 
2   $P \leftarrow \emptyset$ 
3  foreach pair of adjacent edges  $e, f$  from  $H$  do
4      if  $H - \{e, f\}$  is connected then
5           $H \leftarrow H - \{e, f\}$ 
6           $P \leftarrow P \cup (e, f)$ 
7  return  $P$ 

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To prove that the set output by Greedy-Max-Genus Algorithm always contains at least  $\gamma_M(G)/2$  pairs of adjacent edges we employ the following lemma, which can be easily proved either using Xuong's theorem or directly from Lemma 1.

► **Lemma 6.** *Let  $G$  be a connected graph and let  $e$  be an arbitrary edge of  $G$  such that  $G - e$  is connected. Then*

$$\gamma_M(G) - 1 \leq \gamma_M(G - e) \leq \gamma_M(G).$$

The final ingredient is the following characterisation of graphs with maximum genus 0.

► **Theorem 7.** *The following statements are equivalent for every connected graph  $G$ .*

- (i)  $\gamma_M(G) = 0$
- (ii) *No two cycles of  $G$  have a vertex in common.*
- (iii)  *$G$  contains no pair of adjacent edges whose removal leaves a connected graph.*

The equivalence (i)  $\Leftrightarrow$  (ii) in Theorem 7 was first proved by Nordhaus et al. in [39]. The equivalence (ii)  $\Leftrightarrow$  (iii) is easy to see, nevertheless it is its appropriate combination with Lemma 6 which yields the desired performance guarantee for Greedy-Max-Genus algorithm, as shown in the following theorem.

► **Theorem 8.** *For every connected graph  $G$ , the set of pairs output by Greedy-Max-Genus Algorithm run on  $G$  contains at least  $\gamma_M(G)/2$  pairs of adjacent edges.*

**Proof.** Assume that the algorithm stops after the removal of  $k$  disjoint pairs of adjacent edges from  $G$ . For  $i \in \{0, 1, \dots, k\}$  let  $H_i$  denote the graph obtained from  $G$  by the removal of the the first  $i$  pairs of edges. By Lemma 6, the removal of a single edge from a graph can

lower its maximum genus by at most one. Therefore, the removal of two edges can lower the maximum genus by at most two. It follows that  $\gamma_M(H_i) \geq \gamma_M(G) - 2i$  for each  $i$ ; in particular,  $\gamma_M(H_k) \geq \gamma_M(G) - 2k$ . From Theorem 7 we get that  $\gamma_M(H_k) = 0$ . By combining these expressions we get  $2k \geq \gamma_M(G)$ , which yields  $k \geq \gamma_M(G)/2$ , as desired. ◀

Clearly, any maximal set of pairs of adjacent edges of  $G$  whose removal from  $G$  yields a connected graph can possibly be the output of Greedy-Max-Genus Algorithm run on  $G$ . Hence, as a corollary of Theorem 8 we obtain the following 2-approximate counterpart of Theorem 4.

► **Theorem 9.** *Let  $G$  be a connected graph and let  $P$  be any inclusion-wise maximal set of disjoint pairs of adjacent edges of  $G$  whose removal leaves a connected subgraph. Then  $|P| \geq \gamma_M(G)/2$ .*

#### 4 Notes

Considering a star  $K_{1,2n}$  with every edge doubled and a loop attached to every pendant vertex shows that the bound in Theorems 8 and 9 is best possible. At the same time, the last example shows that processing vertices in the decreasing order with respect to their degrees does not lead to an algorithm with better approximation ratio.

The simplest realisation of the algorithm considers all pairs of edges  $\{e, f\}$  with a common end-vertex and test whether removing the pair does not disconnect the graph. The running time is  $O((\tau + \rho) \sum_{i=1}^n d_i^2)$ , where  $\tau$  is the time required to test the connectivity,  $\rho$  is the time required to update the underlying data structure, and  $d_i$  is the degree of the  $i$ -th vertex. If the input graph is simple, then  $\sum_{i=1}^n d_i^2 = O(m^2/n)$  by [11]. If the input graph is not simple, it can be preprocessed by including in the solution a pair of adjacent parallel edges and/or loops and keeping at least one edge from each set of parallel edges until there are no sets of more than two parallel edges and no adjacent loops. It is easy to see that the resulting graph again satisfies  $\sum_{i=1}^n d_i^2 = O(m^2/n)$ . Therefore, using a linear-time connectivity test the running time is  $O(m^3/n)$ . Trading simplicity for running time and using algorithms for dynamic graph connectivity [51] it is possible to support updates in  $\rho = O(\log^2 n / \log \log n)$  amortized time and queries in  $\tau = O(\log n / \log \log n)$  worst-case time. This would yield running time  $O(m^2 \log^2 n / (n \log \log n))$ .

In our opinion, obtaining a simple algorithm (i. e. one notably simpler than the tools used in the exact algorithms) with approximation ratio better than 2 would be a significant achievement.

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