CS E6204 Lecture 3
Genus Distribution of a Graph

Abstract

The principal genus distribution problem is to count the number of cellular imbeddings of a given graph. Complete distributions have been obtained for a few basic families of graphs. Various properties of genus distributions and of related invariants are examined, especially the properties of the average genus.

* This lecture is based on Chapter 3 of [BWGT], contributed by Jonathan L. Gross.

1. Introduction

An ubiquitous question in topological graph theory:
- can a given graph can be imbedded in a given surface?

$$G \to S_j \quad ??$$

This readily extends to the following problem:
- given the graph G and the surface S_j,

count the number of different imbeddings of $G \to S_j$.

(We are using the Iverson truth function.)

$$\sum_{\rho} (\rho : \overbrace{G \to S_j}^{?}) \qquad \rho \text{ varies over all rotations systems}$$

A contrasting classical problem with its origins in geometry:
- for a fixed surface S_j,

how many different **maps** are there to S_j,

where what varies is the graph that serves as the 1-skeleton.

In what follows, all imbeddings are taken to be **cellular**, except where clear from context that non-cellular imbeddings are under consideration. Two cellular imbeddings are considered to be **the same** if their rotation systems are combinatorially equivalent.

DEFINITIONS

- The ***number of imbeddings*** of G in S_h is the number $g_h(G)$ of rotation systems for G that induce a cellular imbedding in S_h;
- the ***orientable genus range*** of a graph G is the set of integers h for which $g_h(G) > 0$;
- the ***minimum genus*** is the number
$$\gamma_{\min}(G) = \min\{h\colon\ g_h(G) > 0\}$$
- the ***maximum genus*** is the number
$$\gamma_{\max} = \max\{h\colon\ g_h(G) > 0\}$$

The following result is a variation on an elementary “intermediate value theorem for genus”.

Theorem 1.1 *The orientable genus range of a graph G is the consecutive set of integers*

$$\{h\colon \gamma_{\min}(G)\ \leq\ h\ \leq\ \gamma_{\max}(G)\}.$$

Proof We can change any rotation system of a graph into any other by effecting a sequence of transpositions of edge-ends, each of which changes the genus of the induced surface by at most 1. In particular, there is such a sequence that goes from a minimum-genus imbedding to a maximum-genus imbedding. ■

DEFINITIONS The ***genus distribution*** of a graph G is the integer-valued function $h \mapsto g_h(G)$, and the ***genus distribution polynomial*** of G is

$$I_G(x) \;=\; \sum_{h\geq 0} g_h(G)\, x^h.$$

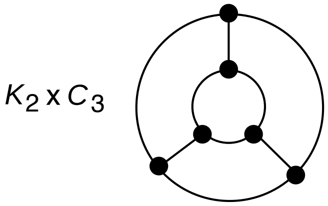
These concepts were introduced by Gross and Furst [GrFu].

Theorem 1.2 *For any graph G,*

$$\sum_{h\geq 0} g_h(G) \;=\; \prod_{v\in V(G)} [\deg(v)-1]!.$$

Proof The sum on the left and the product on the right both count each imbedding of G exactly once. ■

For relatively small graphs, the orientable genus distribution can be calculated by elementary *ad hoc* methods. For example, in Fig. 1, the graph $K_2 \times C_3$ has six vertices, each of degree 3, and so the total number of orientable imbeddings is $64 = 2^6$.



genus of surface	0	1	2
number of embeddings	2	38	24

Figure 1: A graph and its orientable genus distribution.

A ***bar-amalgamation*** of two disjoint graphs G and H is obtained from $G \cup H$ by joining a vertex of G and a vertex of H with an edge, referred to as the ***bar***, as illustrated in Fig. 2.

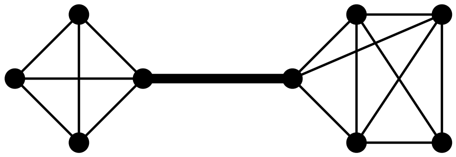


Figure 2: A bar-amalgamation of K_4 and $K_5 - e$.

The following theorem of Gross and Furst [GrFu] is useful in simplifying genus distribution calculations.

Theorem 1.3 *The genus distribution of a bar-amalgamation of two graphs is the convolution of their respective genus distributions, multiplied by the product of the degrees of the two vertices of the bar (not counting the bar).*

The outcome is very much more complicated when two graphs are directly amalgamated at a vertex, without the bar. Amalgamations at two 2-valent vertices help to construct genus distributions for 4-regular graphs, a very important case. Pasting $2 : n$ approaches the ultimate problem of pasting $m : n$.

[GrKhPo] pasting 2:2

[Gr10a] self-pasting 2:2

[KhPoGr] pasting 2:n

Of course, two graphs can be amalgamated along an edge in each graph:

[PoKhGr10A] pasting 2-2:2-2

[PoKhGr10A] self-pasting 2-2:2-2

2. Enumerating Imbeddings by Surface Type

Even at the outset of the programme to provide explicit calculations of imbedding distributions, it was clear that a variety of techniques would be needed. In this section, we consider three infinite families: closed-end ladders, cobblestone paths, and bouquets.

Closed-end ladders

The ***closed-end ladder*** L_n is the graph obtained from the Cartesian product $P_n \times K_2$ by doubling the edges at the ends of the path, as illustrated in Fig. 4. Such ladder-like graphs played a crucial role in the solution of the Heawood map-coloring problem (see Ringel [Rin]).

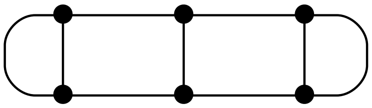


Figure 3: The 3-rung closed-end ladder L_3.

A topological lemma based on a face-tracing argument was used by Furst, Gross and Statman [FuGrSt] to partition the possible rotation systems of the ladder L_n according to the induced surface genus. This permitted the number $g_h(L_n)$ to be represented as a sum whose terms are products of binomial coefficients.

A succession of combinatorial identities led to the following closed formula:

$$g_h\left(L_n\right)=\begin{cases}2^{n-1+h}\binom{n+1-h}{h}\dfrac{2n+2-3h}{n+1-h} & \text{for } h\leq\left\lfloor\dfrac{n+1}{2}\right\rfloor,\\ 0 & \text{otherwise.}\end{cases}$$

Table 1 shows the genus distribution for some small ladders.

Table 1: The genus distribution of small ladders.

$g_h(L_n)$	g_0	g_1	g_2	g_3	g_4	total
L_1	2	2	0	0	0	4
L_2	4	12	0	0	0	16
L_3	8	40	16	0	0	64
L_4	16	112	128	0	0	256
L_5	32	288	576	128	0	1024

Subsequently, McGeoch [McG] calculated the genus distributions of the related families of graphs known as circular ladders and Möbius ladders. Also, Tesar [Te] calculated the genus distribution of the family known as Ringel ladders.

- The method of [PoKhGr10A] and [PoKhGr10A] for recalculating the genus distributions of these ladder graphs is iterative edge-amalgamation.

Figure 4: Obtaining a ladder L_n by iterative edge-amalgamation.

Single-root partials of (G, e)

The imbeddings of single-edge-rooted graphs can be differentiated into two distinct types, depending on whether the two occurrences of the root-edge are in the same or in different fb-walks of an imbedding. The number $g_i(G, e)$ is the sum of the following ***single-root partials***:

$$\begin{aligned} s_i(G,e) &= \text{The number of imbeddings of } G \text{ such that} \\ &\quad\ e \text{ occurs twice on the same fb-walk.} \\ d_i(G,e) &= \text{The number of imbeddings of } G \text{ such that} \\ &\quad\ e \text{ occurs on two different fb-walks.} \end{aligned}$$

Double-root partials of (G, e, f)

Table 2: Double-root partials of (G, e, f).

Partial	*Counts these imbeddings in* S_i
$dd_i(G, e, f)$	e and f both occur on two fb-walks
$ds_i(G, e, f)$	e occurs on two fb-walks and f on one fb-walk
$sd_i(G, e, f)$	e occurs on one fb-walk and f on two fb-walks
$ss_i(G, e, f)$	e occurs on one fb-walk and f on one fb-walk

Some First-order Sub-partials of (G, e, f)

The following three numbers are called sub-partials of $dd_i(G, e, f)$:

$dd_i^0(G, e, f)$ = the number of imbeddings of type-dd_i such that neither fb-walk at e is incident on f.

$dd_i'(G, e, f)$ = the number of imbeddings of type-dd_i such that exactly one fb-walk at e is incident on f.

$dd_i''(G, e, f)$ = **the number of imbeddings of type-**dd_i **such that both fb-walks at** e **are incident on** f**.**

In complicated constructions many more sub-partials may be needed. For closed-end ladders, the only one we need is $dd_i''(G, e, f)$.

We introduce the use of productions

$$d_i(G) * dd''_j(H) \longrightarrow 2d_{i+j}(W) + 2s_{i+j+1}(W)$$

$$s_i(G) * dd''_j(H) \longrightarrow 4d_{i+j}(W)$$

and picture-proofs of their correctness:

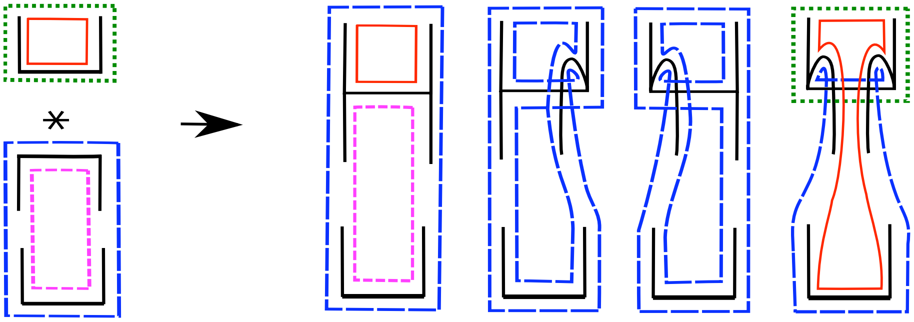


Figure 5: $d_i(G) * dd''_j(H) \longrightarrow 2d_{i+j}(W) + 2s_{i+j+1}(W)$

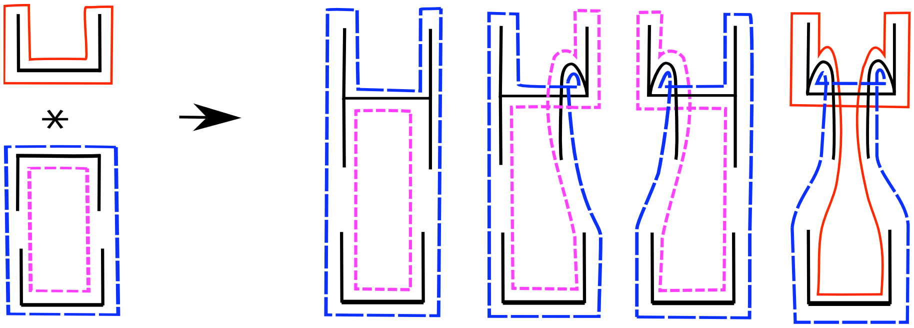


Figure 6: $s_i(G) * dd''_j(H) \longrightarrow 4d_{i+j}(W)$

Cobblestone paths

The ***cobblestone path*** J_n is the graph obtained by doubling each edge of the n-vertex path P_n and then adding a loop at each end, as illustrated in Fig. 7.

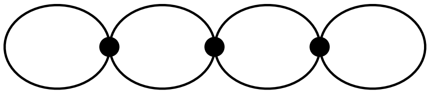


Figure 7: The cobblestone path J_3.

The genus distribution of cobblestone paths was calculated recursively by Furst, Gross and Statman [FuGrSt].

$$g_h(J_n) \ = \ 3^h \cdot 4^{n-1} \binom{n-h}{h} \ + \ 2 \cdot 3^{h-1} \cdot 4^{n-1} \binom{n-h}{h-1}.$$

This could now by rederived using vertex-amalgamations as in [GrKhPo]. Table 3 shows the genus distribution for some of the smaller cobblestone paths.

Table 3: The genus distribution of some cobblestone paths.

$g_h(J_n)$	g_0	g_1	g_2	g_3	total
J_1	4	2	0	0	6
J_2	16	20	0	0	36
J_3	64	128	24	0	216
J_4	256	704	336	0	1296

Bouquets

The ***bouquet*** B_ℓ is the graph with one vertex and ℓ loops, as illustrated in Fig. 8. One of the properties of bouquets important to topological graph theory is that every regular graph can be derived by assigning voltages (possibly permutation voltages) to some bouquet (see Gross and Tucker [GrTuA] [GrTuC]).

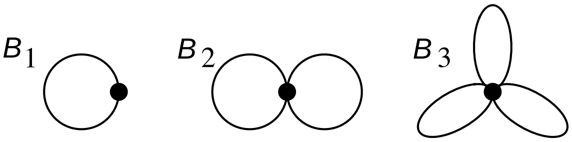


Figure 8: Some small bouquets.

Permutation-group algebra is a key to calculating the distribution of imbeddings of bouquets. Gross, Robbins and Tucker [GrRoTu] established the equation

$$g_h(B_n) \;=\; (n-1)! \cdot 2^{n-1} \cdot e_{n-2h+1}(n)$$

The quantity $e_k(\ell)$ is the cardinality of the set of permutations $\pi \in \Sigma_{2\ell}$, corresponding to an arbitrary fixed cycle ζ of length 2ℓ for which there is a full involution β such that $\pi = \zeta \circ \beta$, and such that π has k cycles. The value of $e_k(\ell)$ is given by a formula of Jackson [Ja].

The closed formula above for $g_h(B_\ell)$ leads to this recursion:

initial conditions:

$$\begin{array}{l} g_0(B_0) \;=\; g_0(B_1) \;=\; 1; \quad g_h(B_0) \;=\; g_h(B_1) \;=\; 0 \;\text{ for } h \geq 1; \\ g_0(B_2) \;=\; 4,\; g_1(B_2) \;=\; 2; \quad \text{and } \; g_h(B_2) \;=\; 0, \;\text{ for } h \geq 2. \end{array}$$

recursion for $h > 2$:

$$\begin{aligned} (\ell+1)\, g_h(B_\ell) \;&=\; 4(2\ell-1)(2\ell-3)(\ell-1)^2(\ell-2)\, g_{h-1}(B_{\ell-2}) \\ &\qquad + 4(2\ell-1)(\ell-1)\, g_h(B_{\ell-1}). \end{aligned}$$

This recursion enables us to calculate the numerical values for the genus distribution of bouquets in Table 4.

Table 4: The genus distribution of some bouquets.

$g_h(J_n)$	g_0	g_1	g_2	total
B_0	1	0	0	1
B_1	1	0	0	1!
B_2	4	2	0	3!
B_3	40	80	0	5!
B_4	672	3360	1008	7!
B_5	16128	161280	185472	9!

Rieper [Rie] extended the group-character approach of [GrRoTu] in his analysis of the genus distribution of ***dipoles***. (The ***dipole*** D_ℓ is the graph with two vertices joined by ℓ edges.)

3. Total imbedding distributions

When non-orientable imbeddings of a graph G are also included, the total number of imbeddings increases by a factor of $2^{\beta(G)-1}$, since for any given rotation system and fixed spanning tree T, each of the $\beta(G)$ edges not in T may be twisted or untwisted.

The ***total imbedding distribution*** of a graph G is the bivariate polynomial

$$\ddot{I}_G(x,y) \;=\; I_G(x) + \tilde{I}_G(y) \;=\; \sum_{h\geq 0} g_h(G)x^h \;+\; \sum_{k\geq 1} \tilde{g}_k(G)y^k.$$

The calculation of total imbedding distributions appears to be quite difficult, in part because the possible twisting of edges complicates the recurrences that one might derive. In order to calculate the genus or crosscap number for a given general rotation system ρ without doing face-tracing, we can choose a spanning tree T, and then calculate the entries of the ***overlap matrix*** $M_{\rho,T} = [m_{i,j}]$, in which

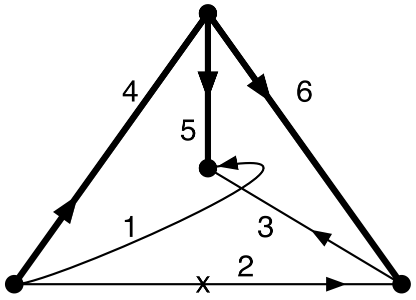
$$m_{i,j} = \begin{cases} 1 & \text{if } i \neq j \text{ and } \mathit{pure}(\rho)\,\big|_{T+e_i+e_j} \text{ is non-planar,} \\ -1 & \text{if } i = j \text{ and edge } i \text{ is twisted,} \\ 0 & \text{otherwise.} \end{cases}$$

Here, the notation $\mathit{pure}(\rho)|_{T+e_i+e_j}$ means the restriction of the underlying pure part of the rotation system ρ to the subgraph $T + e_i + e_j$. Mohar [Mo] derived the following general property of the overlap matrix.

Theorem 3.1 *Let G be a graph, let T be a spanning tree of G, and let ρ be a general rotation system of G. Then*

$$rank(M_{\rho,T}) = \begin{cases} 2h & \text{if the induced surface } S(\rho) \text{ is } S_h, \\ k & \text{if the induced surface } S(\rho) \text{ is } N_k. \end{cases}$$

For example, in Fig. 9, the edges of the spanning tree are labelled 4, 5 and 6. Thus, the rows and columns correspond to c-otree edges 1, 2 and 3. The cross on the bottom edge indicates that it is twisted. Since the rank of the overlap matrix is 3 and the imbedding is non-orientable, the surface for that imbedding must be N_3.



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

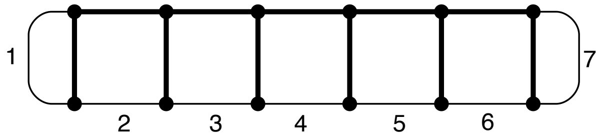
overlap matrix

Figure 9: A graph and its overlap matrix.

At first, the concept of an overlap matrix seemed to be purely of theoretical interest. Indeed, whereas calculating the surface type by face-tracing requires $O(m)$ time for a graph with m edges, calculating the rank of an overlap matrix deteriorates to $O(m^2)$ time.

However, Chen, Gross and Rieper [ChGrRiA] discovered that regrouping the total set of imbeddings according to the rank of the overlap matrix sometimes facilitates calculation of the total imbedding distribution.

For example, consider a tree T in the ladder graph for which the co-tree is a path, as in Fig. 10, and in the cobblestone path graph for which a co-tree is almost a path, as in Fig. 11. These yield a 'tridiagonal' overlap matrix, which is convenient for calculating the rank because there are zeros everywhere except possibly on entries on a narrow band near the diagonal. Each 'x' in the matrix of Fig. 10 indicates an entry that may be either 1 or 0.



$$\begin{matrix} x & x & 0 & 0 & 0 & 0 & 0 \\ x & x & x & 0 & 0 & 0 & 0 \\ 0 & x & x & x & 0 & 0 & 0 \\ 0 & 0 & x & x & x & 0 & 0 \\ 0 & 0 & 0 & x & x & x & 0 \\ 0 & 0 & 0 & 0 & x & x & x \\ 0 & 0 & 0 & 0 & 0 & x & x \end{matrix}$$

Figure 10: The ladder L_6 with a spanning tree, and the form of the corresponding tridiagonal overlap matrix.

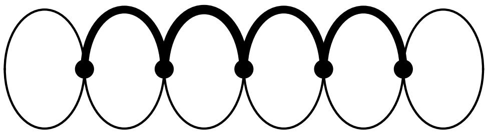


Figure 11: The cobblestone path J_5 with a spanning tree.

The following total imbedding distribution polynomial for closed-end ladders was obtained in [ChGrRiA]:

$$2^n \sum y^{n+1-r} \prod_{h=1}^{r} \left[rd\left(\tfrac{2^{i_h}}{3}\right) \, + \, rd\left(\tfrac{2^{i_h+1}}{3}\right) y \right] - I_{L_n}\left(y^2\right) \, + \, I_{L_n}(x),$$

where $rd(x)$ means the nearest integer to x, and the sum is taken over all r-tuples of positive integers i_1, i_2, $\ldots$, i_r with sum equal to $n+1$. This total imbedding distribution polynomial was obtained for cobblestone paths:

$$\sum 2^{n+r-1} y^{n+1-r} \prod_{h=1}^{r} \left[rd\left(\tfrac{2^{i_h}}{3}\right) + rd\left(\tfrac{2^{i_h+1}}{3}\right) y \right] - I_{J_n}\left(y^2\right) + I_{J_n}(x).$$

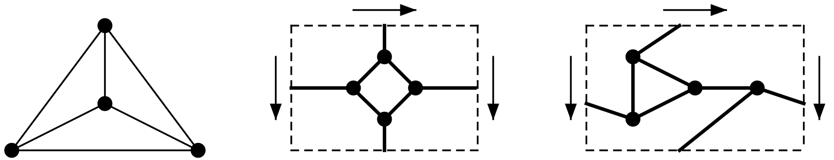
4. Congruence Classes

A second enumerative aspect of graph imbeddings regards two imbeddings as equivalent if they ‘look alike’ when vertex and edge labels are removed. Two imbeddings $\iota_1\colon G \to S$ and $\iota_2 : G \to S$ are ***congruent***, denoted by $\iota_1 \simeq \iota_2$, if there exist a graph automorphism $\alpha\colon G \to G$ and a surface homeomorphism $\eta\colon S \to S$ for which the diagram in Fig. 12 is commutative.

$$\begin{tikzcd}
G \arrow[r, "\iota_1"] \arrow[d, "\alpha"'] & S \arrow[d, "\eta"] \\
G \arrow[r, "\iota_2"'] & S
\end{tikzcd}$$

Figure 12: The commutativity condition for an imbedding congruence.

For example, Fig. 13 shows how the sixteen different orientable imbeddings of the complete graph K_4 are partitioned into congruence classes:



two like this in S_0 six like this in S_1 eight like this in S_1

Figure 13: Partitioning the 16 imbeddings of K_4 into congruence classes.

Burnside's lemma is used to count congruence classes. Each automorphism of a graph G induces a permutation on the rotation systems of G that preserves the congruence class, but does not necessarily preserve the equivalence class, as illustrated in Fig. 14.

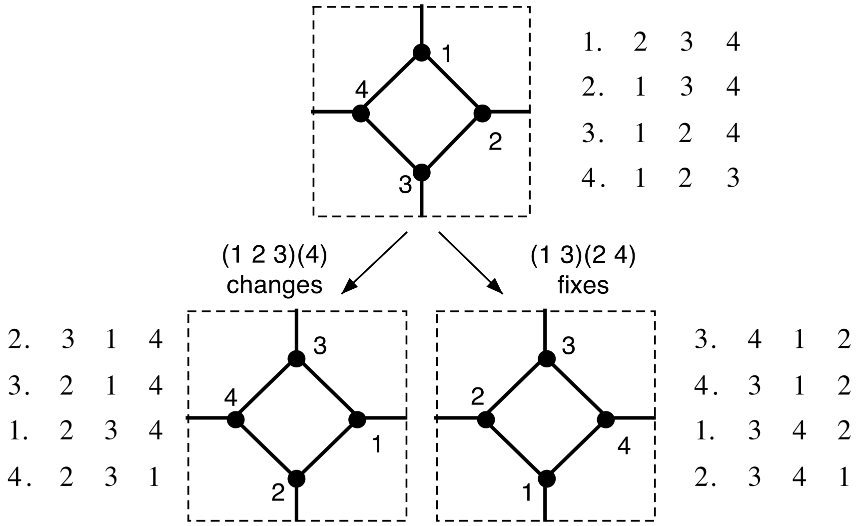


Figure 14: The induced action of two permutations on a rotation system.

Fig. 14 indicates the induced action on a given rotation system of the permuations (1 2 3)(4) and (1 3)(2 4). Although rows 1 and 4 of the resulting rotation system for (1 2 3)(4) (lower left) are the same rotations as in the given rotation system (top), the rows 2 and 3 are the reverse rotations. By way of contrast, rows 1, 2, 3 and 4 of the resulting rotation system for the permutation (1 3)(2 4) (lower right) are the same as the corresponding rows of the given permutation.

Mull, Rieper and White [MuRiWh] showed how to count congruence classes of imbeddings of complete graphs into oriented surfaces.

5. The Unimodality Problem

A sequence $\{a_m\}$ is ***unimodal*** if there exists an integer M such that

$$a_{m-1} \leq a_m \text{ for all } m \leq M \text{ and } a_m \geq a_{m+1} \text{ for all } m \geq M.$$

A typical unimodal sequence first rises and then falls. A sequence $\{a_m\}$ is ***strongly unimodal*** if its convolution with every unimodal sequence yields a unimodal sequence. An equivalent criterion for unimodality (see [KeGe]) is that

$$a_m^2 \geq a_{m+1}a_{m-1} \quad \text{for all } m.$$

It is easily proved that every strongly unimodal sequence is unimodal, which affirms the appropriateness of the name 'strongly unimodal'. All known genus distributions are strongly unimodal. The pioneering calculations are summarized in the next theorem, for which the first two families were studied by Furst, Gross and Statman [FuGrSt] and the third by Gross, Robbins and Tucker [GrRoTu].

Theorem 5.1 *The genus distributions of closed-end ladder graphs, cobblestone paths, and bouquets are strongly unimodal.*

We observe that an imbedding of the bouquet B_ℓ has $\ell+1$ faces in the sphere S_0, $\ell-1$ faces in the torus S_1, $\ell-3$ faces in the double-torus S_2, and so on. This suggests that the genus distribution of the bouquet B_n might resemble this sequence of Stirling cycle numbers

$$\begin{bmatrix} 2n \\ n+1 \end{bmatrix}, \begin{bmatrix} 2n \\ n-1 \end{bmatrix}, \begin{bmatrix} 2n \\ n-3 \end{bmatrix}, \dots,$$

where $\left[{n \atop k}\right]$ denotes the number of ways to partition n distinct objects into k cycles.

Using group character theory, Stahl [StA] proved that the genus distribution of bouquets is asymptotically proportional to this sequence. He also proved [StC] that the resemblance to Stirling numbers also holds for various graphs of small diameter, including partial suspensions of trees and of cycles, which serves as further evidence for unimodality. Whether the genus distribution of every graph is strongly unimodal remains an interesting open problem.

6. Average Genus

The average value of the genus of the imbedding surface for a graph G, taken over all orientable imbeddings, is called the ***average genus*** and denoted by $\gamma_{\text{avg}}(G)$.

Obviously, a graph has average genus 0 if and only if it has maximum genus 0. Thus, in consideration of Nordhaus *et al.* [NoRiStWh], a graph has average genus 0 if and only if no vertex lies on more than one cycle.

As a corollary to Theorem 1.3, Gross and Furst [GrFu] proved that the average genus acts additively on bar-amalgamations. (Analogously, both γ_{min} and γ_{max} act additively on bar-amalgamations.)

Theorem 6.1 *The average genus of a bar-amalgamation of two graphs G and H is $\gamma_{\text{avg}}(G) + \gamma_{\text{avg}}(H)$.*

Suppose that r independent edges of a $2r+s$ cycle are doubled and that a loop is added at each vertex not on a doubled edge, as illustrated in Fig. 15. Such a graph is called a ***necklace*** of type (r, s). Gross, Klein and Rieper [GrKlRi] calculated the average genus of all such graphs.

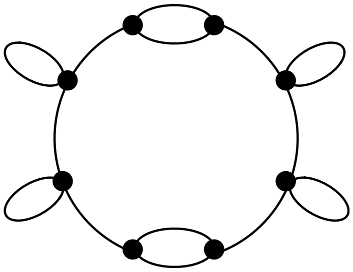


Figure 15: A necklace of type $(2, 4)$.

Theorem 6.2 *The average genus of a necklace of type* (r, s) *is* $1 - \left(\frac{1}{2}\right)^r \left(\frac{2}{3}\right)^s$.

Since the number of different necklaces of type (r, s) grows arbitrarily large as the numbers r and s increase, we infer:

> **Arbitrarily many non-homeomorphic 2-connected graphs can have the same average genus**.

By Xuong's theorem (see Chapter 2), the maximum genus of a necklace is 1. If r or s increases, then the average genus of a necklace of type (r, s) approaches 1, which is part of the general pattern that a randomly chosen imbedding is more likely to be nearer to the maximum genus than to the minimum genus.

Theorem 6.2 also established the number 1 as the first known upper limit point of average genus, thereby raising the questions of the prevalence of upper limit points and of the existence of lower limit points. These are discussed in greater detail below.

The six smallest values of the average genus of any graph are

$$\frac{1}{3}, \ \frac{1}{2}, \ \frac{5}{9}, \ \frac{2}{3}, \ \frac{19}{27} \ \text{ and } \frac{3}{4}$$

(see [GrKlRi]). Fig. 16 shows a necklace realizing each of them.

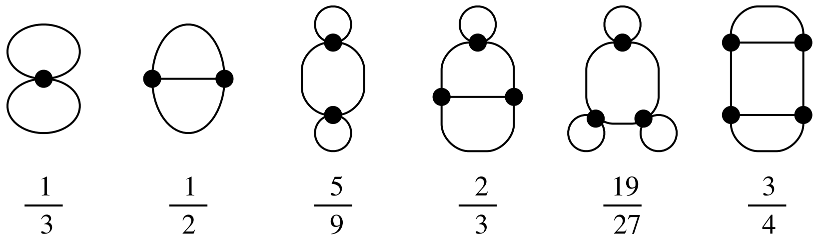


Figure 16: The graphs with the six smallest positive values of the average genus.

Chen and Gross [ChGrC] found that, except for necklaces, there are just eight 2-connected graphs of average genus less than 1. Their proof is based on the minimum number of paths that one must add to a cycle to obtain a given 2-connected graph — that is, on the number of steps in a 'Whitney synthesis' (also called an 'ear decomposition'). The bouquet B_3, the dipole D_4 and the complete graph K_4 have average genus $\frac{2}{3}$, $\frac{5}{6}$ and $\frac{7}{8}$, respectively. Fig. 17 shows the other five such graphs and their average genus. In combination with Theorem 1.3, this yields a complete classification of those graphs with average genus less than 1.

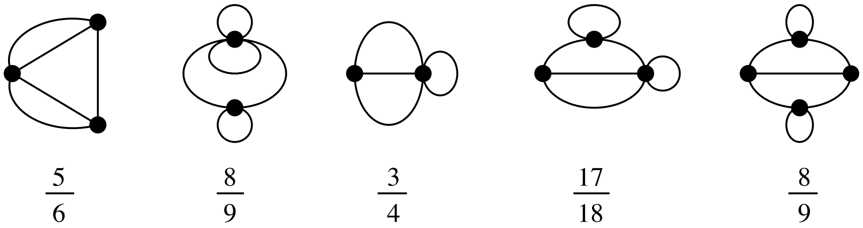


Figure 17: The five sporadic 2-connected graphs with average genus less than 1.

Further, it is proved in [ChGrC] that there are exactly three 2-connected graphs with average genus exactly 1. They are shown in Fig. 18.

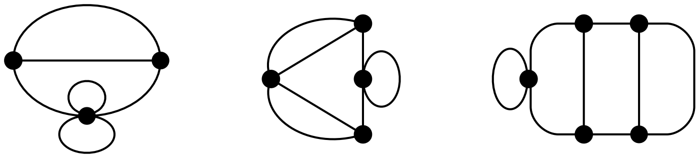


Figure 18: The three 2-connected graphs with average genus 1.

Theorem 6.2 inspired an investigation of the possible limit points of average genus, and Chen and Gross [ChGrA] obtained the following results for 3-connected graphs (simple or not) and for simple 2-connected graphs.

Theorem 6.3 *For each real number r, there are only finitely many 3-connected graphs and finitely many simple 2-connected graphs with average genus less than r.*

Consequently, there are only finitely many 3-connected or simple 2-connected graphs with the same average genus. Moreover, the sets of values of average genus of these large families of graphs have no limit points.

In a sequel, Chen and Gross [ChGrB] gave a systematic method for constructing upper limit points, which we now describe. Let e be an edge of a graph. We ***attach an open ear*** to edge e if we insert two new vertices in the interior of e and then double the edge between them; the two new vertices are called the ***ends*** of that open ear. Similarly, we ***attach a closed ear*** to e if we insert one new vertex w in the interior of e and then attach a loop at w; the vertex w is called the ***end*** of that closed ear. Fig. 19 illustrates both kinds of ear attachments.

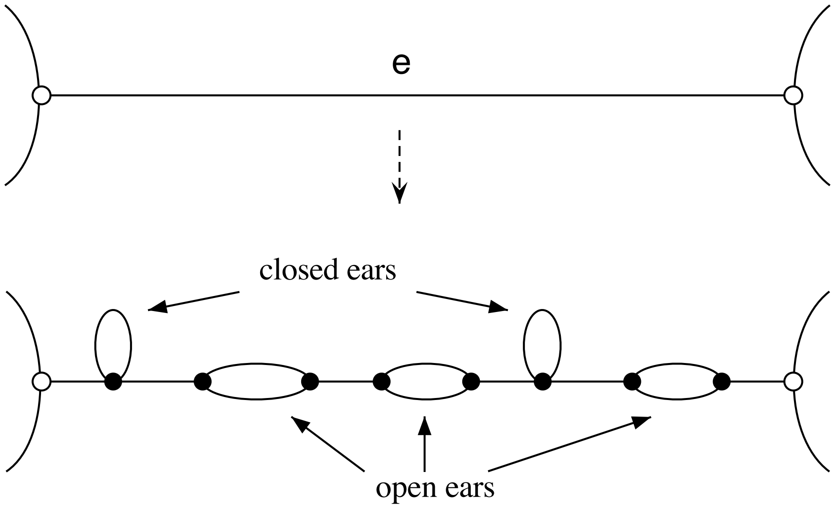


Figure 19: Three open ears and two closed ears serially attached to an edge e.

We say that r open ears and s closed ears are attached ***serially*** to the edge e if the ends of the ears are all distinct, and if no ear has an end between the two ends of an open ear. Theorem 6.4 provides a means for constructing upper limit points; in fact, **all limit points arise from this construction**.

Theorem 6.4 *Let G be a 2-connected graph, and let G_+ be a graph obtained by serially attaching ears to an edge of G. Then*

$$\gamma_{\text{avg}}(G) \;<\; \gamma_{\text{avg}}(G_+) \;<\; \gamma_{\text{avg}}(G) + 1.$$

Chen and Gross [ChGrD] concluded their series of papers by proving that **the set of values of average genus taken over all graphs has no lower limit points**. A linear-time algorithm for isomorphism testing of graphs of bounded average genus was derived by Chen [Ch].

Some bounds have been obtained for the average genus. In this summary of what is known about bounds, it has been conjectured that part (c) can be improved. In the following theorem, part (a) is due to Gross, Klein and Rieper [GrKlRi] and parts (b) and (c) are due to Chen, Gross and Rieper [ChGrRiB]:

Theorem 6.5 *Let G be a graph.*

(a) If H is a subgraph of G, then $\gamma_{\text{avg}}(H) \leq \gamma_{\text{avg}}(G)$.

(b) If G is 3-regular, then $\gamma_{\text{avg}}(G) \geq \frac{1}{2}\gamma_{\max}(G)$.

(c) If G is a simple, 2-connected graph, then $\gamma_{\text{avg}}(G) \geq \frac{1}{16}\beta(G)$, where $\beta(G)$ is the cycle rank.

7. Stratification of Imbeddings

Superimposing an adjacency structure on the distribution of orientable imbeddings was first explored as a possible aid to calculating the minimum genus and maximum genus of a graph. It subsequently appeared to offer some insight into the problem of deciding whether two graphs are isomorphic.

For any graph G, the ***stratified graph*** SG is defined as follows. The vertices of SG are the orientable imbeddings of G. Two imbeddings ι_1 and ι_2 are V***-adjacent*** if there is a vertex v of G for which moving a single edge-end at v is sufficient to transform a rotation system for ι_1 into a rotation system for ι_2; they are E***-adjacent*** if there is an edge e of G for which moving both ends of e can transform a rotation system for ι_1 into a rotation system for ι_2. In either case, the two imbeddings are adjacent.

The induced subgraph of SG on the set of imbeddings into the surface S_h is called the h^{th} ***stratum*** of SG and is denoted by S_hG. The cardinality of S_hG is clearly $g_h(G)$.

Gross and Tucker [GrTuB] proved that trying to descend to the minimum genus can be obstructed by ***traps***, which are false minima, from which it is impossible to descend to a global minimum without first ascending. The ***depth of a trap*** is the minimum increment in genus that one must ascend on any path to the true minimum.

Traps of arbitrary depth were subsequently constructed by Gross and Rieper [GrRi]. This is consistent with Thomassen's result [Th] that the minimum genus problem is NP-complete. However, Gross and Rieper [GrRi] also proved that no false maxima exist, so that it is possible to ascend from any imbedding to a maximum imbedding, even though strict ascent might not always be possible. This is consistent with the work of Furst, Gross, and McGeoch [FuGrMc] that establishes a polynomial-time algorithm for the maximum genus.

Gross and Tucker [GrTuD] proved that the link of each vertex of the stratified graph is a complete invariant of the graph. They also demonstrated how two graphs with similar genus distributions may have markedly different imbedding strata. These findings support the plausibility of a probabilistic approach to graph isomorphism testing, based on the sampling of higher-order imbedding distribution data.

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