# Notes the real moduli spaces $\overline{M}_{0,n}$ and related combinatorics

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**Abstract**

A vanishing result of some homology classes is proved and a tautological construction of a space of the same rational homology type is performed. A graph studied in Computational Biology appears in these spaces.

## 1

Let $G_n$ be the following graph. The vertices of $G_n$ are the right coset classes $S_n/D(n)$, of the symmetric group, modulo the dihedral group . $D(n)$ is the symmetry group of the regular n-gon.

T is a set of $n(n-3)/2$ involutions from $S_n$. For every pair (k, l), $0 < k < l < n$, where (k,l) is different from (1, n-1), we define d:=d(k, l)(x)=l+k-x , if x is between k and l. Otherwise, x is a fixed point.

Two vertices are joined by an edge if there are two permutations a and b in their equivalence classes, and if there is t in T, such that a=bt.

**Remark 1.** *For any r in D(n) and t in T, $rtr^{-1}$ is in T.*

### 1.1 Two-dimensional complexes

We build a sequence of two dimensional complexes.

Let B(n) the following 2-dimensional cellular complex. Its 1-skeleton is given by G(n). For any u and v in T, such that u and v commute, there is a face around the vertices of G(n), represented by the permutations: a, av, avu, and au.

Note: the vertices are classes of type: $xD(n)$ . In the construction above, we choose a permutation a in this class, and we apply a right multiplication (not a left one). So, the graph and the complexes of this section are NOT Schreier graphs.

Note: [Shafarevich] [15] contains the definition of a 2-complex as an oriented graph and a set of cycles (boundaries). In a similar way, we can define CW- complexes, in an inductive way.

As we will prove, rank $H_1$(B(n)) = rank $H_1(\overline{M_{0,n}}(R))$. So, the study of B(n) is important. The first barycentric subdivision transforms any cellular complex into a simplicial one.

## 2 The homology groups of $\overline{M_{0,n}}(R)$ and a rational homology model of these spaces

We will begin to study the first homology group. The same analysis can be applied to higher homology groups, giving a spaces of the same homology as the real moduli spaces. (Theorems 1 and 2)

To keep track of the first homology group, we will use the cellular decomposition of M=$\overline{M}_{0,n}(R)$, after Devadoss . We apply the dual block complex, [13]pp.380, and restrict to level two of its filtration.

Let $K_{n-1}$ be the n-3-convex polytope whose partial order set of its faces is isomorphic with the partial order set of an n-gon with several non-intersecting diagonals. The partial orders are given by inclusions. $K_{n-1}$ is called the associahedron. There is such a convex polytope [Ziegler-Lectures on Polytope p.310] $K_{n-1}$ has the acyclic carrier property , so we can apply the classical theorems from [Munkres pp 225]. The codimension k faces of the associahedron are indexed by n-gons with k non-intersecting diagonals.

DIAG is the following set of $n(n-3)/2$ involutions from $S_n$. For every pair (k, l), $0 < k < l < n$, where (k,l) is different from (1, n), we define d:=d(k, l)(x)=l+k-x , if x is between k and l. Otherwise, x is a fixed point. Let P be a fixed n-gon, with edges labeled 1,2,3...n. For every diagonal of P we can associate an element of DIAG in the following way: any diagonal determines a partition of 1,2...n. Take the one which doesn't contain n: it's between 2 numbers, k and l. Then the associated d will be d(k,l), and we say that d(k,l) is supported by the diagonal of the n-gon P. **Throughout the paper, the word "diagonal" means a diagonal of the n-gon, or the involution carried by the diagonal.**

Take $n!$ copies of $K_{n-1}$. For every permutation of $S_n$, label the edges of the n-gon with $\sigma(1), \sigma(2).....\sigma(k), ....\sigma(n)$. So the codimension k faces are labeled by decorated n-gons with k non-intersecting diagonals. Now we build our space $\overline{M}_{0,n}(R)$. Two codimension k faces of different $K_{n-1}$'s are identified (glued) if the permutations $\sigma_1$ and $\sigma_2$ which color the edges of the n-gons satisfy the following condition "flip" or gluing condition: there are $d_1, d_2, ...., d_i$ couple of elements of DIAG, supported by the diagonals of the second face, such that $\sigma_1 = \sigma_2 \circ d_1 \circ d_2 \circ ... \circ d_i$. ( $\circ$ means composition of functions ).

The top dimensional faces (without diagonals) are identified by the action of $D_n$, the dihedral group. So we can begin with $(n-1)!/2$ copies of $K_{n-1}$, indexed over $S_n/D_n$. Two codimension k faces are identified if their classes modulo the dihedral group $D_n$ contain 2 permutations which satisfy the flip condition from the previous paragraph.

**The Homology** is encoded in the gluing process above. M(our moduli space) is a smooth compact (n-3)-manifold, non-orientable if the dimension is higher than 1.

Recall the construction of the dual block complex. Let X be a compact homology n-manifold. Let sdX be the first barycentric subdivision. The simplices of sdX are $[\bar{a}, \bar{b}...\bar{z}]$ where $a \supset b..... \supset z$ and $\bar{\sigma}$ is the barycenter of $\sigma$ , a simplex of X.

Given a simplex $\sigma$, D($\sigma$), the block of $\sigma$, is the union of the open simplices of sdX, where $\sigma$ is the final vertex; i.e. "$\sigma$ = z" in the notation above. We have dim $\sigma$ + dim D($\sigma$) = dim manifold.

2.0.Let $X_p$ be the dual p-skeleton of X, the union of all D($\sigma$) such that dim D($\sigma$) is smaller or equal to p. $\mathbf{D}_p = H_p(X_p\ ,\ X_{p-1})$. The boundary operator is the boundary operator in the exact sequence of the triple $(X_p\ ,\ X_{p-1}\ ,\ X_{p-2})$. $\mathbf{D}_p = H_p(X_p\ ,\ X_{p-1})$ is the free abelian group generated by the blocks of dimension p of X, arbitrarily oriented, i.e. the blocks from the previous statement label the elements of a basis. How can we deal with the boundary operator of the dual block complex? Fortunately it has a nice geometric meaning. The dual blocks form a CW decomposition of X. Let a and b be 2 cells, dim(a)=p and dim(b)=p-1. $\partial a$ is a formal sum of p-1 cells, with integer coefficients. The coefficient of b is given by "the incidence coefficient", which is the degree of a map that sends the boundary of a (i.e. $S^{p-1}$) to a bouquet of p-1 spheres = $X_{p-1}/X_{p-2}$, and then projected to a p-1 sphere. So the boundary map shows how the boundary of the cell is patched by p-1 spheres.

2.1 We would like to apply the previous settings to X = $\overline{M}_{0,n}(R)$. The associahedra give a cellular, not a simplicial decomposition of X. We have to take the first barycentric subdivision of X. Fortunately, the barycenters of the faces of the associahedra are already labelled by n-gons with several diagonals, where the edges of the n-gons bear a permutation.

A maximal simplex in X is a sequence of n-3 barycenters. Its dual block, of dimension 0, is its barycenter, which can be labelled by the simplex itself. In the notation from 2.0 section, $\mathbf{D}_0$ is the free abelian group generated by these simplices.

A codimension 1 simplex of a simplex above is a face of the simplex above. Its dual block is a segment between 2 maximal simplices which share the same face (X is a manifold !). $\mathbf{D}_1$ is the free abelian group generated by these segments, arbitrarily oriented.

There are 2 types of segments: the segments inside the same associahedron, and the segments between 2 different associahedra.
Similarly, $\mathbf{D}_2$ is the free abelian group generated by 4 segments which form the boundary of a 2-cell, arbitrarily oriented. Any dim 2 block is shared by exactly 4 dim 1 blocks and exactly 4 dim 0 blocks, thereby building a structure similar with the structure of 4 cubes in 3 dimensions.

The boundary morphisms between D's are "normal": a segment goes to the difference of its vertices, and a 2-face goes to a sum of edges, correlated by signs.

$H_1(\overline{M}_{0,n}(R)) = Ker(\partial_1)/Im(\partial_2)$

The barycenters of the maximal simplices above and the edges among them form a new graph, called GG(n). There is a following pictorial transformation between G(n) and GG(n): -the vertices of G(n) become circles. Between these circles, instead of one edge e , there are m(e) edges. m(e) is the following number: any edge e is decorated by a diagonal of the n-gon. m(e) is the number of diagonals which do not intersect e. The tips and the tails of these edges are inside the circles and there are connected by a system of pipes given by the barycentric subdivision of the associahedra.

An element of $D_1$ is a formal sum of edges, decorated with reals.

**Theorem 1**. There is an isomorphism between the first homology groups *with real coefficients* of B(n) and $\overline{M}_{0,n}$.

**Proof:** Let F be the following function: If the m(e) edges between the codimension 1 faces of two associahedra are decorated by real numbers in GG(n), then F associates their sum to the edge e in G(n). Using the fact that the associahedron is homeomorphic with a closed ball, it is easy to prove the statement above. The restriction of F to the 1-cycles in homology gives the stated isomorphism. Let FF be this restriction. The result is true only for homology with real coefficients. There are 3 questions to be answered in this proof:

1. If the definition of FF is independent of the numbers (it depends only on the homology class). The answer is *Yes* to all questions . The image of a boundary is a boundary. By a boundary, we mean a formal sum of 4 edges, colored by + or -1, according to their orientation , which are geometric boundaries of 2-blocks etc.

2. If we can define an inverse of FF. We can define a function GG from the homology of $B(n)$ to $H_1(M)$, which is the restriction of a function G, defined in the following way: the edge e colored by number x goes to the sum of the m(e) edges from GG(n),colored by the same number x/m(e) - a kind of trace-diagonal process. We do not have any obstructions: the associahedron is aspherical, so it is possible to assign numbers to the edges inside them , such that the result is a flux in GG(n). ( a flux is an assignment of numbers to edges such that the sum for every vertex is zero). A physics of this process is given by the concept of "pressure": the pressure of a gas inside the associahedron is zero. it is just a distribution of pressures given by the numbers from the external faces.

3. If they are inverse to each other. It is easy, to see that this is the case.

In a similar way, we can define a cellular complex $BB(n)$ of dimension $n-3$, whose real homology is isomorphic with the real homology of our spaces. The k dimensional faces of $BB(n)$ are given by k commuting diagonals. More exactly, the $k^{th}$ skeleton of $BB(n)$ is obtained from the $(k-1)^{th}$, by attaching k-dimensional cubes given by k commuting diagonals.

The vertices of a k-cube are given by products of at most k commuting diagonals: $a(d_1)(d_2)(d_3)..(d_h)$, where h $\leq$ k. Any 2 diagonals commutes.

**Remark**: Initially , the barycentric subdivision transforms the real moduli spaces into simplicial complexes. The dual block complex gives an algebraic chain (device) useful to compute the homology. From these algebraic devices, we returned back to geometry , using the cellular complex BB(n), described in the last paragraph.

The dual block complex gives us the opportunity to withdraw the associahedra and to use standard cubes.

**Theorem 2** $BB(n)$ and $\overline{M}_{0,n}$ have the same real homology.

**Proof:**
The simplices came from the barycentric subdivision of the associahedra. There are 2 types of simplices. A simplex of type A, of dimension k is labelled by an ordered sequence of k+1 n-gons. We draw another diagonal , to get an n-gon from a previous one .

The dual block complex of A is a union of simplices of type: $[\bar{a}, \bar{b} ... \bar{A}]$ where $a \supset b ..... \supset A$ and $\bar{A}$ is the barycenter of $A$ , a simplex of X.

As in the case of the first homology group, the second type of k-simplices (type B) is contained in only one associahedron Their dual block complexes do not modify the homology, which is given by the cellular homology chain of $BB(n)$.

The simplices of type A are contained in the intersection between several associahedra. For k=1, there were only two associahedra which can share the same n-1-simplex. For k greater than 1, there are $2^{k+1}$ associahedra which share the simplex. Its dual block complex is a cube.

The theorem is a particular case of the Acyclic Carrier Theorem See [Munkres, page 74, Thm. 13.3]. We used two properties of associahedra:

1. They are contractible spaces. 2. The dual block complexes are combinatorial cubes of two types: type A appear in $BB(n)$; the second type appear in only one associahedron. Their union does not affect the homology.

## 2.1 A Vanishing Result of some homology classes

The above space , of the same rational homology type, gives us the opportunity to work on a simplified model: the assocahedron does not appear, we are working with the combinatorial data of the chromosome inversion problem. Moreover, we can find trivial 1-homology classes.

Because of the homology isomorphism above, it is enough to study $BB(n)$, to get the desired results of this section. A partial study of these spaces is given in [**?**].

The notes below is a study of real vector spaces or subspaces generated by formal sums of oriented edges in G(n). We found 1 special type of cycles in B(n):

1. Cycles given by k non-intersecting diagonals in the n-gon, and by k numbers of zero sum. (picture 1 for k=3).

These cycles are boundaries, they are zero in homology. A cycle of this type is the 1-skeleton of a k-dimensional cube. For every k numbers $a_i$ with zero sum, we can decorate the vertices of the cycle with + or - $a_i$ in such a way we get a cycle. We can write the 1-skeleton like a sum of cycles of length 4, so it is zero in homology.

# 3 The Chromosome Inversion Graph G(n). An old problem

The Chromosome Inversion Problem was first stated in 1982 by Watterson, Ewens, Hall and Morgan, in a desire to construct a phylogenetic tree of evolution, and to define a genetic distance [17]. In their paper , a first attempt of an algorithm and a conjecture of a diameter of a graph G(n) appeared. A fundamental approach came in 1996, in the seminal article of Bafna and Pevzner [2]. See also [14].

## 3.1 Mathematical formulations

In the paper [17] , the objects of study are circular chromosomes, without a fixed 12 o'clock position, without top and bottom. Mirror images are the same. Mathematically:

Let $G_n$ be the following graph. The vertices of $G_n$ are the right coset classes $S_n/D(n)$, of the symmetric group, modulo the dihedral group . $D(n)$ is the symmetry group of the regular n-gon.

T is a set of $n(n-3)/2$ involutions from $S_n$. For every pair (k, l), $0 < k < l < n$, where (k,l) is different from (1, n-1), we define d:=d(k, l)(x)=l+k-x , if x is between k and l. Otherwise, x is a fixed point.

Two vertices are joined by an edge if there are two permutations a and b in their equivalence classes, and if there is t in T, such that a=bt.

**Remark 2.** *For any r in D(n) and t in T, $rtr^{-1}$ is in T.*

**Remark 3.** *Any graph has a metric , induced by the smallest number of edges between any 2 vertices. Applying the first remark, we can say that the distance between 2 vertices which contain the permutations $\sigma_1$ and $\sigma_2$ is k, if there are $d_1, d_2, ...., d_k$ several reversals of T,and R in D(n) such that $\sigma_1 = \sigma_2 \circ R \circ d_1 \circ d_2 \circ ... \circ d_k$. ( $\circ$ means composition of functions ), and k is minimal with this property .*

In the case of Genome Rearrangements studied by Bafna and Pevzner, the vertices of a graph are given by all permutations of S(n). Instead of $n(n-3)/2$ reversals, the full set of $n(n-1)/2$ reversals are considered.

**Remark 4.** *In spite of their similarity, we did not find the mathematical equivalence between the problems above. Instead, we can perform the steps of the solution of the Gollan Conjecture .*

**Lemma 5.** *The diameter of the graph $G_n$ is $\leq$ n-2. ( The "ratchet" algorithm).*

Proof ( [17]): Let a and b be two vertices of the graph. They can be represented as labelled points of a circle , the labelling being given by two permutations from a and b. Starting from a point A on the second circle, we travel clockwise until we first come to a point not in the position from its first circle. We make a reversal, to create a neighborhood point of A as on the first circle. We consider the next labelled point which is not in the right position, and so on . We can begin with any A, and we need not to correct the position of the last point. So, the diameter of the graph $G_n$ is $\leq$ n-2.

By a circular permutation, we mean a right coset class in the $S_n$, modulo the dihedral group. (i.e we label n points on a circle in the three dimensional space using permutations).

**Definition 6.** ***Breakpoint graph of a circular permutation*** $\sigma$*.For every vertex of $G_n$, we will associate a bi-colored graph. Let $i \sim j$ if $|i-j| = 1$ or n-1. $\sigma = \sigma(1)\sigma(2)..\sigma(k)..\sigma(n)$. A pair of consecutive elements $\sigma(i)$ and $\sigma(i+1)$ is called a breakpoint if the absolute value of their difference is not 0 or n-1. Define an edge colored graph G($\sigma$) with n vertices on the circle, labelled in the order given by the permutation. We join i and j by a black edge if (i,j) is a breakpoint of $\sigma$. We join i and j by a grey edge if $i \sim j$ , but i and j are not consecutive in $\sigma$.*

**Theorem 7.** *(circular Gollan conjecture), For every n, the distance $d(\gamma_n)$ between the vertices represented by the identity and by the Gollan permutation is at least n-3.*

Let us recall the Gollan permutation:

$$\gamma_n = \begin{cases} (3, 1, 5, 2, 7, 4, ...n-3, n-5, n-1, n-4, n, n-2) & n \;\; even \\ (3, 1, 5, 2, 7, 4, ...n-6, n-2, n-5, n, n-3, n-1) & n \;\; odd. \end{cases}$$

The theorem above is a consequence of the 2 fundamental lemmas from Pevzner's work [2] [14]. It is possible to apply these lemmas in the case of the circular breakpoint graph.

We prove:

1.There are at most 3 disjoint alternating cycles in G($\gamma_n$).

2.d(a) $\geq$ b(a) - c(a), where b is the number of black edges of G(a), and c is the maximal number of disjoint alternating cycles of G(a).

**Remark**: Nothing was published about the circular permutations.

## 4 topics which motivated us in the study of these spaces and combinatorics questions

Our topological study of the compactified moduli spaces M(0,n) has developed as a doctoral project about some conjectures stated in [12]. There are many things to say about these spaces. Let us recall some of them, which motivate us in our research.

1.Kontsevich asks in his seminal paper [10] what are the algebraic structures needed for the cohomological study of the Deligne-Mumford compactification $\overline{M}_{g,n}$. We believe the answer is the Pevzner-Hannenhalli Theory.

2.Topologically speaking, $\overline{M}_{0,n}(R)$ are Eilenberg-MacLane spaces $K(\pi, 1)$, where the fundamental group is described as a kernel of an epimorphism f. It is an usual situation for the fundamental group of a blow-up [5].

Our spaces have a topological fundamental nature. The same aspect is given by the Algebraic Geometry: the moduli space of stable n-pointed curves of genus 0 has been extensively studied as one of the fundamental models of moduli problems (see Mumford). They come equipped with a natural real structure (Manin).

Gelfand ,Kapranov and Zelevinsky's papers contain the first detailed study of these spaces, as Chow quotient $(RP^1)^n//PGL(2, R)$ [7] [8].

3. The study of Thurston, Sleator and Tarjan on the rotation graph, using hyperbolic geometry. Their amazing proof used hyperbolic geometry and numerical data. We still do not have a pure combinatorics proof of their result [16]. Their work was motivated by the Dynamic Finger Conjecture, recently proved by R.Cole (2000).

4. Computational Biology. The Chromosome inversion problem, stated in 1982 was fully observable at the early stage of our pure math investigation. It took several months and a considerably amount of luck to understand that the non-trivial combinatorics of these spaces is not explicitly studied in Algebraic Geometry and it is much better understood since 1996 [Pevzner, Bafna, Caprara, Tarjan, Shamir, Hannenhalli]. The geometry of these spaces , studied by Kapranov, Manin, Davis, Scott , Januszkiewicz and Devadoss, shows that the graph of the "circular permutations" has the diameter n-2. Unfortunately, we did not find the formal way to write a proof .

### 4.1 A dictionary between the geometric approach of the rotation graph and the geometric approach of the chromosome inversion problem, a la Thurston, Sleator, Tarjan. Comparison between the combinatorial data inserted in $\overline{M}_{0,n}$ and in $M_n(\mathbf{C})$

### 4.2 The Braid Groups after Krammer

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Let G be the Cayley graph of the symmetric group $S_n$, with respect to the set of all transpositions. Every graph has a metric, given by the shortest path between two points. The length function is given by the distance between a fixed vertex (in our case it is the vertex given by the identity permutation) and another vertex.

In our case, the length function has a nice combinatorial formula: l($\sigma$) = n - c($\sigma$), where c($\sigma$) is the number of cycles of in the decomposition of $\sigma$.

We draw n points in the plane. We join k and l, if l = $\sigma$(k). c($\sigma$) is the number of independent cycles.

**Note 1:** if the n points are the vertices of a regular n-gon, and if the cycles do not intersect, then $\sigma$ is called a non-crossing permutation. The partition of n in cycles is called a non-crossing partition.

**Note 2:** The number of non-crossing partitions equals the number of the vertices of the associahedron , which is equal to the number of triangulations of the n-gon, which is equal to the well known Catalan numbers

$$1/(n+1)\binom{2n}{n}$$

**Note 3:** Let X be the set of all vertices of the above defined graph G, which are on the geodesics between the identity and the n-cycle $(2, 3, ...n, 1)$. X is the set of non-crossing partition ( or permutations).

**Note 4:** A presentation of the Braid Group is given by the generators indexed over X. The relations are given by the relations between permutations: if a=bc, we have the same relation among the labelled generators.

**Note 5:** The graph and the distance defined above generate a partial order on $S_n$. $a \leq b$ if a and b are on the same geodesic which join them with the identity, and a is closer than b. This partial order gives a simplicial complex structure on X : k ordered permutations form a (k-1)-simplex if they are totally ordered. Amazingly, X is a compact K($\pi$, 1) of dimension n-1, where the fundamental group is given by the Braid Group.

### 4.3 Similar data for the reversal distance. A short review of Pevzner- Hannenhalli Theory.

### 4.4 Future Research

- construction of combinatorial homology classes using the model above.

- to find representations of the fundamental group of these spaces, as Yoshida did it for n=5.

### 4.5 A Question of Davis et al

Recently, Krammer proved a long standing problem in group theory: the braid groups are linear. A fundamental tool was a new description of the braid group , having generators given by the set of non-crossing partitions of $n$ elements. We can say that the generators are the vertices of the associahedron. The challenge is to answer a similar question from Davis et al. article, using Pevzner - Hannenhalli's theory of sorting by reversals, and Caprara's theorems on the relation between permutations and breaking point graphs. Davis et al's group is a group A, given by :

-involutory generators $\alpha_T$, for each proper sub-interval T of [1, n-2]. The relations are: if the distance between the intervals X and Y is at least 2, then $\alpha_X$ and $\alpha_Y$ commute. If X $\subset$ Y, then $\alpha_Y \alpha_X \alpha_Y = \alpha_Z$. Z denotes the image of X under the order-reversing involution of Y. The generators are the reversals from T. The relations are given by the relations among the reversals.

- Let G the Cayley graph of the symmetric group, with respect to the set of $n(n-1)/2$ transpositions (i,j). Take $\lambda$ a cycle of length n, which is at the distance n-1 from the identity. Let Q be the set of all permutations which are on the geodesics from the identity to $\lambda$. The set Q, together with the relations given by permutation composition, is a presentation of the braid group $B_n$.

- The graph $G(n)$ from our second section, the Gollan permutation, and similar construction could play a role in the study of Davis's A- group.

### 4.6 Thurston, Tarjan and Sleator graph

A combinatorial proof of their results, or a proof which uses the spaces above, is our work in progress.

### 4.7 Signed permutations

If we take the reversal graph of signed permutation, there is a space whose building blocks are glued in a manner prescribed by this graph: the edges show the incidence relations among the big cells. We are convinced that there is a nice interplay among the already developed theory from Computational Biology and its math counterpart, studied by Bott, Taubes, Axelrod and Singer. The geometric theory of these spaces is not so developed as the theory for $\overline{M}_{0,n}(R)$.

### 4.8 Computational Biology

The forces which drive Computational Biology, and Algebraic Geometry are so different, that it is too much to predict the future interactions among them. To speculate: we already know the power of Physics and Computer Sciences predictions in pure mathematics. Maybe the future will show predictions given by Genetics.

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