BUILDING PLANAR POLYGON SPACES FROM THE PROJECTIVE BRAID ARRANGEMENT

NAVNATH DAUNDKAR AND PRIYAVRAT DESHPANDE

ABSTRACT. The moduli space of planar polygons with generic side lengths is a smooth, closed manifold. It is known that these manifolds contain the moduli space of distinct points on the real projective line as an open dense subset. Kapranov showed that the real points of the Deligne-Mumford-Knudson compactification can be obtained from the projective Coxeter complex of type A (equivalently, the projective braid arrangement) by iteratively blowing up along the minimal building set. In this paper we show that these planar polygon spaces can also be obtained from the projective Coxeter complex of type A by performing an iterative cellular surgery along a sub-collection of the minimal building set. Interestingly, this sub-collection is determined by the combinatorial data associated with the length vector called the genetic code.

1. INTRODUCTION

A length vector is a tuple of positive real numbers. The moduli space of planar polygons associated with a length vector \( \alpha = (\alpha_1, \ldots, \alpha_m) \), denoted by \( M_\alpha \), is the collection of all closed piecewise linear paths in the plane up to orientation preserving isometries with side lengths \( \alpha_1, \alpha_2, \ldots, \alpha_m \). Equivalently,

\[
M_\alpha = \{(v_1, v_2, \ldots, v_m) \in (S^1)^m : \sum_{i=1}^m \alpha_i v_i = 0\}/\text{SO}_2,
\]

where \( S^1 \) is the unit circle and the group of orientation preserving isometries \( \text{SO}_2 \) acts diagonally. The moduli space of planar polygons (associated with \( \alpha \)) viewed up to isometries is defined as

\[
\overline{M}_\alpha := \{(v_1, v_2, \ldots, v_m) \in (S^1)^m : \sum_{i=1}^m \alpha_i v_i = 0\}/\text{O}_2.
\]

A length vector \( \alpha \) is called generic if \( \sum_{i=1}^m \pm \alpha_i \neq 0 \). For such a length vector \( \alpha \), the moduli spaces \( M_\alpha \) and \( \overline{M}_\alpha \) are closed, smooth manifolds of dimension \( m - 3 \). In the rest of this paper, the length vectors are assumed to be generic unless stated otherwise.

The manifold \( M_\alpha \) admits an involution \( \tau \) defined by

\[
\tau(v_1, v_2, \ldots, v_m) = (\bar{v}_1, \bar{v}_2, \ldots, \bar{v}_m),
\]

where \( v_i = (x_i, y_i) \) and \( \bar{v}_i = (x_i, -y_i) \). Observe that \( \tau \) maps a polygon to its reflected image across the \( X \)-axis. Since we are dealing with only generic length vectors, the involution \( \tau \) does not have fixed points. It is clear that \( M_\alpha \) is a double cover of \( \overline{M}_\alpha \).

The moduli spaces of (planar) polygons have been studied extensively. For example, Farber and Schutz [3] proved that the integral homology groups of \( M_\alpha \) are torsion-free. They also described the Betti numbers in terms of the combinatorial data associated with
the length vector. The mod-2 cohomology ring of $\overline{M}_\alpha$ was computed by Hausmann and Knutson in [5].

The configuration space of $m$-ordered, distinct points on $\mathbb{R}P^1$ is

$$C_m(\mathbb{R}P^1) := (\mathbb{R}P^1)^m \setminus \Delta,$$

where $\Delta = \{(x_1, \ldots, x_m) \in (\mathbb{R}P^1)^m : \exists i, j \text{ such that } x_i = x_j\}$. The real moduli space of genus zero curves $M_0^\alpha(\mathbb{R})$ is the quotient of $C_m(\mathbb{R}P^1)$ by $\mathbb{P}GL_2(\mathbb{R})$.

There is a Deligne-Mumford-Knudsen compactification $\overline{M}_0^m(\mathbb{R})$ of $M_0^m(\mathbb{R})$. Kapranov [11] showed that $\overline{M}_0^m(\mathbb{R})$ can be obtained from the projective Coxeter complex of type $A_{m-2}$ (equivalently the projective braid arrangement) by iteratively blowing up along the minimal building set. Moreover, this process results in a regular cell structure on $\overline{M}_0^m(\mathbb{R})$ consisting of $(m - 1)!/2$ copies of the associahedron as top-dimensional cells.

It is known that for any generic length vector the corresponding planar polygon space is also a compactification of the real moduli space of genus zero curves. Also for every $m$, there is a unique class of length vectors for which $M_\alpha$ is the Coxeter complex and $\overline{M}_\alpha$ is the projective Coxeter complex. Therefore, it is natural to ask the following question.

**Question 1.** Is there a way to obtain $M_\alpha$ (respectively $\overline{M}_\alpha$) from the Coxeter complex of type $A$ (respectively the projective Coxeter complex of type $A$) by some iterative topological operation?

In this article, we answer this question affirmatively. In order to achieve this, we introduce the notion of the (projective) cellular surgery on certain regular cell complexes (see Definition 6.3). The cellular surgery involves removing a subcomplex homeomorphic to the trivial tubular neighborhood of an embedded sphere by a complex which is a tubular neighborhood of a sphere of complementary dimension. The projective surgery is performed when there is a free $\mathbb{Z}_2$-action on the ambient space which also descends to tubular neighborhoods. For a given generic length vector $\alpha$ we first introduce a partial order on the collection of genetic codes, called the genetic order. We use this notion to describe the subcomplexes $G_\alpha$ on which cellular surgery needs to be performed and subcomplexes $P G_\alpha$ on which the projective surgery is to be performed. Interestingly, these complexes form a subcollection of the minimal building set.

Note that the collection of polygons in $M_\alpha$ (respectively $\overline{M}_\alpha$) with exactly two parallel sides is a codimension-1 submanifold of $M_\alpha$ (respectively $\overline{M}_\alpha$). It turns out that the collection $A_\alpha$ (respectively $\overline{A}_\alpha$) of such codimension-1 submanifolds of $M_\alpha$ (respectively $\overline{M}_\alpha$) forms a submanifold arrangement. Consequently, there is a cell structure on both $M_\alpha$ and $\overline{M}_\alpha$ induced by $A_\alpha$ and $\overline{A}_\alpha$, respectively. These cell structures on $M_\alpha$ and $\overline{M}_\alpha$, denoted by $K_\alpha$ and $\overline{K}_\alpha$, respectively. We prove the following theorem,

**Theorem 1.1.** Let $G$ be the genetic code of a length vector $\alpha = (\alpha_1, \ldots, \alpha_m)$. Then the iterated cellular surgery on the Coxeter complex $CA_{m-2}$ (respectively, on projective Coxeter complex $\mathbb{P}CA_{m-2}$) along the elements of $G_\alpha$ (respectively $P G_\alpha$) produces the cell complex homotopy equivalent to $K_\alpha$ (respectively $\overline{K}_\alpha$).

This article is organised as follows: In Section 2, we give the basics of braid arrangement, Coxeter complex, and planar polygon spaces. We also introduce the genetic order and derive some of its properties. We then introduce submanifold arrangements and study the induced cell structure. In Section 4, we give a description of Hausmann’s theorem in the language developed in previous sections. In Section 6, we introduce the notion of cellular surgery on a simple cell complex and prove Theorem 1.1.
2. The braid arrangement, Coxeter complex and motivation

2.1. The braid arrangement. In this subsection, we set up notation and gather some results related to the Coxeter complex.

Definition 2.1. A finite collection, $A$, of codimension-1 subspaces in the Euclidean space is called an arrangement of hyperplanes (or a hyperplane arrangement).

Definition 2.2. The braid arrangement is the collection $B_m = \{H_{ij} : 1 \leq i < j \leq m\}$, where

$$H_{ij} = \{(x_1, \ldots, x_m) \in \mathbb{R}^m \mid x_i - x_j = 0\}.$$  

An arrangement of hyperplanes is said to be essential if the intersection of all hyperplanes is the origin. The braid arrangement $B_m$ is not essential, since

$$\bigcap H_{ij} = \{(t, \ldots, t) \in \mathbb{R}^m \mid t \in \mathbb{R}\} \neq \{0\}.$$  

Nevertheless, there is a way to make $B_m$ essential by considering the quotient $\mathbb{R}^m / \bigcap H_{ij}$. Consider

$$V := \{(x_1, \ldots, x_m) \in \mathbb{R}^m \mid \sum_{i=1}^{m} x_i = 0\},$$

then it is easy to see that the collection

$$B_V = \{H_{ij} \cap V \mid 1 \leq i < j \leq m\}$$

is an essential arrangement in $V$. The arrangement $B_V$ is called an essentialization of $B_m$. Let $SV$ be the unit sphere in $V$.

Definition 2.3. The intersection of hyperplanes in $B_V$ gives a simplicial decomposition of $SV$. This decomposition of $SV$ is called the Coxeter complex of type $A_{m-1}$ and it is denoted by $CA_{m-1}$. The projective Coxeter complex $\mathbb{P}CA_{m-1}$ of type $A_{m-1}$ is the quotient of Coxeter complex $CA_{m-1}$ by the antipodal action.

It is clear that $CA_{m-1}$ has $m!$ copies of the $(m-2)$-simplex as its top-dimensional cells.

Example 2.1. The Coxeter complex $CA_3$ is the 2-dimensional sphere cellulated by 24 triangles and $\mathbb{P}CA_3$ is the projective plane cellulated by 12 triangles (see Figure 2.1).
The collection of all possible intersections of hyperplanes in the hyperplane arrangement \( \mathcal{A} \) forms a lattice under reverse inclusion as the partial order. We denote this lattice by \( \mathcal{I}(\mathcal{A}) \), which is known as the intersection lattice. Let \( \mathcal{I}(\mathcal{B}_m) \) be the intersection lattice of \( \mathcal{B}_m \). It is clear that the lattices \( \mathcal{I}(\mathcal{B}_m) \) and \( \mathcal{I}(\mathcal{B}_n) \) are isomorphic. Moreover, it is isomorphic to the lattice of partitions of the set \([m]\), denoted by \( \Pi_m \). If \( \pi = J_1 - \cdots - J_k \) is a partition of \([m] \) then one can associate to \( \pi \) the following subspace:

\[
X_\pi = \{(x_1, \ldots, x_m) \in V \mid x_i = x_j \text{ whenever } i \text{ and } j \text{ are in } J_s \text{ for some } 1 \leq s \leq k \}
\]

an element of \( \mathcal{I}(\mathcal{B}_V) \). The map

\[
\phi : \Pi_m \to \mathcal{I}(\mathcal{B}_V)
\]

defined by

\[
\phi(\pi) = X_\pi
\]
is an isomorphism.

De Concini and Procesi [1] identified a special collection of elements of the intersection lattice of an arrangement such that the blow-ups along these subspaces commute for a given dimension and the resulting arrangement has normal crossings.

For given intersection \( X \in \mathcal{I}(\mathcal{A}) \) the subarrangement at \( X \) is

\[
\mathcal{A}_X := \{H \in \mathcal{A} \mid X \subseteq H\}.
\]

**Definition 2.4.** An intersection \( X \in \mathcal{I}(\mathcal{A}) \) is said to be reducible if there exist \( Y \) and \( Z \) in \( \mathcal{I}(\mathcal{A}) \) such that \( \mathcal{A}_X = \mathcal{A}_Y \cup \mathcal{A}_Z \), otherwise \( X \) is irreducible.

**Definition 2.5.** The minimal building set \( \text{Min}(\mathcal{A}) \) of \( \mathcal{A} \) is the collection of all irreducible elements of \( \mathcal{I}(\mathcal{A}) \).

**Example 2.2.** Consider the braid arrangement \( \mathcal{B}_m \). The minimum building set \( \text{Min}(\mathcal{B}_m) \) contains intersections corresponding to those partitions of \([m]\) which have at most one block of size greater or equal to 2.

Now we prove that for an element \( X \in \mathcal{I}(\mathcal{B}_V) \), the induced cell decomposition on the unit sphere in \( X \) is a lower-dimensional Coxeter complex.

**Lemma 2.1.** Let \( X \in \mathcal{I}(\mathcal{B}_V) \) and \( S_X = X \cap CA_{m-1} \). Then \( S_X \) is isomorphic to the Coxeter complex \( CA_{\dim(X)-1} \).

**Proof.** Recall that \( X = X_\pi \) for some partition \( \pi = (J_1, \ldots, J_k) \) of \([m]\). Moreover, \( \dim(X_\pi) = k - 2 \). Note that \( S_X \) is a sphere in \( X \). We can think of the \( k \) blocks of \( X \) as the elements \( \{1, 2, \ldots, k\} \). Then the induced cell structure on \( S_X \) is equivalent to the cell structure on the unit sphere in \( \mathbb{R}^k \) induced by the braid arrangement. Therefore, \( S_X \cong CA_{k-1} \). This proves the lemma.

### 2.2. Motivation.

Our article is motivated by the work of Hu [8] relating the Deligne-Knudsen-Mumford compactification to the moduli space of spatial polygons, the work of Kapronov [10] expressing the aforementioned compactification as an iterative blow up and the work of Devadoss [2] explaining the relationship over reals using combinatorial arguments. We briefly explain some of these ideas here.

**Definition 2.6.** Let \( \alpha = (\alpha_1, \ldots, \alpha_m) \) be a generic length vector. The spatial polygon spaces is defined as follows:

\[
N_\alpha = \{(v_1, v_2, \ldots, v_m) \in (S^2)^m : \sum_{i=1}^m \alpha_i v_i = 0\}/SO_3,
\]

where \( SO_3 \) acts diagonally.
The spatial polygon spaces have been studied widely. For example, the integer cohomology ring of \( N_\alpha \) was computed by Hausmann and Knutson in [5].

The moduli space of \( m \)-punctured Riemann spheres (or the moduli space of genus zero curves) \( \mathcal{M}_0^m \) is an important object in geometric invariant theory. There is the Deligne-Knudson-Mumford compactification \( \overline{\mathcal{M}}_0^m \) of this space which has been studied widely. We refer the reader to [10], [11]) for comprehensive introduction.

In [8], Hu introduced the notion of "stable polygons" (see [8, Definition 4.13]). Roughly speaking, a stable polygon is obtained from the following procedure: Let \( P = (v_1, \ldots, v_m) \) be a polygon and \( J \subset [m] \) such that \( v_i = v_j \) for \( i, j \in J \). That is, sides of \( P \) indexed by \( J \) are parallel. Now introduce a new polygon without parallel edges, all whose sides except the longest one are indexed by \( J \). The longest side is set to \( \sum_{j \in J} \alpha_j - \epsilon \), where \( \epsilon \) is a carefully chosen small positive real number. Denote this new polygon by \( P_J \). Follow the same procedure for all sets of parallel sides and obtain such polygons without parallel edges. The stable polygon is a tuple of all such newly constructed polygons without parallel sides whose first coordinate is \( P \).

Let \( Y \) be the collection of subvarieties of \( N_\alpha \) defined in [8, Section 6]. The following theorem gives a relation between the moduli space of stable polygons \( \mathcal{M}_{\alpha,\epsilon} \), the Deligne-Knudson-Mumford compactification \( \overline{\mathcal{M}}_0^m \) and spatial polygon space \( N_\alpha \).

**Theorem 2.1** ([8, Theorem 7.3, Theorem 6.5]). With the above notations

1. The moduli space \( \mathcal{M}_{\alpha,\epsilon} \) is a complex manifold biholomorphic to \( \overline{\mathcal{M}}_0^m \).
2. The space \( \mathcal{M}_{\alpha,\epsilon} \) can be obtained from \( N_\alpha \), by iteratively blowing up along the elements of \( Y \).

Recall the definition of configuration space \( m \)-ordered, distinct points of \( \mathbb{R}P^1 \) from the Introduction.

**Definition 2.7.** The real moduli space of \( m \)-punctured Riemann spheres is

\[
\mathcal{M}_0^m(\mathbb{R}) = \frac{C_m(\mathbb{R}P^1)}{\mathbb{P}Gl_2(\mathbb{R})}.
\]

Let \( \mathbb{P}(B_{m-1}) \) be the projective braid arrangement in \( \mathbb{P}V \) and \( \mathcal{M}(\mathbb{P}(B_{m-1})) \) be its complement. Let \( (\mathbb{P}CA_{m-1})# \) denote the space obtained from \( \mathbb{P}CA_{m-1} \) by iterated blow-ups along the minimal building set of \( \mathbb{P}(B_{m-1}) \).

Let \( \overline{\mathcal{M}}_{0}^{m+1}(\mathbb{R}) \) be the real points of the Deligne-Mumford-Knudson compactification \( \overline{\mathcal{M}}_{0}^{m+1} \). Kapranov [11] remarkably proved the following.

**Theorem 2.2.** With the above notations

1. There are homeomorphisms \( \mathcal{M}(\mathbb{P}(B)) \cong \mathcal{M}_0^{m+1}(\mathbb{R}) \) and \( \overline{\mathcal{M}}_0^{m+1}(\mathbb{R}) \cong (\mathbb{P}CA_{m-1})# \)
2. The real moduli \( \overline{\mathcal{M}}_0^{m+1}(\mathbb{R}) \) is tiled by associahedra.

It is known that for a generic \( \alpha \), the polygon space \( \overline{\mathcal{M}}_\alpha \) contains \( \mathcal{M}_0^m(\mathbb{R}) \) as an open dense set. In particular, \( \overline{\mathcal{M}}_\alpha \) form a compactification of \( \mathcal{M}_0^m(\mathbb{R}) \) (see [12], [9] and [13] for more details). Therefore, it is natural to ask the following questions.

**Question 2.** Is there a real version of Theorem 2.1?

**Question 3.** Is there an analogue of Theorem 2.2 for planar polygon spaces?

By a theorem of Hausmann [6, Proposition 2.9] it follows that the planar polygon spaces are related by iterated surgery. Using a suitable cell structure (first defined by Panina [13]) we show that the surgery operation can be defined at the level of CW complexes and the genetic code of the given length vector can be used to keep track of how these spaces change.
3. Planar polygon spaces

This section is devoted to planar polygon spaces; we define genetic codes and prove some results. In the end, we introduce a collection of codimension-1 submanifolds that form a submanifold arrangement and a induced cell structure on $M_\alpha$ and $\overline{M}_\alpha$. This cell structure coincides with the one that Panina described in [13].

We denote the set $\{1, \ldots, m\}$ by $[m]$. There are two important combinatorial objects associated with the length vector $\alpha = (\alpha_1, \alpha_2, \ldots, \alpha_m)$.

**Definition 3.1.** A subset $I \subset [m]$ is called $\alpha$-short if

$$\sum_{i \in I} \alpha_i < \sum_{j \not\in I} \alpha_j$$

and $\alpha$-long otherwise.

We may write short for $\alpha$-short when the context is clear. The collection of short subsets may be very large. There is another combinatorial object associated with length vectors which further compactifies the the short subset data. Note that the diffeomorphism type of a planar polygon spaces does not depend on the ordering of the side lengths of polygons. Therefore, we assume that the length vector satisfies $\alpha_1 \leq \alpha_2 \leq \cdots \leq \alpha_m$.

**Definition 3.2.** For a length vector $\alpha$, consider the collection of subsets of $[m]$

$$S_m(\alpha) := \{J \subset [m] : m \in J \text{ and } J \text{ is short} \}$$

and a partial order $\leq$ on $S_m(\alpha)$ by $I \leq J$ if $I = \{i_1, \ldots, i_t\}$ and $\{j_1, \ldots, j_t\} \subseteq J$ with $i_s \leq j_s$ for $1 \leq s \leq t$. The genetic code of $\alpha$ is the set of maximal elements of $S_m(\alpha)$ with respect to this partial order.

If $A_1, A_2, \ldots, A_k$ are the maximal elements of $S_m(\alpha)$ with respect to $\leq$ then the genetic code of $\alpha$ is denoted by $\langle A_1, \ldots, A_k \rangle$; we will use the notation $G(\alpha)$ when it is convenient to do so.

**Example 3.1.** Let $\alpha = (1, \ldots, 1, m - 2)$ ($m$-tuple) be a length vector. Then the genetic code of $\alpha$ is $\langle m \rangle$. Moreover, $M_\alpha \cong S^{m-3}$ and $\overline{M}_\alpha \cong \mathbb{R}P^{m-3}$.

For a generic length vector $\alpha$, consider the collection of all short subsets

$$S(\alpha) := \{J \subset [m] \mid J \text{ is } \alpha\text{-short} \}.$$ 

**Theorem 3.1** ([7, Lemma 4.2]). For a generic length vector $\alpha$, the collection $S(\alpha)$ is determined by $S_m(\alpha)$. Moreover, $S(\alpha)$ can also be reconstructed from the genetic code of $\alpha$.

Observe that the partial order defined above doesn’t depend on the length vector. In particular, this partial order remains a partial order on the set of all subsets of $[m]$ containing $m$. This fact will help us to introduce the partial order on the collection of genetic codes.

**Definition 3.3.** Let $G(\alpha) = \langle A_1, \ldots, A_k \rangle$ and $G(\beta) = \langle B_1, \ldots, B_l \rangle$ be two genetic codes. We say that

$$\langle A_1, \ldots, A_k \rangle \preceq \langle B_1, \ldots, B_l \rangle$$

if for each $1 \leq i \leq k$ there exist $1 \leq j \leq l$ such that $A_i \leq B_j$. We call this partial order the genetic order.

**Remark 3.1.** Since $G(\alpha)$ consists of maximal elements of the poset $(S_m(\alpha), \leq)$, it completely determines the set $S_m(\alpha)$. Therefore, it follows from [6, Lemma 1.2] that if the genetic code of length vectors $\alpha$ and $\beta$ are same then the corresponding planar polygon spaces are diffeomorphic. Moreover, $G(\alpha) \preceq G(\beta)$ is equivalent to $S_m(\alpha) \subset S_m(\beta)$. Finally, in Definition 3.3 we may have $l \leq k$, for example, $\langle 126, 36 \rangle \preceq \langle 136 \rangle$. 


3.1. Saturated chains. Recall that in a poset \((P, \leq)\) an element \(y\) is said to cover another element \(x\) if \(x \leq y\) and \(x \neq y\). A saturated chain is a totally ordered subset \(C\) if there does not exist \(z \in P \setminus C\) such that \(x \leq z \leq y\) for some \(x, y \in C\) and that \(C \cup \{z\}\) is a chain.

We now characterize saturated chains in the poset of genetic codes. In particular, we first show that if the collection \(S_m(\beta)\) is obtained by adding just one element to the collection \(S_m(\alpha)\) then the code \(G(\beta)\) covers the code \(G(\alpha)\) in the genetic order.

**Proposition 3.2.** The genetic code \(G(\beta)\) covers \(G(\alpha)\), denoted \(G(\alpha) \preceq G(\beta)\), if and only if
\[
S_m(\beta) = S_m(\alpha) \cup \{I\} \text{ for some } J \subset [m].
\]

**Proof.** Let \(G(\beta)\) cover \(G(\alpha)\). Hence the collection \(S_m(\alpha)\) is a subcollection of \(S_m(\beta)\). On the contrary, assume that there exists \(J_1, J_2 \in S_m(\beta) \setminus S_m(\alpha)\). Let \(G'\) denote the genetic code obtained by adding \(J_1\) as a gene to \(G(\alpha)\). Then \(G(\alpha) \preceq G' \preceq G(\beta)\). This is a contradiction to the fact that \(G(\beta)\) covers \(G(\alpha)\). Therefore, we have \(S_m(\beta) = S_m(\alpha) \cup \{J\}\) for some \(J \subset [m]\).

Now we prove the converse by contradiction. Let there be a genetic code \(H\) such that \(G(\alpha) \preceq H \preceq G(\beta)\). Then, there is a gene \(I_1\) of \(H\) which is not a part of \(G(\alpha)\) and another gene \(I_2\) of \(G(\beta)\) which is not a part of \(H\) (see Remark 3.1). This implies, \(I_1, I_2 \in S_m(\beta) \setminus S_m(\alpha)\), a contradiction. This concludes the proposition. \(\square\)

**Remark 3.2.** Recall from [7, Lemma 4.1] that the collection \(S(\alpha)\) is determined by \(S_m(\alpha)\). Suppose \(S_m(\beta) = S_m(\alpha) \cup \{J\}\) for some \(J \subset [m]\). Let \(J' < J\) with \(m \in J'\). Note that \(J' \subset S_m(\beta)\). Since \(S_m(\beta) = S_m(\alpha) \cup \{J\}\), \(J' \subset S_m(\alpha)\). Consequently, \(S_m(\alpha)\) generates all \(\beta\)-short subsets except \(J\). Therefore, \(S(\beta) = S(\alpha) \setminus \{J'^c\}\) \(\cup \{J\}\).

Now we express the covering relation at the level of genetic codes and then show how to construct saturated chains.

**Proposition 3.3.** Let \(\tilde{G}\) and \(G\) be two monogenic codes of the same size such that \(S_m(\tilde{G}) = S_m(G) \cup J\) for some \(J \subset [m]\). Then \(\tilde{G} = \langle J \rangle\).

**Proof.** First we note that \(J\) contains \(m\). Suppose \(G = \langle S \rangle\) where \(S \subset [m]\) containing \(m\). Then we have \(G \preceq \langle S, J \rangle \preceq G\). Proposition 3.2 implies \(\tilde{G}\) covers \(G\). Therefore, \(\tilde{G} = \langle S, J \rangle\). But \(\tilde{G}\) is monogenic covering \(G\). Thus \(\tilde{G} = \langle J \rangle\). \(\square\)

**Proposition 3.4.** Let \(G = \langle \{g_1, \ldots, g_r, m\} \rangle\) and \(\tilde{G} = \langle \{h_1, \ldots, h_r, m\} \rangle\) be two genetic codes. Then \(\tilde{G}\) covers \(G\) if \(h_i = g_i + i\) for \(i \geq 1\) and \(g_i = g_1 + i\) for \(i \geq 2\).

**Proposition 3.5.** Let \(G = \langle \{g_1, \ldots, g_r, m\} \rangle\) and \(\tilde{G} = \langle \{h_1, \ldots, h_{r+1}, m\} \rangle\) be two genetic codes. Then \(\tilde{G}\) covers \(G\) if \(h_i = i\) for \(1 \leq i \leq r + 1\) and \(g_j = j + 1\) for \(1 \leq j \leq r\).

**Proposition 3.6.** Let \(G = \langle \{g_1, \ldots, g_r, m\} \rangle\) be a genetic code and \(G_i = \{g_1, \ldots, g_{i-1}, g_i - 1, g_{i+1}, \ldots, g_r, m\}\) for \(1 \leq i \leq r\). Then \(G\) covers the genetic code \((G_1, \ldots, G_r)\).

**Proof.** The proof follows from the observation \(S_m(G) = S_m((G_1, \ldots, G_r)) \cup \{g_1, \ldots, g_r, m\}\) and Proposition 3.2. \(\square\)

**Remark 3.3.** We observe that the converse of Proposition 3.4 and Proposition 3.5 is also true. Since we dont need the converse in the context of this paper, we opt not to write it here.

We now explain a procedure to construct a saturated chain of genetic codes. For simplicity we write the set \(\{i_1, \ldots, i_k\}\) as \(i_1 \ldots i_k\). Let \(G = \langle 25m \rangle\). A genetic code covered by \(G\) can be obtained using Proposition 3.6. For example, \(G\) covers \(\langle 24m, 15m \rangle\). We denote
this genetic code by $C_1$. Then our first task is to obtain a saturated chain starting from $\langle 24m \rangle$ to $C_1$. Using Proposition 3.6 for $\langle 15m \rangle$. In particular, we get the genetic code $C_2 = \langle 24m, 05m, 14m \rangle = \langle 24m, 5m \rangle$ which is covered by $C_1$. In the next step we reduce $C_2$ to $C_3 = \langle 24m, 4m \rangle = \langle 24m \rangle$. Thus we are done with the first task and the saturated chain is

\[(3.1) C_3 = \langle 24m \rangle \not\prec \langle 24m, 5m \rangle \not\prec \langle 24m, 15m \rangle \not\prec \langle 25m \rangle = G.\]

The next task is to keep using Proposition 3.6 to reach from $C_3$ to $\langle 23m \rangle$. More precisely, we get this saturated chain as

\[(3.2) \langle 23m \rangle \not\prec \langle 4m, 23m \rangle \not\prec \langle 14m, 23m \rangle \not\prec C_3.\]

Now we can use Proposition 3.4 to conclude that $\langle 23m \rangle$ covers $\langle 13m \rangle$. Then, we will reduce $\langle 13m \rangle$ to $\langle 12m \rangle$ using Proposition 3.6. Then we get the saturated chain

\[(3.3) \langle 12m \rangle \not\prec \langle 3m, 12m \rangle \not\prec \langle 13m \rangle.\]

Now there is an obvious way to reduce $\langle 12m \rangle$ to $\langle m \rangle$, which is

\[(3.4) \langle m \rangle \not\prec \langle 1m \rangle \not\prec \langle 2m \rangle \not\prec \langle 12m \rangle.\]

Finally, we use (3.1), (3.2), (3.3), and (3.4) to obtain a saturated chain which starts with $\langle m \rangle$ and ends with $\langle 25m \rangle$ as follows

$$\langle m \rangle \not\prec \langle 1m \rangle \not\prec \langle 2m \rangle \not\prec \langle 12m \rangle \not\prec \langle 3m, 12m \rangle \not\prec \langle 13m \rangle \not\prec \langle 23m \rangle \not\prec \langle 4m, 23m \rangle$$

$$\not\prec \langle 14m, 23m \rangle \not\prec \langle 24m \rangle \not\prec \langle 24m, 5m \rangle \not\prec \langle 24m, 15m \rangle \not\prec \langle 25m \rangle.$$ 

Given any monogenic code $G$, the general idea of constructing a saturated chain of genetic codes which starts with $\langle m \rangle$ and ends with $G$ is similar. More precisely, start with a genetic code $G = \langle \{g_1, \ldots, g_r, m\} \rangle$. Then use Proposition 3.6 repeatedly to get the covering chain that starts from $\langle \{g_1, \ldots, g_r, m\} \rangle$ and reaches $G$ and then from $\langle \{g_1, \ldots, g_r, m\} \rangle$ to $\langle \{g_1, \ldots, g_r, m\} \rangle$. One can use these ideas iteratively to construct a saturated chain from $\langle \{g_1, g_1 + 2, \ldots, g_1 + r, m\} \rangle$ to $G$. Then one can use Proposition 3.4 to proceed further. Then again by using similar ideas to get a saturated chain starts from $\{1, 2, \ldots, r, m\}$ to $\langle \{g_1, g_1 + 2, \ldots, g_1 + r, m\} \rangle$. Then, there is an obvious saturated chain starts from $\langle \{m\} \rangle$ and ends with $\{1, 2, \ldots, r, m\}$. Finally, we can combine all these saturated chains to get the saturated chain from $\langle \{m\} \rangle$ to $G = \langle \{g_1, \ldots, g_r, m\} \rangle$.

These ideas can be generalized to construct a saturated chain from $\langle \{m\} \rangle$ to any genetic code $G = \langle G_1, \ldots, G_k \rangle$ by constructing saturated chain between $\langle G_i \rangle$ and $\langle \{m\} \rangle$ for each $1 \leq i \leq k$ and fixing all other genes in $G$.

**Remark 3.4.** The answer to the question – would any arbitrary collection of subsets of $[m]$ that contain $m$ be a genetic code? – is no. Since, in a genetic code any two genes can’t be comparable and the complement of a gene can’t be a short subset. For an arbitrary collection, any of the previous two conditions may fail. However, it is possible to have a genetic code that does not correspond to any length vector. Note that, we can define a short subset system abstractly as a collection of subsets of $[m]$ that satisfy: singletons are there, it is an abstract simplicial complex and if a subset is there in the collection then its complement is not there. This definition gives rise to genetic codes that do not correspond to any length vector. For example, $\langle 2469 \rangle$ is a genetic code that doesn’t correspond to any length vector [7, Lemma 4.6].

Another way of looking at (realizable) genetic codes is via hyperplane arrangements. Equations of the form $\sum \pm x_i = 0$ define a set of hyperplanes in $\mathbb{R}^m$. Connected components of the complement of the union of these hyperplanes are called chambers. An $m$-tuple in a chamber gives us a generic
length vector. It is not hard to check that changing the length vector in a chamber does not change the diffeomorphism type of the corresponding polygon spaces. The same is true for genetic codes: there is a one-to-one correspondence between chambers of this arrangement in (the positive orthant of) $\mathbb{R}^m$ and (realizable) genetic codes in $[m]$. One can describe saturated chains of genetic codes using chambers of this arrangement. Providing full details here will involve introducing more vocabulary and some technical results. Since this language of arrangements and chambers is not directly relevant to the aim of this paper, we won't provide any details. However, for the interested reader we only mention that the partial order on chambers is defined using ‘the set of separating hyperplanes’ and the covering relation is given by ‘wall crossing’.

3.2. Submanifold arrangements. There are smoothly embedded closed codimension-1 submanifolds of planar polygon spaces corresponding to 2-element short subsets. In fact, the collection of all such submanifolds forms a submanifold arrangement. In this section, we study some combinatorial properties of this arrangement. We also study the induced cell structure.

**Definition 3.4.** Let $X$ be a finite dimensional smooth, closed manifold. A submanifold arrangement is a finite collection $A = \{N_1, \ldots, N_r\}$ of codimension-1 submanifolds such that,

1. each element of $A$ is smoothly embedded as a closed subset;
2. for every point $x \in \bigcup_{i=1}^{r} N_i$ has a coordinate neighbourhood $V_x$ such that the collection $\{N_i \cap V_x, \ldots, N_r \cap V_x\}$ is a hyperplane arrangement in $V_x$ with $x$ as the origin;
3. the intersections of members of $A$ induces a regular cell structure on $X$ and each cell is combinatorially equivalent to simple convex polytope of an appropriate dimension.

There is an important combinatorial object associated with the submanifold arrangement.

**Definition 3.5.** The intersection poset $I(A)$ is the set of connected components of all possible intersections of $N_i$’s ordered by reverse inclusion.

Corresponding to every 2-element short subset $\{i, j\}$ we have polygonal configurations with $i$-th and $j$-th sides are in the same direction. Collection of such polygonal configurations forms codimension-1 submanifold of $M_\alpha$. In particular we write

$$N_{i,j} = \{(v_1, \ldots, v_i, \ldots, v_j, \ldots, v_m) \in M_\alpha : v_i = v_j\}.$$  

Let $$\alpha(i, j) = (\alpha_1, \ldots, \alpha_i, \ldots, \alpha_j, \ldots, \alpha_i + \alpha_j, \ldots, \alpha_m)$$ be the $(m-1)$-tuple such that $\alpha_i$ and $\alpha_j$ are absent in $\alpha(i, j)$. Observe that $\alpha(i, j)$ is a generic length vector. It is easy to see that $N_{i,j} \cong M_{\alpha(i,j)}$. Similarly we define

$$\overline{N}_{i,j} = \{(v_1, \ldots, v_i, \ldots, v_j, \ldots, v_m) \in \overline{M}_\alpha : v_i = v_j\}.$$  

We also have $\overline{N}_{i,j} \cong M_{\alpha(i,j)}$. For a length vector $\alpha$, we define the finite collections of submanifolds of $M_\alpha$ and $\overline{M}_\alpha$ as follows

$$A_\alpha := \{N_{i,j} : \{i, j\} \text{ is } \alpha \text{-short}\},$$  

$$\overline{A}_\alpha := \{\overline{N}_{i,j} : \{i, j\} \text{ is } \alpha \text{-short}\}.$$  

Let $\alpha$ be a generic length vector. Let

$$\Pi_m(\alpha) = \{\pi \in \Pi_m : \text{blocks of } \pi \text{ are } \alpha\text{-short}\}$$  

and

$$\overline{\Pi}_m(\alpha) = \{\overline{\pi} : \pi \in \Pi_m \text{ and } M_{\alpha(\pi)} \text{ is disconnected}\}.$$  

Let $L_\alpha = \Pi_m(\alpha) \sqcup \overline{\Pi}_m(\alpha)$ be the poset under the reverse refinement as a partial order.
Lemma 3.1. The intersection posets $\mathcal{I}(\mathcal{A}_\alpha)$ and $\mathcal{I}(\overline{\mathcal{A}}_\alpha)$ are isomorphic to the posets $\mathcal{L}_\alpha$ and $\Pi_m(\alpha)$, respectively.

\textbf{Proof.} Consider the following intersection 

$$X = N_{i_1j_1} \cap N_{i_2j_2} \cap \cdots \cap N_{i_rj_r}.$$ 

Then by clubbing together pairwise intersecting 2-element short subsets 

$$\{i_l, j_l : 1 \leq l \leq r\}$$ 

we can write 

$$X = N_{i_1} \cap N_{i_2} \cap \cdots \cap N_{i_s},$$ 

where $N_{i_t} = \bigcap_{(i,j) \in I_t} N_{ij}$ for $1 \leq t \leq s$. Note that $I_1 - I_2 - \cdots - I_s$ is a partition of \{i_1, j_1, \ldots, i_r, j_r\}. By putting together remaining singletons we get the partition of $[m]$. Let’s denote this partition by $\pi$. Recall that if $X$ is disconnected then it is the disjoint union of tori. We label one of the connected component of $\pi$ and the other one by $\pi$. Otherwise, label $X$ by $\pi$. Conversely, we define an element of $\mathcal{I}(\mathcal{A}_\alpha)$ corresponding to a partition $\pi = J_1 - \cdots - J_k$ of $[m]$ with all $J_i$’s are short. Consider the following intersection. 

$$X = \bigcap_{(i,j) \in J_1} N_{ij} \cap \cdots \cap \bigcap_{(i,j) \in J_k} N_{ij}.$$

As done above if $X$ is disconnected we label one of the connected component by $\pi$ and the other one by $\pi$.

Note that if the intersection corresponding to 2-element short subsets $\{i_l, j_l : 1 \leq l \leq r\}$ 

$$X = \overline{N}_{i_1j_1} \cap \overline{N}_{i_2j_2} \cap \cdots \cap \overline{N}_{i_rj_r},$$ 

is nonempty then $\overline{X}$ is connected. Now the isomorphism between $\mathcal{I}(\overline{\mathcal{A}}_\alpha)$ and $\Pi_m(\alpha)$ is clear. \hfill $\square$

Remark 3.5. Let $\alpha$ be a generic length vector, and $\pi = J_1 - \cdots - J_k$ be a partition of $[m]$ with all $J_i$’s are $\alpha$-short. Consider the shorter length vector $\alpha(\pi) = (\alpha_{J_1}, \ldots, \alpha_{J_k})$ where $\alpha_{J_l} = \sum_{i \in J_l} \alpha_i$ for $1 \leq l \leq k$. Let 

$$X = \bigcap_{(i,j) \in J_1} N_{ij} \cap \cdots \cap \bigcap_{(i,j) \in J_k} N_{ij}$$

and 

$$\overline{X} = \bigcap_{(i,j) \in J_1} \overline{N}_{ij} \cap \cdots \cap \bigcap_{(i,j) \in J_k} \overline{N}_{ij}.$$ 

Then it is easy to see that $X \cong M_{\alpha(\pi)}$ and $\overline{X} \cong \overline{M}_{\alpha(\pi)}$.

Corollary 3.6.1. Both the collections $\mathcal{A}_\alpha$ and $\overline{\mathcal{A}}_\alpha$ are locally isomorphic to either braid arrangement or the product of braid arrangement.

\textbf{Proof.} Let $X \in \mathcal{I}(\mathcal{A}_\alpha)$ be a connected submanifold. Then without loss of generality assume that $X = J_1 - J_2 - \cdots - J_k$, where $J_i$’s are $\alpha$-short. Consider the collection 

$$\mathcal{I}(\mathcal{A})_X = \{Y \in \mathcal{I}(\mathcal{A}_\alpha) : X \subseteq Y\}.$$ 

Note that any element of $\mathcal{A}_X$ has the labelled by the refined partition of $X$. Therefore, the poset $\mathcal{I}(\mathcal{A})_X$ is isomorphic to the poset of all refinements of $X$. This concludes 

$$\mathcal{I}(\mathcal{A})_X \cong \prod_{i=1}^k \mathcal{I}(\mathcal{B}_{|J_i|}).$$ 

Similar arguments work for $\overline{\mathcal{A}}_\alpha$.

The following result is an immediate consequence of the above corollary.
Corollary 3.6.2. The collections $\mathcal{A}_\alpha$ and $\overline{\mathcal{A}}_\alpha$ induces a regular cell structure on $M_\alpha$ and $\overline{M}_\alpha$, respectively such that each cell is combinatorially equivalent to some simple polytopes.

The following proposition is now clear.

Proposition 3.7. The collections $\mathcal{A}_\alpha$ and $\overline{\mathcal{A}}_\alpha$ are submanifold arrangements in $M_\alpha$ and $\overline{M}_\alpha$, respectively.

We denote the cell structures induced from the submanifold arrangements $\mathcal{A}_\alpha$ and $\overline{\mathcal{A}}_\alpha$ on $M_\alpha$ and $\overline{M}_\alpha$ by $K_\alpha$ and $\overline{K}_\alpha$, respectively.

Remark 3.6. It can be observed that the cell structure $K_\alpha$ induced by the submanifold arrangement coincides with the cell structure introduced by Panina in [13]. Panina also showed that for a generic length vector $M_\alpha$ is a PL-manifold.

Example 3.2. Let $\langle m \rangle$ be the genetic code of $\alpha$. Then we have

$$\overline{\mathcal{A}}_\alpha = \{N_{ij} : \{i, j\} \subset [m - 1]\}.$$ 

Note that for any proper subset of $[m - 1]$ is $\alpha$-short if the genetic code of $\alpha$ is $\langle m \rangle$. Therefore, corresponding to any partition of $[m - 1]$, we have nonempty intersection of $\overline{N}_{i,j}$’s. Therefore, it is easy to see that

$$\mathcal{I}(\overline{\mathcal{A}}_{\langle m \rangle}) \cong \Pi_{m-1} \setminus \{\hat{1}\},$$

where $\Pi_{m-1}$ is the lattice of partitions of $[m - 1]$. Note that $M_\alpha \cong S^{m-3}$ and the arrangement

$$\mathcal{A}_\alpha = \{N_{ij} : \{i, j\} \subset [m - 1]\}$$

is the braid arrangement $B_{m-1}$ intersected with $S^{m-3}$.

Figure 3.1. $\overline{K}_{\langle 5 \rangle} \cong PCA_3$ and $\mathcal{I}(\overline{\mathcal{A}}_\alpha) \cong \Pi_4 \setminus \{\hat{1}\}$. 

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Proposition 3.8. The cell complex $K_{(m)}$ (respectively $\overline{K}_{(m)}$) is isomorphic to the Coxeter complex (respectively projective Coxeter complex) of type $A_{m-2}$.

Proof. Recall that $M_{(m)} \cong S^{m-3}$ and $\overline{M}_{(m)} \cong \mathbb{R}P^{m-3}$. Moreover, the submanifold arrangement $A_{(m)}$ is isomorphic to the braid arrangement $B_{m-1}$; see Example 3.2. Therefore, it is evident that $K_{(m)} \cong CA_{m-2}$ and $\overline{K}_{(m)} \cong \mathbb{P}CA_{m-2}$. □

4. A THEOREM OF HAUSMANN

Let $\alpha$ and $\beta$ be two length vectors such that $S_m(\beta) = S_m(\alpha) \cup J$ for some $J \subset [m]$. Hausmann [6] used techniques from Morse theory to obtain a relation between corresponding planar polygon spaces $M_\alpha$ and $M_\beta$. He proved the following theorem.

Theorem 4.1 ([6, Proposition 2.9]). The space $M_\beta$ is obtained from $M_\alpha$ by an $O(1)$-equivariant surgery of index $|J| - 2$, i.e.,

$$M_\beta \cong (M_\alpha \setminus S^{|J| - 2} \times D^{m-1-|J|}) \cup_{S^{|J| - 2} \times S^{m-2-|J|}} (D^{|J| - 1} \times S^{m-2-|J|}),$$

where $O(1)$ acts antipodally on $D^{m-1-|J|}$ and $D^{|J| - 1}$.

Note that using Proposition 3.2, we can say that if the genetic code $G$ covers $G'$ then $M_G$ is obtained from $M_{G'}$ by an $O(1)$-equivariant surgery. In fact, one can iterate this process over any saturated chain of genetic codes. Note that $M_{(m)} \cong S^{m-3}$ and $\overline{M}_{(m)} \cong \mathbb{R}P^{m-3}$. The iterated version of Theorem 4.1 is given by the following proposition.

Proposition 4.2. Let $\langle m \rangle = G_1 \preceq G_2 \preceq \cdots \preceq G_r = G$ be the saturated chain of genetic codes. Then the space $M_G$ is obtained from $S^{m-3}$ by an iterated $O(1)$-equivariant surgery in $r$ steps.

Proof. Note that $S_m(G_{i+1}) = S_m(G_i) \cup J_i$ for $1 \leq i \leq r - 1$. Therefore, $M_{G_{i+1}}$ is obtained from $M_{G_i}$ by an $O(1)$-equivariant surgery along $S^{|J_i| - 2}$. Observe that $S_m(G_r) = \{m\} \cup \bigcup_{i=1}^{r-1} J_i$. Now the propositions follows from iteratively applying Theorem 4.1. □

Remark 4.1. Observe that Theorem 4.1 doesn’t describe how to keep track of iterations, also there is no CW-complex analogue of the procedure.

We now define a projective version of the surgery operation for certain quotient manifolds. Let $M$ be a smooth manifold of dimension $n$ with a free $\mathbb{Z}_2$-action. Suppose the
$k$-dimensional sphere $S^k$ and its trivial tubular neighbourhood $S^k \times D^{n-k}$, embeds $\mathbb{Z}_2$-equivariantly in $M$. Let $\overline{M}$ denote the quotient of $M$ by the free $\mathbb{Z}_2$-action. Note that $\mathbb{R}P^k$ and the quotient $\frac{S^k \times D^{n-k}}{(x,y) \sim (-x,-y)}$ embed in $\overline{M}$. With this information we introduce the following notations.

1. \[
\mathcal{D}^\mathbb{P}(k) := \frac{S^k \times D^{n-k}}{(x, y) \sim (-x, -y)},
\]

2. \[
\mathcal{D}_P(k) := \frac{D^k \times S^{n-k}}{(x, y) \sim (-x, -y)},
\]

3. \[
\partial(\mathcal{D}_P(k)) = \frac{S^k \times S^{n-k-1}}{(x, y) \sim (-x, -y)} = \partial(\mathcal{D}_P(k+1)).
\]

**Remark 4.2.** The space $\partial(\mathcal{D}_P(k))$ is the total space of the sphere bundle of the $(n-k)$-direct sum of canonical line bundles over $\mathbb{R}P^k$ and $\mathcal{D}_P(k)$ is the total space of the disc bundle of the $(n-k)$-direct sum of canonical line bundles over $\mathbb{R}P^k$.

With the above notations, we define projective cellular surgery.

**Definition 4.1.** An index $k$-projective surgery on a manifold $\overline{M}$ along $\mathbb{R}P^k$, produces a manifold $\mathcal{P}S_k(\overline{M})$ defined as follows

\[
\mathcal{P}S_k(\overline{M}) := \left(\overline{M} \setminus \mathcal{D}_P(k)\right) \cup_{\partial(\mathcal{D}_P(k))} (\mathcal{D}_P(k+1)).
\]

**Proposition 4.3.** We now have the following:

1. The index-0 surgery on a manifold $M$ along $S^0$, produces a manifold homeomorphic to the connected sum $M\#(S^1 \times S^{n-1})$.

2. The index-0 projective surgery on a manifold $\overline{M}$ along $\mathbb{R}P^0$, produces a manifold homeomorphic to the connected sum $\overline{M}\#\mathbb{R}P^n$.

**Proof of (1).** Without loss of generality $M = S^n$. Let $D^+$ and $D^-$ be two small and disjoint antipodal discs containing the north pole and south pole, respectively. Then the surgery on $S^n$ along $S^0$ tells us that, remove $D^+$ and $D^-$ from $S^n$ and attach $D^1 \times S^{n-1}$ to $S^n \setminus (D^+ \cup D^-)$. This clearly gives $S_0(S^n) = S^1 \times S^{n-1}$. Observe that $S_0(S^1 \times S^{n-1}) = S^1 \times S^{n-1}$. Without loss of generality, we can assume that there is a bigger disc $D$ such that $D^+ \cup D^- \subseteq D$ Now observe that the index-0 surgery on $S^n$ is an equivalent operation to removing $D$ from $S^n$ and attaching $(S^1 \times S^{n-1}) \setminus D'$ to $S^n \setminus D$, for some disc $D'$ in $S^1 \times S^{n-1}$. This is same as the connected sum of $S^n$ and $S^1 \times S^{n-1}$. The same idea works for general $M$.

**Proof of (2).** We make the following observations:

1. \[
\mathcal{D}_P(0) = \frac{S^0 \times D^n}{(x, y) \sim (-x, -y)} = D^n,
\]

2. \[
\mathcal{D}_P(1) = \frac{D^1 \times S^{n-1}}{(x, y) \sim (-x, -y)} = \frac{S^n \setminus (D^+ \cup D^-)}{x \sim -x} = \mathbb{R}P^n \setminus D^n,
\]
This proves the result. □

**Theorem 4.4 ([6, Proposition 2.9])**. If the genetic code $G$ covers $G'$, i.e., $S_m(G) = S_m(G') \cup J$ for some $J \subset [m]$ then $\bar{M}_G$ is homeomorphic to $\mathbb{P}S_{|J|-2}(\bar{M}_{G'})$.

One can iterate the projective surgery to any chain $G_1 \preceq G_2 \preceq \cdots \preceq G_r = G$ such that for each $1 \leq i \leq r-1$, $G_i$ is covered by $G_{i+1}$. We denote the space after iterated projective surgery as $\mathbb{P}S_{(j_1,\ldots,j_r)}(M_{G_1})$ where $j_i = |J_i|-2$ such that $S_m(G_{i+1}) = S_m(G_i) \cup J_i$. In fact we have $S_m(G_r) = S_m(G_1) \cup \bigcup_{i=1}^{r-1} J_i$. With this, we have the following version of Theorem 4.1.

**Proposition 4.5.** The planar polygon space $\bar{M}_G$ is homeomorphic to $\mathbb{P}S_{(j_1,\ldots,j_r)}(\mathbb{R}P^{m-3})$.

5. **Combinatorial surgery on a meet semi-lattice**

The notion of combinatorial blow-up was introduced by Feichtner and Kozlov in [4]. Here, we introduce a similar notion in the contexts of surgery.

**Definition 5.1.** Let $\mathcal{L}$ be a meet semilattice. For an element $x \in \mathcal{L}$, we define a poset $CS_x(\mathcal{L})$, the combinatorial surgery on $\mathcal{L}$ along $x$, as follows:

- **elements of $CS_x(\mathcal{L})$:**
  1. $y \in \mathcal{L}$, $y \neq x$ and $y \preceq x$
  2. $[x, y]$, $y < x$

- **order relations in $CS_x(\mathcal{L})$:**
  1. $y > z$ in $CS_x(\mathcal{L})$ if $y > z$ in $\mathcal{L}$
  2. $[x, y] > [x, z]$ in $CS_x(\mathcal{L})$ if $y > z$ in $\mathcal{L}$
  3. $[x, y] > z$ in $CS_x(\mathcal{L})$ if $y \geq z$ in $\mathcal{L}$.
  4. $y < [x, 0]$ if $y \vee x \in \mathcal{L}$.

**Remark 5.1.** The element $[x, 0]$ can be thought of as a result of combinatorial surgery along $x$.

**Theorem 5.1.** The poset $CS_x(\mathcal{L})$ is a meet semilattice. Moreover, for $x \in \mathcal{L}$, the posets $\mathcal{L}$ and $CS_x(\mathcal{L})$ are of equal rank $k$ the rank of $\mathcal{L}$, then

$$rk([x, y]) = k - rk(x) + rk(y) + 1.$$ 

**Example 5.1.** Let $G = \langle \{2, 6\} \rangle$ be the genetic code and $\mathcal{I}(A_G)$ be the corresponding meet semilattice. Let $(1, 2, 345, 6) \in \mathcal{I}(A_G)$. We denote this partition by 345. Then

$$CS_{345}(\mathcal{I}(A_G)) = \left( \mathcal{I}(A_G) \setminus \mathcal{I}(A_G)_{\geq 345} \right) \cup \left\{ [345, y] : y < 345 \right\}$$

$$\cong \left( \mathcal{I}(A_G) \setminus \mathcal{I}(A_G)_{\geq 345} \right) \cup \left\{ (126, \pi) : \pi < (1, 2, 345, 6) \right\}$$

$$= \mathcal{I}(A_{\langle\{1,2,6\}\rangle}),$$

where $(126, \pi)$ denotes an unordered partition of $[6]$. Observe that the genetic code $\langle\{1, 2\}\rangle$ covers $\{(2, 6)\}$ with respect to the genetic order.
Let $G$ and $G'$ be two genetic codes of $m$-length vectors such that $G'$ covers $G$. It follows from Proposition 3.2 that there exists a subset $J \subseteq [m]$ with $S_m(G') = S_m(G) \cup J$. With this, the following result is straightforward.

**Proposition 5.2.** $CS_J(\mathcal{I}(A_G)) \cong \mathcal{I}(A_{G'})$.

6. **Cellular surgery on simple cell complexes and the proof of Theorem 1.1**

Let $K$ be a simple cell complex of dimension $n$ such that there is a subcomplex homeomorphic to the $k$-sphere $S^k$. Let us denote this subcomplex by $KS^k$. Moreover, assume that for any $k$-simplices $\sigma, \sigma' \in KS^k$, $Lk(\sigma, K) \cong Lk(\sigma', K) \cong S^{n-k-1}$.

**Definition 6.1.** The index $k$ cellular surgery on $K$ along $KS^k$ is defined in two steps:

Step 1: Truncate all cells whose closure intersects $KS^k$.

Step 2: Let $D(KS^k)$ be the cellular disc with the boundary $KS^k$. Note that the boundary complex of the truncated part around $KS^k$ is $KS^k \times Lk(\sigma, K)$ for $\sigma \in KS^k$. Now attach another simple cell complex $D(KS^k) \times Lk(\sigma, K)$ to $K$ along $KS^k \times Lk(\sigma, K)$.

In particular, if $\tilde{K}$ denotes the cell complex obtained by the cellular surgery on $K$ then

$$\tilde{K} := \left( K \setminus KS^k \times D(Lk(\sigma, K)) \right) \bigcup_{KS^k \times Lk(\sigma, K)} \left( D(KS^k) \times Lk(\sigma, K) \right).$$

Let $K$ be a simple cell complex with free $\mathbb{Z}_2$-action such that $S^k$ embeds in $K$ as an $\mathbb{Z}_2$-equivariant subcomplex. Assume that, for any $k$-simplices $\sigma, \sigma' \in KS^k$ we have $Lk(\sigma, K) \cong Lk(\sigma', K) \cong S^{n-k-1}$ such that the quotient of $Lk(\sigma, K)$ by $\mathbb{Z}_2$-action is again a cell complex. With these assumptions, we are ready to define the projective version of a cellular surgery on the quotient of $K$ by the $\mathbb{Z}_2$-action.

**Definition 6.2.** Let $PKS^k$ and $\overline{K}$ be the quotients of $KS^k$ and $K$ by the $\mathbb{Z}_2$-action, respectively. The index $k$ projective cellular surgery on $\overline{K}$ along $PKS^k$ is a cell complex $\overline{\tilde{K}}$ defined as

$$\overline{\tilde{K}} := \left( \overline{K} \setminus KS^k \times_\mathbb{Z}_2 D(Lk(\sigma, K)) \right) \bigcup_{KS^k \times_\mathbb{Z}_2 Lk(\sigma, K)} \left( D(KS^k) \times_\mathbb{Z}_2 Lk(\sigma, K) \right),$$

where $KS^k \times_\mathbb{Z}_2 D(Lk)$ denotes the quotient of $KS^k \times D(Lk)$ by diagonal $\mathbb{Z}_2$-action. Similarly, $KS^k \times_\mathbb{Z}_2 Lk(\sigma, K)$ and $D(KS^k) \times_\mathbb{Z}_2 Lk(\sigma, K)$ are defined.
Let $CA_{m-1}$ be the Coxeter complex corresponding to the braid arrangement $B_m$. Let $X \in \text{Min}(B_m)$. Recall that $X$ can be represented by the partition of $\{m\}$ with at most one block of size greater equal 2. Let $X = J - i_1 - i_2 - \cdots - i_k$. Consider the subcollection
$$B_X = \{H \in B_m : X \subset H\}$$
of $B_m$. It is easy to see that the following isomorphism
$$B_X = \{H_{ij} \in B_m : \{i, j\} \subset J\} \cong B_{|J|}.$$Let $\sigma \in S_X$ be a cell such that $\dim(\sigma) = \dim(S_X)$. From the above discussion, it is clear that $\text{Lk}(\sigma, CA_{m-1}) \cong CA_{|J|-1}$.

**Definition 6.3.** Let $X \in \text{Min}(B_m)$. Cellular surgery on $CA_{m-1}$ along $S_X$ is defined as

1. Truncate all cells which are adjacent to $S_X$.
2. Note that the boundary complex of the truncated part around $S_X$ is $X \times CA_{|J|-1}$. Let $D(S_X)$ be the cellular disc whose boundary is $S_X$. Attach the complex $D(S_X) \times CA_{|J|-1}$ along the boundary $S_X \times CA_{|J|-1}$.

Similarly, we can define a cellular surgery on the projective Coxeter complex by replacing $S_X$ and $CA_{m-1}$ by $\mathbb{P}S_X$ and $\mathbb{P}CA_{m-1}$ respectively in the Definition 6.3. Note that after truncating cells adjacent to $\mathbb{P}S_X$, the boundary of the truncated part will be $S_X \times O(1)CA_{|J|-1}$. Accordingly, attach the $D(S_X) \times O(1)CA_{|J|-1}$ to the truncated complex.

**Remark 6.1.** We have the following observations.

1. It is easy to see that truncation of all cells adjacent to $S_X$ in $CA_{m-1}$ is an equivalent operation to removing $S^{m-|J|-1} \times D^{|J|-1}$ tubular neighbourhood of $S_X$, since $S_X \cong S^{m-|J|-1}$ and $D^{|J|-1}$ is the $(|J| - 1)$-dimensional disc. In step 2 of the above definition, we attach $D^{m-|J|} \times S^{|J|-2}$ since, $CA_{|J|-1} \cong S^{|J|-2}$. Therefore, the Definition 6.3 is a cellular analogue of the surgery on manifolds.

2. If $\dim(X) = 0$ then the cellular surgery on $CA_{m-1}$ along $S_X$ gives the cell complex homeomorphic to $S^1 \times S^{m-3}$. On the other hand, the cellular surgery on $\mathbb{P}CA_{m-1}$ along $\mathbb{P}S_X$ gives a cell complex which is homeomorphic to $\mathbb{R}P^{m-2} \# \mathbb{R}P^{m-2}$.

**Example 6.1.** Let $X = 123$ be an element of the minimal building set $\text{Min}(B_4)$. Note that $S_{123} = S^0 = \{123, 1\}$ is a 0-dimensional sphere. We can see that the subarrangement $B_X$ is isomorphic to the braid arrangement $B_3$. Note that there are 6 triangles that are adjacent to 123. Therefore, if we truncate all these triangles, the boundary of the truncated part will be a hexagonal circle, $CA_2$ (see the red hexagonal circle in Figure 6.1). Similarly, truncating cells adjacent to 123 creates the disjoint union of two hexagonal circles as the boundary of the truncated part. Note that this boundary is isomorphic to the complex $S_{123} \times CA_2$. Let $D(S_{123})$ be the cellular disc with the boundary $S_{123}$. In the next step of cellular surgery along $S_{123}$ we have to attach a hexagonal cylinder $D(S_{123}) \times CA_2$, to the truncated complex along with the boundary complex $S_{123} \times CA_2$ of the truncated part in the step-1. Now it is easy to see that the complex obtained after the cellular surgery is the torus cellulated by 18 squares and 12 triangles.

**Example 6.2.** Let $X \in \text{Min}(B_4)$ such that it is represented by an unordered partition $123 - 4$. Without loss of generality we can omit the singletons and write $X = 123$. Consider the 0-dimensional projective Coxeter complex $\mathbb{P}S_{123}$ in $\mathbb{P}X$. Similarly, as in the previous
example we have \( PB_{2X} \cong B_3 \). Now truncating cells of \( PCA_3 \) adjacent to \( S_{123} \) gives boundary of truncated part to be \( S_{123} \times_{O(1)} CA_2 \), a hexagonal circle. Note that the boundary \( \partial(D(S_{123}) \times_{O(1)} CA_2) = S_{123} \times_{O(1)} CA_2 \). Now in the next step we attach \( D(S_{123}) \times_{O(1)} CA_2 \) to \( S_{123} \times_{O(1)} CA_2 \). Note that \( D(S_{123}) \times_{O(1)} CA_2 \) is a cell complex homeomorphic to the Mobius band. Now it is easy to see that the resulting complex after the projective cellular surgery is cellulated by 6 triangles and 9 squares (see Figure 6.2).

Let \( \langle m \rangle = G_1 \preceq G_2 \preceq \cdots \preceq G_r = G \) be a saturated chain of genetic codes such that \( G_{i+1} \) covers \( G_i \) for \( 1 \leq i \leq r - 1 \) and \( S_m(G) = \{ m \} \cup \bigcup_{i=1}^{r-1} J_i \). Note that \( m \notin J_{r}^c \). Therefore, \( J_{r}^c \)'s are short subsets with respect to the genetic code \( \langle m \rangle \). Note that each \( J_{r}^c \) represents the partition \( J_{r}^c = j_1 - j_2 - \cdots - j_k \) of \( [m] \). Now it follows from the Example 2.2 that \( \{ J_1^c, \ldots, J_{r-1}^c \} \subseteq \text{Min}(B_{m-1}) \). Consider the collections

\[
\mathcal{G}_G = \left\{ S_{J_1}, S_{J_2}, \ldots, S_{J_{r-1}} \right\}
\]
and

\[ \mathbb{P}G = \left\{ \mathbb{P}S_{jk}, \mathbb{P}S_{j_1}, \ldots, \mathbb{P}S_{j_{r-1}} \right\}. \]

**Theorem 6.1.** Let \( G \) be the genetic code of a length vector \( \alpha \). Then the iterated cellular surgery on \( \mathbb{P}CA_{m-2} \) (respectively on \( \mathbb{P}CA_{m-2} \)) along the elements of \( G \) (respectively \( \mathbb{P}G \)) produces the cell complex \( \hat{K}_\alpha \) (respectively \( \hat{\mathbb{P}}G \)) homotopy equivalent to \( K_\alpha \) (respectively \( \mathbb{P}G \)).

**Proof.** Following the inductive argument, it is enough to prove the theorem for a saturated chain of length 1. Let \( G \preceq G' \) be a saturated chain of length 1. It follows from the Proposition 3.2 that, \( S_m(G') = S_m(G) \cup J \) for some \( J \subset [m] \). Since \( J' \) is the maximal short subset (i.e., adding an extra element in \( J' \) makes it into long), the subcomplex \( S_{j'} \) of \( K_\alpha \) is isomorphic to the Coxeter complex \( CA_{|J|-1} \) of dimension \( |J| \). Note that \( J \) is short subset with respect to the genetic code \( G' \). We also have \( G' = \langle G, J \rangle \). Since \( J \) is maximal short subset the subcomplex \( S_J \) of \( K_{G'} \) represents the Coxeter complex \( CA_{m-2-[J]} \). Now we see that the \( \text{Lk}(\sigma, K_{G'}) \) is isomorphic to the Coxeter complex for \( \sigma \in S_{j'} \). Note that collapsing \( \mathbb{P}G \) is isomorphic to the Coxeter complex for \( \sigma \). Following the inductive argument, it is enough to prove the theorem for a saturated chain of length 1. Therefore, \( \text{Lk}(\sigma, K_{G'}) \cong S^{m-|J|-2} \) if \( \dim(\sigma) = |J| - 1 \). The cell structure on \( S^{m-|J|-2} \) is induced by the collection

\[ \{N_{i,j} : \{i, j\} \subset J'\}. \]

Note that the above collection is isomorphic to the braid arrangement \( B_{m-[J]} \). Therefore, \( \text{Lk}(\sigma, K_{G'}) \cong CA_{m-2-[J]} \). Let \( K_{G'} \) be the complex obtained by the index \( |J| - 1 \) cellular surgery on \( K_{G} \) along \( S_{j'} \). Then

\[ \hat{K}_G = \left( K_G \setminus S_{j'} \times D(CA_{m-2-[J]}) \right) \bigcup_{S_{j'} \times CA_{m-2-[J]}} D(S_{j'}) \times CA_{m-2-[J]} \].

Now if we collapse \( D(S_{j'}) \times CA_{m-2-[J]} \) onto \( CA_{m-2-[J]} \), \( \hat{K}_G \) becomes homotopy equivalent the complex \( (K_G \setminus S_{j'}) \cup S_J \). It follows from Section 4 that \( 
\hat{K}_G \cong M_{G'} \). Note that collapsing \( D(S_{j'}) \times CA_{m-2-[J]} \) onto \( CA_{m-2-[J]} \) doesn’t change the homeomorphism type of \( \hat{K}_G \). Therefore, \( (K_G \setminus S_{j'}) \cup S_J \cong M_{G'} \). Now it follows from Remark 3.2 that the cell complex \( (K_G \setminus S_{j'}) \cup S_J \) is induced from the submanifold arrangement \( A_{\alpha} \). Therefore, \( (K_G \setminus S_{j'}) \cup S_J = K_{G'} \).

Let \( \mathbb{P}S_{j'} \) be the projective Coxeter complex \( \mathbb{P}CA_{[J]-1} \) in \( \hat{K}_G \) represented by a partition \( J' \) of \( [m] \) and let \( \mathbb{P}S_J \) be the subcomplex of \( \hat{K}_{G'} \) isomorphic to the projective Coxeter complex \( \mathbb{P}CA_{m-2-[J]} \). The index \( |J| - 1 \) projective cellular surgery on \( \hat{K}_G \) along \( \mathbb{P}S_{j'} \) gives

\[ \hat{\mathbb{P}}G = \left( K_G \setminus S_{j'} \times (1) \right) \bigcup_{S_{j'} \times (1) \times CA_{m-2-[J]}} D(S_{j'}) \times (1) \times CA_{m-2-[J]} \].

Note that \( S_{j'} \times (1) \times CA_{m-2-[J]} \) and \( D(S_{j'}) \times (1) \times CA_{m-2-[J]} \) are the total spaces of disc bundles over \( \mathbb{P}S_{j'} \) and \( \mathbb{P}S_J \), respectively. Therefore, \( J' \times (1) \times CA_{m-2-[J]} \) and \( J' \times (1) \times CA_{m-2-[J]} \) are homotopy equivalent to \( \mathbb{P}S_{j'} \) and \( \mathbb{P}CA_{m-2-[J]} \), respectively. Therefore, \( \hat{\mathbb{P}}G \) is homotopy equivalent to the complex \( (K_G \setminus \mathbb{P}S_{j'}) \cup \mathbb{P}S_J \). Now the theorem follows from similar arguments as did for the cellular surgery.

Since the projective cellular surgery along zero dimensional subspaces coincides with the blow-up, the following result is straightforward.

**Corollary 6.1.1.** Let \( \langle \{k, m\} \rangle \) be the genetic code of \( \alpha \). Then \( K_\alpha \) is obtained from the \( \mathbb{P}CA_{m-2} \) by an iterated blow-up along the subspaces \( \{1, 2, \ldots, i, \ldots, m\} \) for \( 1 \leq i \leq k \).
Now we characterize planar polygon spaces that are $\overline{M}_0^m(\mathbb{R})$.

**Proposition 6.2.** Let $\alpha = (\alpha_1, \ldots, \alpha_m)$ be a generic length vector. Then there is a homeomorphism $\overline{M}_0^m(\mathbb{R}) \cong \mathcal{K}_\alpha$ if and only if the genetic code of $\alpha$ is $\langle \{4, 5\} \rangle$.

**Proof.** Devadoss [2] showed that $\overline{M}_0^m(\mathbb{R}) \cong \mathcal{M}_a$ is tiled by $(m-1)!/2$ copies of the associahedron of dimension $m - 3$. Recall that the number of facets of this associahedron is $\binom{m-1}{2} - 1$. Any top dimensional cell of $\mathcal{K}_\alpha$ has at most $m$ many facets. Observe that $m = \binom{m-1}{2} - 1$ if and only if $m = 5$. In this case the top dimensional cell (i.e., 2-dimensional) of $\mathcal{K}_\alpha$ has 5-facets and it is isomorphic to a pentagon. Recall that $\overline{M}_0^m(\mathbb{R}) \cong \mathcal{K}_\alpha$ is the connected sum of 5 copies of $\mathbb{R}P^2$. Since $\mathcal{K}_\langle\{4, 5\}\rangle$ is tiled by 12 pentagons and homeomorphic to the connected sum of 5 copies of $\mathbb{R}P^2$, $\overline{M}_0^m(\mathbb{R}) \cong \mathcal{K}_\alpha$ for the genetic code $\langle \{4, 5\} \rangle$.

We now illustrate the idea of the Theorem 6.1 through the following example.

**Example 6.3.** Consider the saturated chain of genetic codes $\langle 5 \rangle \leq \langle 15 \rangle \leq \langle 25 \rangle \leq \langle 125 \rangle$. Note that $\mathcal{G}_{\langle 125 \rangle} = \{S_{234}, S_{134}, S_{34}\}$. Now we explain how to obtain the cell complex $\tilde{K}_{\langle 125 \rangle}$ (resp. $\tilde{K}_{\langle 125 \rangle}$) by performing the cellular surgery on $CA_3$ (resp. $\mathbb{P}CA_3$) along $\mathcal{G}_{\langle 125 \rangle}$ (resp. $\mathcal{G}_{\langle 125 \rangle}$). We start with performing surgery on $CA_3$ along $S_{234}$. Then we get the complex $\tilde{K}_{15}$ isomorphic to the torus. Note that, if we collapse the hexagonal cylinder onto one of its boundary components we get the complex again isomorphic to the torus. It is easy to see that this complex is isomorphic to the complex $K_{\langle 15 \rangle}$. Later we follow the same process for $S_{134}$ and get the complex $K_{\langle 25 \rangle}$. Now we need to do the surgery along $S_{34}$. Note that $S_{34}$ represents the hexagonal circle in $K_{\langle 25 \rangle}$. In this case, the first step is to truncate all the cells adjacent to $S_{34}$. After truncating adjacent cells we get the two disjoint complexes, each of them is isomorphic to the complex obtained from torus removing the hexagonal disc. In the second step, we attach the two disjoint unions of the hexagonal disc to the hexagonal boundary of each complex obtained in the previous step. Then we get the complex isomorphic to the disjoint union of two tori. Note that, if we collapse the attached hexagonal disc of to the point then again the resulting complex is isomorphic to the disjoint union of the torus which is exactly the complex $K_{\langle 125 \rangle}$ (see Figure 6.3).

At every step of the iterated cellular surgery on $CA_3$, we can take the quotients by antipodal action and get the cellular surgery on $\mathbb{P}CA_3$. In particular, at the last step, we get the complex isomorphic to $\tilde{K}_{\langle 125 \rangle}$, the torus.

The following arrows summarize the above process.

\[
\begin{align*}
CA_3 & \xrightarrow{234} \tilde{K}_{15} \xrightarrow{h.e.} K_{\langle 15 \rangle} \xrightarrow{134} \tilde{K}_{\langle 25 \rangle} \xrightarrow{h.e.} K_{\langle 25 \rangle} \xrightarrow{34} \tilde{K}_{\langle 125 \rangle} \xrightarrow{h.e.} K_{\langle 125 \rangle}.
\end{align*}
\]

\[
\begin{align*}
\mathbb{P}CA_3 & \xrightarrow{234} \tilde{K}_{15} \xrightarrow{h.e.} K_{\langle 15 \rangle} \xrightarrow{134} \tilde{K}_{\langle 25 \rangle} \xrightarrow{h.e.} K_{\langle 25 \rangle} \xrightarrow{34} \tilde{K}_{\langle 125 \rangle} \xrightarrow{h.e.} K_{\langle 125 \rangle}.
\end{align*}
\]

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Figure 6.3. Iterated cellular surgery on $CA_3$ along $G_{(125)}$
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**Indian Institute of Science Education and Research Pune, India.**

*Email address:* navnath.daundkar@acads.iiserpune.ac.in

**Chennai Mathematical Institute, India**

*Email address:* pdeshpande@cmi.ac.in