Every adult knows that the relation in question can and does exist between entire strangers,
different in language, color, tastes, class, civilization, morals, religion, character:
in everything, in short, except their bodily homology
and the reproductive appetite common to all living organisms.

— George Bernard Shaw, *Getting Married* (1908)

17 Homology

Homology is an equivalence relation between 'cycles' in topological spaces. Homology is related to homotopy-equivalence, but it is a much coarser relation: Two homotopic cycles are always homologous, but homologous cycles may not be homotopic. The homology relation also includes objects that are more general than cycles in the usual sense (images of circles), such as weighted sums of cycles, higher-dimensional manifolds, and even vector and tensor fields.

Homology classes of cycles of any particular dimension define a group, just as homotopy classes of loops define the fundamental group. Like the fundamental group, ***homology groups*** are topological invariants; if two spaces are homeomorphic, they have the same homology. However, two spaces with the same homology might not be homeomorphic, or even homotopy equivalent. Homology groups have much nicer algebraic structure than the fundamental group; they are (essentially) vector spaces. Consequently, homology is an ***effective*** topological invariant. Most basic algorithmic questions about homology can be answered efficiently, using variants of standard algorithms for effective linear algebra.

This presentation closely follows Zomorodian [34], who I'm sure does a better job.

17.1 Oriented Simplices, Chains, and Boundary Maps

Let X be a finite simplicial complex (that is, a proper Δ-complex). The restriction to simplicial complexes is purely to simplify notation. All of the definitions presented here can be generalized to cubical complexes, polytopal complexes, Δ-complexes, and CW-complexes with a little more effort.

For technical reasons, we need to assign an arbitrary ***orientation*** to each simplex in X. An orientation of a simplex is an equivalence class of permutations of its vertices, where two permutations are considered equivalent if they have the same parity. We specify any oriented simplex by a sequence of its vertices in brackets: $\sigma = [x_0, x_1, x_2, \ldots, x_k]$. For any oriented simplex σ, let $\boldsymbol{-\sigma}$ denote the same simplex in the opposite orientation. Thus, we can specify an oriented triangle with vertices x, y, and z in six different ways:

$$[x,y,z] = -[x,z,y] = [z,x,y] = -[z,y,x] = [y,z,x] = -[y,x,z].$$

Fix a non-negative integer k. Let $\boldsymbol{X_k}$ denote the set of oriented k-dimensional simplices in X, and let $\boldsymbol{n_k} := |X_k|$. A ***k-chain*** over X is a function $\alpha : X_k \to \mathbb{Z}$, such that $\alpha(-\sigma) = -\alpha(\sigma)$.[1] Equivalently, a k-chain is simply a vector of n_k integers, one for each k-simplex in X. For notational convenience, k-chains are usually represented by *formal sums* $\sum_i \alpha_i \Delta_{k,i}$, where each α_i is an integer and each $\Delta_{k,i}$ is the ith oriented k-simplex in X. The set of all k-chains form an abelian group under addition, isomorphic to $\mathbb{Z}^{n_k}$, called the ***kth chain group*** $\boldsymbol{C_k(X)}$.

In fact, chains can be generalized to use any coefficient ring R instead of the integers. For example, if we set $R = \mathbb{Z}_2$, then a k-chain is a 0-1 vector, or equivalently, a subset of the k-faces. If $R = \mathbb{Q}$, chains are *ration* vector; if $R = \mathbb{R}$, then chains are *real* vectors; if $R = \mathbb{C}$, then chains are *complex* vectors; and so on. In all of these cases, and in fact whenever the coefficient ring R is a field, the group $C_k(X)$ is actually a ***vector space***. In general, however, and in particular for integer coefficients, $C_k(X)$ is not a

[1] Alternately, we can define a k-chain to be an unrestricted function $\alpha : X_k \to \mathbb{Z}$ that assigns both an orientation $\operatorname{sgn}(\alpha(\sigma))$ and a non-negative value $|\alpha(\sigma)|$ to any unoriented k-simplex σ.

vector space but merely a ***R-module*** (no scalar division). It may be useful to think of the chain group as a vector space *most* of the time, even then R is not a field, although there are some subtleties that violate this intuition. I'll stick to integer coefficients for most of the lecture.

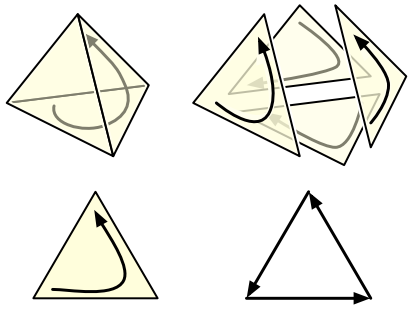
The ***boundary $\partial\sigma$*** of an oriented k-simplex σ is a $(k-1)$-chain, defined as the following weighted sum of the facets of σ:

$$\partial[x_0, x_1, \ldots, x_k] := \sum_{i=0}^{d} (-1)^i [x_0, x_1, \ldots, \widehat{x_i}, \ldots, x_k],$$

where $[x_0, x_1, \ldots, \widehat{x_i}, \ldots, x_d]$ indicates the facet opposite vertex x_i. For example, we have

$$\begin{aligned}
\partial[w,x,y,z] &:= [x,y,z] - [w,y,z] + [w,x,z] - [w,x,y] \\
\partial[x,y,z] &:= [y,z] - [x,z] + [x,y] \\
\partial[x,y] &:= [y] - [x] \\
\partial[x] &:= []
\end{aligned}$$

(The empty simplex has no boundary.) It is easy to check that this function is well-defined; equivalent vertex permutations yield equivalent boundary chains. Indeed, this is the reason for the alternating signs in the summation. Moreover, the boundary function is antisymmetric: we have $\partial(-\sigma) = -\partial\sigma$ for any oriented simplex σ. For any positive integer k, the boundary function extends linearly to k-chains, giving us the ***kth boundary homomorphism ∂_k***: $C_k(X) \to C_{k-1}(X)$. Because the map ∂_k is linear, it can be represented by a $n_{k-1} \times n_k$ integer matrix with all entries in the set $\{-1, 0, 1\}$.



Top: an oriented 3-simplex and its boundary chain. Bottom: An oriented 2-simplex and its boundary chain.

Lemma 17.1. *$\partial_{k-1} \circ \partial_k = 0$ for every integer $k \geq 2$.*

Proof: Because the boundary functions are linear, it suffices to prove that the boundary of the boundary of a k-simplex is the empty $(k-2)$-chain.

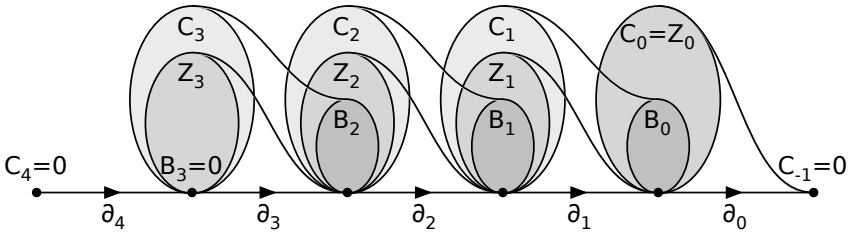
$$\begin{aligned}
&\partial_{k-1}(\partial_k[x_0, \ldots, x_d]) \\
&\quad = \sum_{i=0}^{d} (-1)^i \partial_{k-1}[x_0, \ldots, \widehat{x_i}, \ldots, x_d] \\
&\quad = \sum_{i=0}^{d} (-1)^i \left(\sum_{j=0}^{i-1} (-1)^j [x_0, \ldots, \widehat{x_j}, \ldots, \widehat{x_i}, \ldots, x_d] + \sum_{j=i+1}^{d} (-1)^{j-1} [x_0, \ldots, \widehat{x_i}, \ldots, \widehat{x_j}, \ldots, x_d] \right) \\
&\quad = \sum_{0 \leq j < i \leq d} (-1)^{i+j} [x_0, \ldots, \widehat{x_j}, \ldots, \widehat{x_i}, \ldots, x_d] - \sum_{0 \leq i < j \leq d} (-1)^{i+j} [x_0, \ldots, \widehat{x_i}, \ldots, \widehat{x_j}, \ldots, x_d] \\
&\quad = 0
\end{aligned}$$

□

Thus, for an n-dimensional simplicial complex X, we have a sequence of homomorphisms linking the chain groups

$$0 \longrightarrow C_n(X) \xrightarrow{\partial_n} C_{n-1}(X) \xrightarrow{\partial_{n-1}} \cdots \xrightarrow{\partial_2} C_1(X) \xrightarrow{\partial_1} C_0(X) \longrightarrow 0,$$

where $\partial_{k-1} \circ \partial_k = 0$ for all $k > 1$, and 0 denotes the trivial additive group $\{0\}$. Such a sequence of groups and homomorphisms is called an ***exact sequence*** or a ***chain complex***.



A chain complex for a three-dimensional complex; after Zomorodian [34].

17.2 Cycles, Boundaries, and Homology

We now describe two important subgroups of the chain groups $C_k(X)$. A ***k-cycle*** is a k-chain α such that $\partial_k \alpha = 0$. A ***k-boundary*** is a k-chain α such that $\alpha = \partial_{k+1}\beta$ for some $(k+1)$-chain β. Lemma 17.1 implies immediately that every k-boundary is a k-cycle, but in general, not every cycle is a boundary. We sometimes refer to k-boundaries as ***bounding cycles***.

The k-cycles and k-boundaries define subgroups of $C_k(X)$ called the ***kth cycle group $Z_k(X)$*** and the ***kth boundary group $B_k(X)$***. These subgroups can also be defined in terms of the boundary maps as follows:

$$Z_k(X) := \ker \partial_k \quad \text{and} \quad B_k(X) := \operatorname{im} \partial_{k+1}.$$

In linear-algebraic terms, $B_k(X)$ is the row space of the matrix ∂_{k+1}; and $Z_k(X)$ is the right null space (the orthogonal complement of the column space[2]) of ∂_k. All cycle and boundary groups are free abelian groups, meaning they have the form $\mathbb{Z}^c$ for some integer c. Lemma 17.1 implies that $B_k(X) \trianglelefteq Z_k(X) \trianglelefteq C_k(X)$, where $\trianglelefteq$ denotes 'normal subgroup'. (If we use real coefficients instead of integers to define chains, then $B_k(X)$ and $Z_k(X)$ are nested linear subspaces of the real vector space $C_k(X)$.)

∂_k	linear map $C_k \to C_{k-1}$	$n_{k-1} \times n_k$ integer matrix
$B_k(X)$	$\operatorname{im} \partial_{k+1}$	row space of ∂_{k+1}
$Z_k(X)$	$\ker \partial_k$	right null space of ∂_k

Equivalent definitions of the cycle and boundary groups.

We now define an equivalence relation over $Z_k(X)$. Two k-cycles α and β are ***homologous*** if the k-cycle $\alpha - \beta$ is a k-boundary. The equivalence class of a k-cycle α is the ***homology class $[\alpha]$***. Addition of homology classes is well-defined; for any k-cycles α and β, we have $[\alpha + \beta] = [\alpha] + [\beta]$. Thus, the set of homology classes of k-cycles forms a well-defined group under addition, called the ***kth homology group $H_k(X)$***. This group can also be defined as the quotient group of k-cycles mod k-boundaries:

$$H_k(X) := Z_k(X)/B_k(X).$$

[2]This really should be called the ***lumn space***, just to be nsistent.

Homology groups are abelian groups, but *not* free abelian groups in general. Like all finitely-generated abelian groups, each homology group is isomorphic to a product of cyclic groups

$$H_k(X) \cong \mathbb{Z}^{\beta_k(X)} \oplus \bigoplus_i (\mathbb{Z}/d_i\mathbb{Z})$$

for some integers β_k and $1 \le d_1 \le d_2 \le \cdots \le d_m$, where each integer d_i is a divisor of its successor d_{i+1}. The rank β_k of the free component of $H_k(X)$ is called the ***k*th Betti number** of X [2, 25, 24]. The components $(\mathbb{Z}, d_i\mathbb{Z})$ are called ***torsion subgroups***.

As mentioned before, we can define chains—and therefore cycles, boundaries, and homology groups—using any coefficient ring in place of the integers. Let $\boldsymbol{H_k(X;R)}$ denote the kth homology group of X with coefficients in ring R; different choices of R lead to different homology groups. However, integer homology is *universal* in a certain sense; the homology groups with respect to any ring R can be described in terms of the integer homology groups. In particular, if R is a field of characteristic zero (like $\mathbb{Q}$ or $\mathbb{R}$ or $\mathbb{C}$), we have $H_k(X;R) \cong R^{\beta_k}$; the structure for finite fields and other rings is more complex.

17.3 The Euler-Poincaré Formula

The Euler-l'Huilier formula for combinatorial 2-manifolds can be generalized to arbitrary simplicial complexes as follows:

Theorem 17.2 (The Euler-Poincaré Formula [20, 22]). $\sum_{k\ge0}(-1)^k n_k = \sum_{k\ge0}(-1)^k \beta_k$.

Proof: Every finitely-generated abelian group G can be written as $\mathbb{Z}^r \oplus \bigoplus_i (\mathbb{Z}/c_i\mathbb{Z})$ for some integers r and c_i. The integer r is called the *rank* of the group. For any subgroup H of any abelian group G, we have $\operatorname{rank}(G/H) = \operatorname{rank}(G) - \operatorname{rank}(H)$. In particular, $\beta_k(X) = \operatorname{rank}(H_k(X)) = \operatorname{rank}(Z_k(X)) - \operatorname{rank}(B_k(X))$. $B_k(X)$ is the column space of ∂_{k+1}, and therefore has rank equal to the (matrix) rank of ∂_{k+1}. $Z_k(X)$ is the orthogonal complement of the row space of ∂_k, and therefore has rank equal to $n_k - \operatorname{rank}(\partial_k)$. We conclude immediately that

$$\sum_k (-1)^k \beta_k = \sum_k (-1)^k \left(n_k - \operatorname{rank}(\partial_k) - \operatorname{rank}(\partial_{k+1})\right) = \sum_k (-1)^k n_k. \qquad \square$$

The quantity $\boldsymbol{\chi(X)} := \sum_k (-1)^k n_k = \sum_k (-1)^k \beta_k(X)$ is called the ***Euler characteristic*** or *Euler-Poincaré characteristic* of X. Poincaré's first publication of this formula [20] introduces it offhandedly, as though it were obvious, or at least well-known.[3]

[3] "On peut s'en rendre compute de diverses manières; par example si nous désignons par

$$P_1,\ P_2,\ \ldots,\ P_{n-1}$$

les ordres de connexion du polyèdre définis par Riemann et Betti, **on voit qu'on a**

$$\alpha_0 - \alpha_1 + \alpha_2 - \cdots + \alpha_n = 3 - P_1 + P_2 - \cdots - P_{n-1},$$

si n est pair et

$$\alpha_0 - \alpha_1 + \alpha_2 - \cdots - \alpha_n = -P_1 + P_2 - \cdots + P_{n-1},$$

si n est impair." Poincaré is using α_i for what we are calling n_i, and P_i for what we would call $\beta_i - 1$. The definition of the Betti numbers was reduced by 1 after homology became well-known.

17.4 Invariance

A simplicial complex X is a ***refinement*** of another simplicial complex Y if there is a homeomorphism from $|Y|$ to $|X|$ that maps any simplex of Y to (the underlying space of) a subcomplex of X. Standard topological arguments imply that if X is a refinement of Y, then $H_*(X) = H_*(Y)$. This is *almost* enough to prove the following theorem:

Theorem 17.3. *If X and Y are homeomorphic simplicial complexes, then $H_*(X) = H_*(Y)$.*

The missing ingredient is a proof of the following statement, dubbed ***die Hauptvermutung der kombinatorischen Topologie*** ("the main conjecture of combinatorial topology") by Kneser [13]:

Hauptvermutung. *Two triangulations of the same topological space have a common refinement.*

Poincaré [21] stated this conjecture as fact. It was first formulated as a conjecture by Steinitz [27] and Tietze [30]. Kneser [13], Alexandrov and Hopf [1]

The Hauptvermutung has been proved for 2-manifolds by Kerékjártó [11] and Radó [23], for arbitrary 2-dimensional complexes by Papakyriakopoulos [19], for 3-manifolds by Moise [16], and for arbitrary 3-dimensional complexes by Brown [3]. Unfortunately, the Hauptvermutung is *false*; the first counterexample was constructed by Milnor [15], and the first counterexample for manifolds was given by Kirby and Siebenmann [12].

Proving Theorem 17.3 required the development of a more general formulation of homology, called ***singular homology***, which gives identical results for simplicial complexes, but can also be applied to spaces that have no triangulations.

17.5 Examples: Polygonal Schemata

Recall that $\Sigma(g,0)$ denotes the orientable 2-manifold with genus g. Any system of loops defines a CW-complex with one vertex x, one face f, and $2g$ edges $\ell_1, \ldots, \ell_{2g}$, whose underlying space is Σ_g. We can compute the homology groups of Σ by examining the incidence relations between cells in this complex.

In fact, the homology computation is trivial, because *every* cell in this CW-complex has empty boundary! The boundary of any vertex is empty by definition. The boundary of any edge is the difference between its endpoints, but every edge ℓ_i is a loop. Finally, the boundary of the single face f is a sum of its sides, but every edge appears on the boundary of f once in each orientation. Thus the boundary groups B_0, B_1, and B_2 are all trivial, and the cycle groups Z_0, Z_1, and Z_2 are equal to their corresponding chain groups. We conclude:

Theorem 17.4. *$H_0(\Sigma(g,0)) \cong \mathbb{Z}$; $H_1(\Sigma(g,0)) \cong \mathbb{Z}^{2g}$; and $H_2(\Sigma(g,0)) \cong \mathbb{Z}$.*

Together with the Euler-Poincaré formula, this theorem implies that $\chi(\Sigma(g,0)) = 2 - 2g$, as we already know.

Now consider $\Sigma(0,g)$, the *non-orientable* surface of genus $g > 0$. Again, any system of loops defines a CW-complex structure for Σ_{-g} with one vertex, g edges $\ell_1, \ldots, \ell_g$, and one face f. The proof of the Surface Classification Theorem implies that we can assume without loss of generality that exactly one edge, say ℓ_1, appears twice on the boundary of f in the same orientation. Once again, the boundaries of the vertex and the edges are empty, but now we have $\partial f = 2\ell_1$. Thus, we have one nontrivial class of 1-boundaries, and *no* nontrivial 2-cycles.

Just as in the orientable case, we have $H_0 \cong \mathbb{Z}$, because the manifold is connected. The second homology group H_2 is empty, because there are no nontrivial 2-cycles. The first homology group is more interesting; we have $Z_1 = \langle \ell_1, \ldots, \ell_g \rangle$ and $B_1 = \langle 2\ell_1 \rangle$, and therefore

$$H_1 \;=\; \langle \ell_1, \ldots, \ell_g \rangle / \langle 2\ell_1 \rangle \;=\; \langle \ell_1, \ldots, \ell_g \mid 2\ell_1 = 0 \rangle \;\cong\; \mathbb{Z}^{g-1} \oplus (\mathbb{Z}/2\mathbb{Z})$$

(Here $\langle I \mid R \rangle$ denotes the *abelian* group generated by the elements of I, with relators R.) The 1-sided loop ℓ_1 has introduced ***torsion*** into the first homology group.

Theorem 17.5. *$H_0(\Sigma(0,g)) = \mathbb{Z}$, $H_1(\Sigma(0,g)) = \mathbb{Z}^{g-1} \oplus \mathbb{Z}/2\mathbb{Z}$, and $H_2(\Sigma(0,g)) = 0$.*

Together with the Euler-Poincaré formula, this theorem implies that $\chi(\Sigma(0,g)) = 2 - g$, as we already know.

17.6 The Smith-Poincaré Reduction Algorithm

Unlike fundamental groups, there is a well-defined algorithm to compute the homology groups of an arbitrary simplicial complex X, originally due to Poincaré [22], called the ***reduction algorithm***.[4] In addition to the groups themselves, the reduction algorithm computes ***basis*** for each homology group: a set of k-cycles whose homology classes generate $H_k(X)$. Poincaré's reduction algorithm is actually equivalent to an algorithm published four decades earlier by Smith [26] for computing a certain normal form of an integer matrix, although Poincaré was apparently unaware of this fact. Smith's algorithm is in turn a variant of the standard Gaussian elimination algorithm, which was actually discovered by Chinese mathematicians some time before 100AD.

Let $diag(d_1, d_2, \ldots, d_m)$ denote the $m \times m$ square matrix with the integers $d_1, d_2, \ldots, d_m$ along the diagonal, and zeros everywhere else. The ***Smith normal form*** of an $r \times c$ integer matrix M is a matrix product $S\tilde{M}T = M$, where S is an invertible $r \times r$ integer matrix, T is an invertible $c \times c$ integer matrix, and $\tilde{M}$ is an $r \times c$ integer matrix of the form

$$\tilde{M} = \left[\begin{array}{c|c} Diag(d_1, d_2, \ldots, d_m) & 0 \\ \hline 0 & 0 \end{array}\right]$$

where each integer d_i divides its successor d_{i+1}. In particular, the matrices M and $\tilde{M}$ both have rank m. The reduction algorithm for computing Smith normal form modifies the matrix using the following elementary row and column operations: (1) exchange two rows or columns; (2) multiply any row or column by -1; (3) add an integer multiple of one row or column to another. If we want to compute the matrices S and T, we start with S and T identity matrices, update S at each row operation, and update T at each column operation. However, for our application, we only need the matrix $\tilde{M}$.

Finally, Poincaré's algorithm computes the groups B_k, Z_k, and H_k by reducing each boundary matrix ∂_k to its Smith normal form $S_k \tilde{\partial}_k T_k$. Suppose each matrix $\tilde{\partial}_k$ has m_k nonzero diagonal entries $d_{k1} \mid d_{k2} \mid \cdots \mid d_{km_k}$. Then we can express the boundary, cycle, and homology groups as follows:

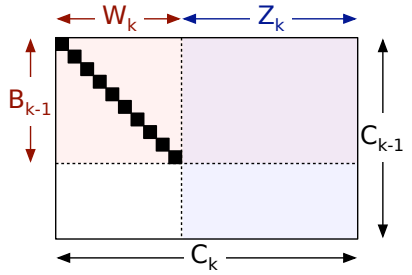
$$\begin{aligned} Z_k &\cong \mathbb{Z}^{n_k - m_k} \\ B_k &\cong \mathbb{Z}^{m_{k+1}} \\ H_k &\cong \mathbb{Z}^{n_k - m_k - m_{k+1}} \oplus \bigoplus_{i=1}^{m_{k+1}} (\mathbb{Z}/d_{ki}\mathbb{Z}) \end{aligned}$$

[4] Actually, Poincaré was only interested in computing Betti numbers the torsion coefficients. Poincaré described addition of (homology classes of) cycles, but at the time, only groups of transformations (such as Lie groups) were considered groups. The homology *groups*, as important objects of study in their own right, were introduced independently by Noether [18] and Vietoris [32], although some special cases appeared in earlier work [31, 33]; see McLarty [14].

If $d_{ki} = 1$, the corresponding group $\mathbb{Z}/d_{ki}\mathbb{Z}$ is trivial and can therefore be omitted from the direct sum decomposition of H_k.

The oriented k-simplices in X define a basis for the chain group $C_k(X)$, and the boundary matrix ∂_k expresses the linear boundary homomorphism with respect to the standard bases of C_{k-1} and C_k. Each elementary row and column operation corresponds to a change of basis in C_{k-1} and C_k, respectively. Exchanging two rows or columns exchanges the indices of two basis elements. Multiplying a row or column by -1 reverses the orientation of a boundary element. If e_i and e_j are the ith and jth basis elements of C_k, then adding column i to column j also replaces e_j with a new basis element $e_i + e_j$. Finally, if $\hat{e}_i$ and $\hat{e}_j$ are the ith and jth basis elements of C_{k-1}, then adding row i to row j also replaces $\hat{e}_i$ with a new basis element $\hat{e}_i - \hat{e}_j$. (The sign difference reflects the asymmetry of multiplying on the left by S and multiplying on the right by T.)

Let $\{e_1, e_2, \ldots, e_{n_k}\}$ be the basis of C_k, and let $\{\varepsilon_1, \ldots, \varepsilon_{n_{k-1}}\}$ be the basis for C_{k-1}, when the reduction algorithm terminates. Thus, $\{e_1, e_2, \ldots, e_{n_k}\}$ is a basis for the column space of $\tilde{\partial}_k$, and $\{\varepsilon_1, \ldots, \varepsilon_{n_{k-1}}\}$ is a basis for the row space of $\tilde{\partial}_k$. The column basis elements $e_{m_k+1}, \ldots, e_{n_k}$ comprise a basis for the cycle group Z_k, and the *scaled* row basis elements $d_1\varepsilon_1, \ldots, d_{m_k}\varepsilon_{m_k}$ comprise a basis for the boundary group B_{k-1}.



Structure of the Smith normal form matrix $\tilde{\partial}_k$

With some additional care, we can ensure that the basis for each boundary group B_k is a subset of the basis for the corresponding cycle group Z_k, except possibly for some nontrivial torsion coefficients $d_{m_k} > 1$. Thus, we can easily obtain a basis for each homology group H_k, where each k-cycle is a basis for one of the factors of its direct-sum decomposition.

The standard algorithm for computing Smith normal form requires $O(n^2)$ elementary row and column operations, each of which requires $O(n)$ exact integer arithmetic operations, where $n = r + c$. Thus, the the reduction algorithm is often incorrectly reported to run in $O(n^3)$ time. Unfortunately, the integers in the matrix can grow signficiantly as the algorithm proceeds; as a result, a straightforward implementation of Smith's algorithm has *doubly exponential* running time. The first polynomial-time algorithms for computing the Smith normal form of an integer matrix was described by Kannan and Bachem [10]; faster algorithms are described by Chou and Collins [4], Iliopoulos [8], and Storjohann [28, 29]; see also the survey by Dumas *et al.* [7].

The numerical difficulties can be avoided entirely by computing homology with $\mathbb{Z}_2$ coefficients; in this setting, the reduction algorithm is straightforward Gaussian elimination, all matrix coefficients are either 0 or 1, and the running time is $O(n^3)$. However, even computing with integer coefficients is often efficient in practice. Donald and Chang [5, 6] have shown that for random 'sparse' matrices, the standard algorithm to compute Smith normal form runs in $O(n^2)$ expected time. For sparse complexes, the running time can also be reduced by simplifying the complex before computing the Smith normal form; effective heuristics for reducing cell complexes without changing their homology type are described by Mrozek and his colleagues [9, 17].

17.7 Matrix Reduction Example

Let's actually use the reduction algorithm to compute the homology of a small simplicial complex. Consider the boundary of the standard 3-simplex Δ_3 as an oriented triangulation of the sphere S^2, with vertices w, x, y, z. We can arbitrarily orient the cells of this complex as follows:

$$\begin{aligned} \text{Vertices: } & w, x, y, z \\ \text{Edges: } & wx, wy, wz, xy, xz, yz \\ \text{Facets: } & wxy, wxz, wyz.xyz \end{aligned}$$

(To simplify notation, I am omitting the brackets and commas.) The boundary maps ∂_1 and ∂_2 are represented by the following matrices:

∂_1	w	x	y	z
wx	-1	1	0	0
wy	-1	0	1	0
wz	-1	0	0	1
xy	0	-1	1	0
xz	0	-1	0	1
yz	0	0	-1	1

∂_2	wx	wy	wz	xy	xz	yz
wxy	1	-1	0	1	0	0
wxz	1	0	-1	0	1	0
wyz	0	1	-1	0	0	1
xyz	0	0	0	1	-1	1

To reduce ∂_1, we first erase the first column by adding the second, third, and fourth columns, and then swap the empty column to the right. Then we clear the last three rows by adding and/or subtracting the first three rows.

$\partial_1 \longmapsto$

	$x-w$	$y-w$	$z-w$	w
wx	1	0	0	0
wy	0	1	0	0
wz	0	0	1	0
xy	-1	1	0	0
xz	-1	0	1	0
yz	0	-1	1	0

$\longmapsto$

$\tilde{\partial}_1$	$x-w$	$y-w$	$z-w$	w
wx	1	0	0	0
wy	0	1	0	0
wz	0	0	1	0
$xy+wx-wy$	0	0	0	0
$xz+wx-wz$	0	0	0	0
$yz+wy-wz$	0	0	0	0

We can now read off $m_1 = 3$ and $d_1 = d_2 = d_3 = 1$ from the reduced matrix $\tilde{\partial}_1$. Moreover, we have the following bases for Z_1 and B_0:

$$\begin{aligned} Z_1 &= \langle xy + wx - wy,\ xz + wx - wz,\ yz + wy - wz \rangle \cong \mathbb{Z}^3 \\ B_0 &= \langle x - w,\ y - w,\ z - w \rangle = \langle \partial wx,\ \partial yw,\ \partial wz \rangle \cong \mathbb{Z}^3. \end{aligned}$$

Similarly, to reduce ∂_2, we first apply column operations to reduce the matrix to lower-echelon form, and then apply row operations to obtain the Smith normal form. In this example, the column operations we apply are inverses of the row operations we used to reduce ∂_1, so that we end with the same basis for the chain group C_1 (except for reordering).

$\partial_2 \longmapsto$

	$xy+wx-wy$	$xz+wx-wz$	$yz+wy-wz$	wx	wy	wz
wxy	1	0	0	0	0	0
wxz	0	1	0	0	0	0
wyz	0	0	1	0	0	0
xyz	1	−1	1	0	0	0

$\longmapsto$

$\tilde{\partial}_2$	$xy+wx-wy$	$xz+wx-wz$	$yz+wy-wz$	wx	wy	wz
wxy	1	0	0	0	0	0
wxz	0	1	0	0	0	0
wyz	0	0	1	0	0	0
$xyz-wxy+wxz-wyz$	0	0	0	0	0	0

Once again, we can read off $m_2 = 3$ and $d_1 = d_2 = d_3 = 1$ from the reduced matrix $\tilde{\partial}_2$. Moreover, we have the following bases for Z_2 and B_1:

$$Z_2 = \langle xyz - wxy + wxz - wyz \rangle \cong \mathbb{Z}$$
$$B_1 = \langle wx - wy + xy,\ wx - wz + xz,\ wy - wz + yz \rangle = \langle \partial wxy,\ \partial wxz,\ \partial wyz \rangle \cong \mathbb{Z}^3.$$

Notice that B_1 and Z_1 are generated by the *same* set of 1-cycles, and thus are identical as groups.

We conclude that the sphere $\partial\Delta_3$ has exactly the homology we would expect from our earlier intuitive analysis.

$$H_0 = C_0/B_0 = \langle w,x,y,z \rangle / \langle x-w,\ y-w,\ z-w \rangle = \langle w \rangle \cong \mathbb{Z}$$
$$H_1 = Z_1/B_1 = Z_1/Z_1 = 0$$
$$H_2 = Z_2 = \langle xyz - wxy + wxz - wyz \rangle \cong \mathbb{Z}$$

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