FINAL
MATH 232A

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As its name may suggest, the fundamental group of a space is one of the most important ideas from algebraic topology. It's an algebraic invariant for topological spaces describing the (closed) loops up to homotopy in that space. Much can be learned about topological spaces through the fundamental group, as well as its generalizations - the higher homotopy groups. While homotopy groups tell us quite a lot about a space, they're limited in accessibility, as computing them have been a challenge. This motivates the construction of another algebraic invariant for topological spaces - homology groups.

Unlike, homotopy groups, homology groups are much more accessible, as they are easier to compute. The drawback in this is that they are less intuitive and more of a challenge to define. However, despite this, we will show the power that homology theory possesses in extracting information about topological spaces.

We begin by discussing simplicial homology, which is much nicer and more intuitive than its more advanced counterpart, singular homology. To do this, we first introduce the structure on which simplicial homology is built upon - Δ-complex structures.

The construction for Δ-complex structures, in a more or less way, is representing a topological space with (generalized) triangles. We define an n-simplex as the convex hull of $n+1$ points, $\{v_0, \cdots, v_n\}$, that sit in $\mathbb{R}^m$, where $\{v_0, \cdots, v_n\}$ do not lie in a hyperplane of dimension less than n (note that this requires $m \geq n$). A simple example is taking the convex hull of the standard (orthonormal) basis elements on $\mathbb{R}^{n+1}$. We denote the n-simplex $[v_0, \cdots, v_n]$, where v_i are the points selected for the construction of the n-simplex. Moreover, we give an orientation on the edges of our n-simplex by the ordering of the vertices, namely that the direction goes from the vertex with the lower subscript to the vertex with the higher one. We refer to a n-simplex as Δ^n. Given an n-simplex $[v_0, \cdots, v_n]$, we give the coordinates of $\sum_{i=0}^{n} t_n v_n$ as $(t_0, \cdots, t_n)$. We call the set of points with none of the coordinates being 0 the interior (denoted as $\mathring{\Delta}^n$), and the set of points whose coodinates have 0 the boundary (denoted as $\partial\Delta^n$). We notice that the coordinates of $[v_0, \cdots, v_n]$ are in one to one correspondence with the coordinates (in under the standard basis) of the n-simplex formed by the standard basis on $\mathbb{R}^{n+1}$ (ie. taking its convex hull).

With all this in place, we can now define a Δ-complex. A Δ-complex on a space X is a collection of maps $\sigma_\alpha : \Delta^n \to X$, where n is indexed by α, such that:

1. $\sigma_\alpha|_{\mathring{\Delta}^n}$ is injective and each point of X is contained in exactly one image of the $\sigma_\alpha|_{\mathring{\Delta}^n}$.
2. Restricting any of the $\sigma_\alpha : \Delta^n \to X$ to a face (ie. an $n-1$-simplex generated by all but one of the vertices that generated Δ^n) gives another map $\sigma_\beta : \Delta^{n-1} \to X$ in our collection. Moreover, the ordering on the vertices is preserved
3. $A \subset X$ is open if and only if for each map σ_α, $\sigma_\alpha^{-1}(A)$ is open in Δ^n.

Despite the technicality of the details, it's important to remind ourselves that the Δ complex on a space X is, in essence, just covering X up in (generalized) triangles. More specifically, what we are doing is that we are mapping n-simplices into our space X in such a way where our n-simplices cover X, but in a 'non-overlapping' way (ie. the interiors of the triangles do not overlap). Moreover, while we can prescribe Δ-complexes to topological spaces, we can also build topological spaces from disjoint simplices by way of identifying faces and taking quotients.

Our next step towards simplicial homology is to define the chain complex of X. We denote $\Delta_n(X)$ as the free abelian group generated by the n-simplices of X. These can be written of the form $\sum_\alpha n_\alpha \sigma_\alpha$, for $n_\alpha \in \mathbb{Z}$. We refer to the elements of $\Delta_n(X)$ as n-chains. We recall from earlier that the faces of an n-simplex, form the boundary. We use this definition to motivate a homomorphism $\partial_n : \Delta_n(X) \to \Delta_{n-1}(X)$, defined by $\partial_n(\sigma_\alpha) = \sum\limits_{i=0}^{n} (-1)^n \sigma_\alpha|_{[v_0,\cdots,\hat{v_i},\cdots,v_n]}$, where $[v_0,\cdots,\hat{v_i},\cdots,v_n]$ is the $n-1$ simplex $[v_0,\cdots,v_{i-1},v_{i+1},\cdots,v_n]$ (that is, we remove the ith vertex). Since the restriction of σ_a to a face is indeed another member of the Δ-complex, we see that ∂_n does indeed map into $\Delta_{n-1}(X)$. We call this map the boundary map, and rightfully so, as it does map n-simplices to their boundaries. Indeed, as we iterate through i, we run through all the $n-1$-simplices that are faces of a given n-simplex. Moreover, the alternating sign takes care of the orientation of our simplicies, so that heuristically, what's happening is that we are 'running around the boundary'. This is best seen in a 2-simplex, where given $[v_0, v_1, v_2]$, we see that $\partial_2([v_0, v_1, v_2])$ gives $[v_1, v_2] - [v_0, v_2] + [v_0, v_1]$, which *literally* runs around the 2-simplex (this is technically an abuse of notation, as ∂_2 is defined on $\Delta_2(X)$, which consists of *maps* from of the 2-simplices to X, and not the simplices themselves; however, seeing the n-chains as simplicies is helpful in this context as to why the map is defined the way it is). This helps motivate two definitions - we call elements of $\ker(\partial_n)$ cycles, while the elements of $Im(\partial_{n+1})$ boundaries. We also observe that $\partial_n \circ \partial_{n+1}$ is the 0 map. Since the context of the boundary maps on chain complexes are quite clear, we will abbreviate them as ∂ when it is convenient to do so. To put things together, we have the groups $\Delta_n(X)$ and the boundary map (technically plural, but they all do the same thing anyways) behaving in the following way

$$\cdots \xrightarrow{\partial} \Delta_{n+1}(X) \xrightarrow{\partial} \Delta_n(X) \xrightarrow{\partial} \Delta_{n-1}(X) \xrightarrow{\partial} \cdots \xrightarrow{\partial} \Delta_1(X) \xrightarrow{\partial} \Delta_0(X) \to 0.$$

Now, we finally have all the tools we need in order to define the simplicial homology groups. Since we have that $\partial_{n+1} \circ \partial_n \equiv 0$, we see that $Im(\partial_{n+1}) \subset \ker(\partial_n)$. We define the nth homology group of X, as $H_n^\Delta(X) = \ker(\partial_n)/Im(\partial_{n+1})$.

Let us now take a moment to appreciate the complexity that is simplicial homology. This gives us a brief taste of what topologists mean when they say 'homology is hard to define.' Here already, we see the difficulty of its construction, and how it's not completely clear (at least not at first glance) what the elements of H_n^Δ represent geometrically. Moreover, the construction of the simplicial homology groups give rise a few questions. Do homotopy equivalent spaces have isomorphic homology groups? More specifically, do homeomorphic spaces have isomorphic homology groups? Better yet, does the homology group of a space depend on the choice of Δ-complex structure? Unfortunately, the answers to these questions are not clear in the context of simplicial homology. So, we shift our gaze to singular homology.

The setting for singular homology is similar to that of simplicial homology. Only now, our class of maps is greatly expanded. Singular homology relies not on a Δ-complex structures to 'restrict' what maps we have, but rather, our maps, which we refer to as singular n-simplicies $\sigma : \Delta^n \to X$, can now be *any* (continuous) map. The analog of $\Delta_n(X)$ is the nth chain group, $C_n(X)$, which is defined as the free abelian group generated by *all* singular n-simplices. We similarly have the boundary map $\partial_n : C_n(X) \to C_{n-1}(X)$, which is defined exactly the same way as it was in the context of simplicial homology. As before, we since we have $\partial_n \circ \partial_{n+1} \equiv 0$, we can define the nth homology group in the same way as before, $H_n(X) = \ker(\partial_n)/Im(\partial_{n+1})$. A remark we can make from here is that if we split up $C_n(X) = \bigoplus_\alpha C_n(X_\alpha)$, where X_α are the path components of X, we note that ∂_n is a restricted to $C_n(X_\alpha)$ maps into $C_{n-1}(X_\alpha)$. From this, we can actually get that $H_n(X) \cong \bigoplus_\alpha H_n(X_\alpha)$. The construction of the singular homology groups are much more complicated than that of the simplicial homology groups, and as such, they are much harder to think about. For example, the groups that make up the chain complex of a space can potentially be massive (as it's generated by *all* continuous mappings from a n-simplex into X).

Let us begin by computing singular homology for the simplest space we can think of - that of a point (we will refer to this space as X). Since there is only one map from any space to a point, we see that each of the $C_n(X) \cong \mathbb{Z}$. We refer to the generator of $C_n(X)$ as σ_n (which is the unique map $\sigma_n : \Delta^n \to X$). Let us now compute the boundary maps. We note that since $\partial_n(\sigma_n) = \sum_{i=0}^{n} (-1)^n \sigma_{n-1}$, the boundary map ∂_n is an isomorphism if n is even and the zero map when n is odd. From this, we calculate that $H_n(X) = 0$ when $n > 0$ and $H_0(X) \cong \mathbb{Z}$. The homology of X is a bit awkward since we have that the homology is trivial *except* for the 0th spot, which is isomorphic to $\mathbb{Z}$. In fact, this is true for every space that's retractable to a point, so for convenience, we introduce reduced homology groups.

The construction for reduced homology groups is similar to that of singular homology groups, except for one of the boundary maps being replaced with a different map. For a space X, instead of having $\partial_0 : C_0(X) \to 0$, we replace it with $\epsilon : C_0(X) \to \mathbb{Z}$, where we have $\epsilon\left(\sum_\alpha n_\alpha \sigma_\alpha\right) = \sum_\alpha n_\alpha$. That is, we have the following sequence:

$$\cdots \xrightarrow{\partial} C_2(X) \xrightarrow{\partial} C_1(X) \xrightarrow{\partial} C_0(X) \xrightarrow{\epsilon} \mathbb{Z} \to 0.$$

As before, we have $\tilde{H}_n(X) = \ker(\partial_n)/Im(\partial_{n+1})$ for $n > 0$, and $\tilde{H}_0(X) = \ker(\epsilon)/Im(\partial_1)$. By this construction, we note that $H_n(X) = \tilde{H}_n(X)$ for $n > 0$, and $H_0(X) \cong \tilde{H}_0(X) \oplus \mathbb{Z}$. Moreover, if X was a singleton set, or any contractible space, we have that $\tilde{H}_n(X) = 0$ for every n. What's more is that we can use the map ϵ to show that given a path connected space, $H_0(X) \cong \mathbb{Z}$, and by extension, if X has k path components, we would have that $H_0(X) \cong \mathbb{Z}^k$.

Now, suppose $f : X \to Y$ is a continuous map. We notice that f induces a map on the chain groups, $f_\sharp : C_n(X) \to C_n(Y)$ where $f_\sharp(\sigma) = f\sigma$ (we can linearly extend $f_\sharp$, and see that it forms a group homomorphism). A simple observation tells us that $f_\sharp \partial = \partial f_\sharp$, and so, we have the following commutative diagram:

$$\begin{tikzcd}
\cdots \arrow[r, "\partial"] & C_{n+1}(X) \arrow[r, "\partial"] \arrow[d, "f_\sharp"] & C_n(X) \arrow[r, "\partial"] \arrow[d, "f_\sharp"] & C_{n-1}(X) \arrow[r, "\partial"] \arrow[d, "f_\sharp"] & \cdots \\
\cdots \arrow[r, "\partial"] & C_{n+1}(Y) \arrow[r, "\partial"] & C_n(Y) \arrow[r, "\partial"] & C_{n-1}(Y) \arrow[r, "\partial"] & \cdots
\end{tikzcd}$$

In general, if $f_\sharp \partial = \partial f_\sharp$, we say that $f_\sharp$ is a chain map. From this, we see that $f_\sharp$ takes cycles to cycles and boundaries to boundaries, and so, $f_\sharp$ induces a homomorphism $f_* : H_n(X) \to H_n(Y)$. Much like the induced map for the fundamental group, the induced map on homology groups behaves nicely in many of the same ways. For example, given $f : X \to Y$ and $g : Y \to Z$, we have that $(gf)_* = g_* f_*$. Moreover, we have that $\mathbb{1}_* = \mathbb{1}$. One of the more nontrivial facts that we also discover is that if $f : X \to Y$ and $g : X \to Y$ are homotopic, then $f_* = g_*$ on the level of homology groups. A direct consequence of this is that if $f : X \to Y$ is a homotopy equivalence, then $f_* : H_n(X) \to H_n(Y)$ is an isomorphism. From this, we see that homotopic equivalent spaces have isomorphic singular homology groups, something that wasn't so obvious under the setting of simplicial homology groups.

Now that we have seen some very nice properties of singular homology, a natural question to ask is exactly how far we can go. In particular, does taking the quotient of a space X by a subspace A play nicely on the level of homology groups? Or better yet, do we have $H_n(X/A) \cong H_n(X)/H_n(A)$? A quick reality check tells us that while this would be nice, it's actually not true. For example, if we take any topological space X and embed it into its cone CX, we have that CX is contractible, which means $H_n(CX) = 0$ for all $n > 0$. Fortunately, hope is not lost, as there is a way we can relate X, A, and X/A in terms of long exact sequences of reduced homology groups, if A is "good". To define what "good" means, we say that for a nonempty closed $A \subset X$, (X, A) is a good pair if A is a deformation retract of some neighborhood of X. In particular, if (X, A) is a good pair, we have the long exact sequence

$$\cdots \to \tilde{H}_n(A) \xrightarrow{i_*} \tilde{H}_n(X) \xrightarrow{j_*} \tilde{H}_n(X/A) \xrightarrow{\partial} \tilde{H}_{n-1}(A) \xrightarrow{i_*} \tilde{H}_{n-1}(X) \to \cdots \to \tilde{H}_n(X/A) \to 0$$

where $i : A \hookrightarrow X$ is the inclusion map and $j : X \to X/A$ is the quotient map. The map ∂ takes inspiration from the boundary map on the level of chain complexes that we know and love, and will be constructed as we go. Some of the consequences of this are that by leveraging the fact that this sequence is exact, we can come up with some nice results as well as easy ways to compute homologies, without even thinking much about what i_*, j_*, or ∂ are doing on the level of homology groups. For example, we can relatively easily compute the homology of the k-sphere, which are $\tilde{H}_k(S^k) = \mathbb{Z}$ and $\tilde{H}_n(S^k) = 0$ for all $n \neq k$ (we note that the homology group and reduced homology groups coincide for $n > 0$, and we can separately compute $H_0(S^k) = \mathbb{Z}$, as it is connected).

In order to show the exactness of the sequence we have above, we first introduce relative homology groups. Relative homology groups, in a sense, measure how different $H_n(X)$ is with $H_n(A)$. Given $A \subset X$, we say that $C_n(X, A) = C_n(X)/C_n(A)$. Since the boundary map takes elements from $C_n(A)$ to $C_{n-1}(A)$, it induces the map $\partial_n : C_n(X, A) \to C_{n-1}(X, A)$, with $\partial^2 = 0$ still holding. We call the elements of $\ker \partial$ the relative cycles, and the elements of $Im\partial$ the relative boundaries. Similar to how the other homology groups were defined, we define $H_n(X, A) = \ker \partial_n / Im(\partial_{n+1})$. One quick remark we make is that for $A \neq \emptyset$, we have that $H_n(X, A) = \tilde{H}_n(X, A)$. Although it may not be expected at first, we also have induced maps for relative homology. If $f : (X, A) \to (Y, B)$ is a map of pairs (that is, $f(A) \subset B$), we can make the construction as we did before and induce a map $f_\sharp$ from the relative chain complex $C_n(X, A)$ to $C_n(Y, B)$, which now induces a map $f_* : H_n(X, A) \to H_n(Y, B)$. Indeed, the fact that map of pairs is needed is makes quite a bit of sense, because if $f(A)$ mapped outside of B, none of the induced maps would make any sense. Moreover, if $f : (X, A) \to (Y, B)$

and $g : (X, A) \to (Y, B)$ are homotopic as maps of pairs (that is, their restriction on A are homotopic too), we have that $f_* = g_*$. So, we see many of the results from absolute homology carrying over to relative homology, under "obvious" conditions, which is pretty nice.

We note that since

$$0 \to C_n(A) \xrightarrow{i} C_n(X) \xrightarrow{j} C_n(X, A) \to 0$$

is exact, we also have the following short exact sequence of chain complexes:

$$\begin{tikzcd}
 & \vdots \arrow[d, "\partial"] & \vdots \arrow[d, "\partial"] & \vdots \arrow[d, "\partial"] & \\
0 \arrow[r] & C_{n+1}(A) \arrow[r, "i"] \arrow[d, "\partial"] & C_{n+1}(X) \arrow[r, "j"] \arrow[d, "\partial"] & C_{n+1}(X, A) \arrow[r] \arrow[d, "\partial"] & 0 \\
0 \arrow[r] & C_n(A) \arrow[r, "i"] \arrow[d, "\partial"] & C_n(X) \arrow[r, "j"] \arrow[d, "\partial"] & C_n(X, A) \arrow[r] \arrow[d, "\partial"] & 0 \\
0 \arrow[r] & C_{n-1}(A) \arrow[r, "i"] \arrow[d, "\partial"] & C_{n-1}(X) \arrow[r, "j"] \arrow[d, "\partial"] & C_{n-1}(X, A) \arrow[r] \arrow[d, "\partial"] & 0 \\
 & \vdots & \vdots & \vdots &
\end{tikzcd}$$

By using the exactness of the rows, the fact that the diagram commutes, and that $\partial^2 = 0$, we are able to construct, after some diagram chasing, a well defined map $\partial : H_n(X, A) \to H_{n-1}(A)$. As we can see, $\partial : H_n(X, A) \to H_{n-1}(A)$ is constructed with boundary map in mind, and furthermore, can be thought of as the boundary map on relative cycles represented in $H_n(X, A)$. Moreover, with a big of diagram chasing, we have the following exact sequence which looks quite similar to the long exact sequence we originally wanted[1]:

$$H_n(A) \xrightarrow{i_*} H_n(X) \xrightarrow{j_*} H_n(X, A) \xrightarrow{\partial} H_{n-1}(A) \to \cdots \to H_0(X, A) \to 0.$$

We remark that by following the same process, we can get the same exact sequence for reduced homology. In fact, we can do something similar with a triple (X, A, B) (with $X \supset A \supset B$).

Now, *if only* we can replace $H_n(X, A)$ with $\tilde{H}_n(X/A)$... Turns out, we can! But with a slight caveat: (X, A) must be a good pair. In order to get there, we need the excision theorem, which tells us that given $Z \subset A \subset X$ where $cl(Z) \subset \mathring{A}$, we have that the inclusion $(X - Z, A - Z) \hookrightarrow (X, A)$ induces an isomorphism $H_n(X - Z, A - Z) \to H_n(X, A)$ for all n. Another way we can say this is that if $A, B \subset X$ such that $\mathring{A} \cup \mathring{B} = X$, then the inclusion $(B, A \cap B) \hookrightarrow (X, A)$ induces an isomorphism $H_n(B, A \cap B) \to H_n(X, A)$ for all n. The proof of the excision theorem is rather long and involved, but the result gets us what we want. Namely if we have

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[1] We note that this construction is purely algebraic. In fact, given a short exact sequence of chain complexes (not necessarily derived from a topological space!), we can construct a long exact sequence of homology groups. This result is known as the Snake Lemma.

a good pair (X, A), then the quotient map $q : (X, A) \to (X/A, A/A)$ induces an isomorphism $q_* : H_n(X, A) \to H_n(X/A, A/A)$ for all n. The way the excision theorem is used is that to prove this, we find a neighborhood of A, which we call V, that deformation retracts back onto A, and we excise A out. We then use a series of isomorphisms to give us that $H_n(X, A)$ and $H_n(X/A, A/A)$ are indeed isomorphic. We note that $H_n(X/A, A/A) \cong \tilde{H}_n(X/A)$, and so, this proposition gives us the final piece required to show $H_n(X, A) \cong \tilde{H}_n(X/A)$, which finally gives us

$$\cdots \to \tilde{H}_n(A) \xrightarrow{i_*} \tilde{H}_n(X) \xrightarrow{j_*} \tilde{H}_n(X/A) \xrightarrow{\partial} \tilde{H}_{n-1}(A) \xrightarrow{i_*} \tilde{H}_{n-1}(X) \to \cdots \to \tilde{H}_n(X/A) \to 0.$$

Let us now take a moment to appreciate this piece of machinery that was just discussed. The long exact sequence actually gives us quite a few results. From the last proposition, we're able to deduce that the identity map $id : \Delta^n \to \Delta^n$ (viewed as a singular n-simplex) generates $H_n(\Delta^n, \partial\Delta^n)$, which will become useful later. Another result we obtain from our proposition is that if $X = \bigvee_\alpha X_\alpha$ where the wedge sum is formed at points $x_\alpha \in X_\alpha$ such that $(X_\alpha, \{x_\alpha\})$ is good, then the inclusion map $i : X_\alpha \to X$ induces an isomorphism $\bigoplus_\alpha : \bigoplus_\alpha \tilde{H}_n(X_\alpha) \to \tilde{H}_n(X)$. That is, the homology group of wedge sums break up into the homology groups of their individual components provided that the point the chosen basepoint is good. Another nice application that uses the excision theorem, as well as our long exact sequence, is that we can use them to show if nonempty open sets $U \subset \mathbb{R}^n$ and $V \subset \mathbb{R}^m$ are homeomorphic, then $m = n$. We notice that in many of these examples, a good pair was required in order to make our machinery run. But what if we didn't have a good pair? It turns out that in general, we have the following isomorphism: $\tilde{H}_n(X \cup CA) \cong H_n(X, A)$.

Now that we've discussed simplicial and singular homology in quite a bit of detail, the natural question is if they agree. That is, given a Δ-complex structure (indeed, the way we defined simplicial homology was based on such construction), are simplicial homology groups and singular homology isomorphic? We'd better hope so, because otherwise, we would be in some trouble. Fortunately, they are. In fact, we can show this in greater generality, that relative simplicial homology groups (which are defined the same way as relative singular homology groups) are isomorphic to relative singular homology groups. Since we have the embedding of $\Delta_n(X) \hookrightarrow C_n(X)$ and $\Delta_n(A) \hookrightarrow C_n(A)$, we have a chain map $\Delta_n(X, A) \to C_n(X, A)$. This induces a homomorphism $H_n^\Delta(X, A) \to H_n(X, A)$, which we can show is actually an isomorphism by considering the k-skeleton of X, recalling that the identity map on Δ^k generates $H_k(\Delta^k, \partial\Delta^k)$, using the long exact sequence we obtained from earlier, and applying the five lemma - a key tool from homological algebra. We note that the case where $A = \emptyset$ reduces down to an isomorphism of absolute homology. To wrap things up, we note that since we have the equivalence between simplicial and singular homology, results from one carries into the other. For example, by the way simplicial homology was constructed, the number of generators for $H_n^\Delta(X)$ is at most the number of n-cells in the Δ-complex. As such, this puts a bound on the number of generators of $H_n(X)$ as well. On the other hand, singular homology tells us that homotopy equivalent spaces have the same homology group. This means that this holds in the context of simplicial homology too, which wasn't very clear at all when we were just considering simplicial homology. Indeed, it's nice to see that this equivalence doesn't just give us closure, but also results that would otherwise be difficult to verify.

Having discussed the two ways to compute homology, we still have a gaping issue that still needs to be further resolved: computation. While computation using simplicial homology is pretty straight forward and doable, it's rather limited in application, as we require a Δ-complex structure to be imposed onto our space. On the other hand, while singular homology is (in theory) able to determine a lot about a much wider class of spaces, it can be an utter pain to make direct computations with (which is why we so frequently had to use roundabout ways to compute, such as using exact sequences). Now *if only* we had a homology theory somewhere in the middle, that can both compute efficiently and across a wide variety of spaces... Fortunately, we do - cellular homology! Cellular homology is, in a sense, a cross between simplicial homology and singular homology, in that it has the computational flavor of simplicial homology, but over a much wider scope of spaces (ie. cell complexes) using facts we know from singular homology. But before we can talk further about cell complexes, we need to take a slight detour into computation on the homology of spheres (ie. S^n).

One of the main ingredients to build up cellular homology is the notion of degree for a map on a sphere. Consider $f : S^n \to S^n$, where n is nonzero. We recall that when $n > 0$, we have $H_n(S^k) = \begin{cases} \mathbb{Z} & n = k \\ 0 & n \neq k \end{cases}$. From this, we see that $f_* : H_n(S^n) \to H_n(S^n)$ must be multiplication by some integer (ie. $f_*(\alpha) = d\alpha$ for some $d \in \mathbb{Z}$). We define the degree of f, $\deg(f)$, to be this integer obtained from the induced map on the nth homology[2]. In a way, the degree measures how f "wraps around" S^n. The degree of f acts as an invariant on spheres to itself, in that it has many nice properties, which include the following (among others, which can be referenced in the very beginning of Section 2.2 of Hatcher)[3]:

1. If f and g are homotopic, then $\deg(f) = \deg(g)$ as $f_* = g_*$.
2. The degree is multiplicative. That is, $\deg(fg) = \deg(f)\deg(g)$, which can be easily seen in that $(fg)_* = f_* g_*$.
3. If f is a reflection, then $\deg(f) = -1$, which also means that the antipodal map has $\deg(-\mathbb{1}) = (-1)^{n+1}$ (as it is a composition of $n+1$ reflections).

Our next order of business to develop is a rather handy lemma about CW complexes, which will be the domain on which we build cellular homology. Let X be a CW complex. Then we have the following:

1. $H_k(X^n, X^{n-1}) = 0$ when $k \neq n$ and is free abelian for $k = n$. Moreover, there is a one to one correspondence between the n-cells and generators for $H_n(X^n, X^{n-1})$.
2. $H_k(X^n) = 0$ when $k > n$.
3. The inclusion map induces an isomorphism $i_* : H_k(X^n) \to H_k(X)$ when $k < n$. If $k = n$, then the induced map is surjective.

Here, (a) can be realized by observing (X^n, X^{n-1}) is a good pair, and X^n/X^{n-1} is a wedge sum of n-spheres, with each n-sphere corresponding to an n-cell of X. (b) and (c) can be

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[2] In particular, we want to make the distinction that we are mapping from our sphere to itself, rather than another sphere. Thus, the integer for the degree is well defined (as otherwise, there would be confusion in regards to whether the degree is the positive or negative integer of a certain magnitude).

[3] Although there is a lot more that we can say about the degree of a map on a sphere, we will omit most of the details that are less relevant for the purposes of cellular homology.

realized by considering the long exact sequence for the pair (X^n, X^{n-1}), although the case where $\dim(X) = \infty$ for (c) requires a bit more work. One observation we can make is that $H_k(X) = 0$ when $k > \dim(X)$.

We now have the tools that we need in order to define cellular homology. For our chain complex, we let our nth chain group be $H_n(X^n, X^{n-1})$. Although this construction of our chain complex is rather strange, there's actually a rather "natural" construction our boundary map. By considering the long exact sequence for (X^n, X^{n-1}) (for each n), and using the lemma that we mentioned above, in the following way: we can construct boundary maps (which we also refer to as degree maps) in the following way:

$$\begin{tikzcd}
 & & & & 0 & & \\
 & 0 \arrow[dr] & & H_n(X^{n+1}) \approx H_n(X) \arrow[ur] & & & \\
 & & H_n(X^n) \arrow[ur] \arrow[dr, "j_n"] & & & & \\
\cdots \arrow[r] & H_{n+1}(X^{n+1}, X^n) \arrow[ur, "\partial_{n+1}"] \arrow[rr, "d_{n+1}"] & & H_n(X^n, X^{n-1}) \arrow[rr, "d_n"] \arrow[dr, "\partial_n"'] & & H_{n-1}(X^{n-1}, X^{n-2}) \arrow[r] & \cdots \\
 & & & & H_{n-1}(X^{n-1}) \arrow[ur, "j_{n-1}"'] & & \\
 & & & 0 \arrow[ur] & & &
\end{tikzcd}$$

Here, we notice that we can construct d_n by composing $j_{n-1}\partial_n$ from their respective long exact sequences. Moreover, our chain groups alongside the maps d_n do indeed form a chain complex, as we notice that $d_n d_{n+1} = 0$, since inside the composition contains $\partial_n j_n$, which is a part of the long exact sequence for $H_n(X^n, X^{n-1})$ (by exactness, this composition must be the zero map). As we've done so for simplicial and singular homology, the nth cellular homology group is defined to be $H_n^{CW}(X) = \ker(d_n)/Im(d_{n+1})$. Moreover, by observing the properties of the maps involved in the construction of H_n^{CW} (ie. $\partial_{n+1}, j_n, \partial_n, j_{n-1}$), we can show that (surprise surprise) $H_n^{CW}(X) \cong H_n(X)$.

Let us now take a moment to understand the construction that we just concocted. Since for each $H_n(X^n, X^{n-1})$, the generators are in one to one correspondence with the n-cells of X, we see that the generators of $H_n(X)$ is bounded above by the n-cells of X. In particular, it is quite evident that if X has no n-cells, then $H_n(X) \cong 0$. Moreover, if there are no $n \pm 1$ cells, then it's easy to see that $H_n(X)$ is a free abelian group with generators in one to one correspondence to the n-cells of X. This is quite similar to some of the properties we previously noted about simplicial homology, except now, it's applied to a much bigger class of spaces (ie. CW complexes).

In fact, it's useful to think of our nth chain group as being free abelian groups generated by the n-cells of X themselves. As we mentioned before, we sometimes call the cellular boundary map d_n the degree map. The reasons for this is that there is a "natural" way to relate the cellular boundary map with the notion of degree. Let $\{e_\alpha^n\}$ be the set of n-cells of X, and $\{e_\beta^{n-1}\}$ be the set of $n-1$-cells of X. For an n-cell e_α^n and an $n-1$-cell e_β^{n-1}, consider the attaching map $a_\alpha : \partial e_\alpha^n \to X^{n-1}$ and the quotient map $\pi_\beta : X^{n-1} \to X^{n-1}/(X^{n-1} \setminus e_\beta^{n-1})$. We notice that ∂e_α^n is homeomorphic to S^{n-1}, as is $X^{n-1}/(X^{n-1} \setminus e_\beta^{n-1})$ (since we are taking our $n-1$ cell and collapsing everything outside of it). So, $\pi_\beta \circ a_\alpha$ can be thought of as a map from S^{n-1} to itself, and so, we can take the degree. We then have the formula $d_n(e_\alpha^n) = \sum\limits_\beta d_{\alpha\beta} e_\beta^{n-1}$, where $d_{\alpha\beta} = \deg(\pi_\beta \circ a_\alpha)$. That is, the coefficient on e_β^{n-1} for the image of e_α^n is, roughly speaking, the number of times the attaching map "wraps around" e_β^{n-1}.

To fully appreciate the work of wonder that is cellular homology, let's see it in action. One of the wonderful thing about cellular homology is that it computes the nth homology directly from the n-cells. What's more is that we can also use it to work backwards and build spaces to fit certain conditions homological descriptions. Given an abelian group G and integer $n \geq 1$, we say that if there's a CW complex X such that $H_n(X) \cong G$ and $\tilde{H}_i(X) \cong 0$ for $i \neq n$, then we say that X is a Moore space, or more specifically, X is a $M(G, n)$. We can use cellular homology to construct Moore spaces in the following manner. First, we know that S^n is a $M(\mathbb{Z}, n)$. Now, we take S^n and attach an $n+1$-cell, e^{n+1}, in such a way where the attaching map has degree m, we see that the resultant space is actually a $M(\mathbb{Z}_m, n)$. By taking wedge sums, we can construct $M(G, n)$ for any finitely generated G. In fact, we can use this idea and extend this construction for infinitely generated abelian groups to construct spaces X that are $M(G, n)$ for G being any abelian group. Furthermore, given any set of abelian groups $\{G_n\}_{n \in \mathbb{N}}$, we can take wedge sums of $M(G_n, n)$ (for different n) in order to construct a space X such that $H_n(X) \cong G_n$.

Another example of cellular homology at play is calculating the homology groups of $\mathbb{R}P^n$. First, we note that we can construct S^n with two k-cells, for each $0 \leq k \leq n$, where we attach each k-cell along the boundary of each of the two $k-1$-cells. That is, given any of the two k-cells e_i^k ($i = 1$ or $i = 2$), $d_k(e_i^k) = e_1^k - e_2^k$. Taking on this view, $\mathbb{R}P^n$ would have one k-cell for each $0 \leq k \leq n$ (we denote the k-cell as e^k). Moreover, because of the antipodal identification, we have that $d_k(e^k) = e^{k-1} - (-1)^{k+1} e^{k-1}$. From this, for the chain complex of $\mathbb{R}P^n$, the kth degree map alternates from the zero map and the $\cdot 2$ map, depending on whether k is odd or even. That is, we have the following chain complex:

$$0 \to \mathbb{Z} \xrightarrow{2} \mathbb{Z} \xrightarrow{0} \cdots \xrightarrow{2} \mathbb{Z} \xrightarrow{0} \mathbb{Z} \to 0 \text{ if } n \text{ is even and}$$
$$0 \to \mathbb{Z} \xrightarrow{0} \mathbb{Z} \xrightarrow{2} \cdots \xrightarrow{2} \mathbb{Z} \xrightarrow{0} \mathbb{Z} \to 0 \text{ if } n \text{ is odd.}$$

So, we see

$$H_k(\mathbb{R}P^n) = \begin{cases} \mathbb{Z} & k = 0,\ k = n \equiv 1 \mod 2 \\ \mathbb{Z}_2 & k \equiv 1 \mod 2,\ 0 < k < n \\ 0 & \text{otherwise} \end{cases}$$

In fact, $\mathbb{R}P^{2n-1}$ is a special case of a class of spaces called lens spaces[4]. The construction of a CW structure for a lens space is similar to that of $\mathbb{R}P^{2n-1}$, albeit much more complicated[5]. Given a lens space $L_m(\ell_1, \cdots, \ell_n)$, where each $\ell_1 \in \mathbb{Z}$ (which are coprime to m) corresponds to a rotation, we can construct the following chain complex:

$$0 \to \mathbb{Z} \xrightarrow{0} \mathbb{Z} \xrightarrow{m} \cdots \xrightarrow{m} \mathbb{Z} \xrightarrow{0} \mathbb{Z} \to 0$$

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[4] The $2n-1$ comes from the fact that we are viewing our construction in $\mathbb{C}^n$. In this case, our unit vectors form a copy of S^{2n-1}, which have an even number of coordinates when viewed as a real space.

[5] The construction can be found on Example 2.43 in Hatcher.

So, we see

$$H_k(L_m(\ell_1, \cdots, \ell_n)) = \begin{cases} \mathbb{Z} & k = 0, 2n-1 \\ \mathbb{Z}_m & k \equiv 1 \mod 2,\ 0 < k < 2n-1 \\ 0 & \text{otherwise} \end{cases}$$

Before talking about more computational techniques, let us now consider some places where homology (in particular, cellular homology) comes up. One of these places is the Euler characteristic. For a finite CW complex X, we say that $\chi(X) = \sum_n (-1)^n c_n$, where c_n is the number of n-cells of X. We note that for the case of platonic solids (which are represented as 2 dimensional complexes), this agrees with the (less general but better known) definition of $V - E + F$. We can also show that $\chi(X) = \sum_n (-1)^n \text{rank} H_n(X)$, which actually shows that the Euler characteristic is a topological invariant, as the homology groups are invariant under homotopy. This (equivalent) definition of Euler characteristic shouldn't be too big of a surprise, because in order to make one of the n-cells not count towards the free part of the nth homology (ie. make it torsion), we need to either attach an $n+1$ cell in a way such that the $n+1$ cell also doesn't contribute to the free part of the $n+1$st homology or attach the n-cell in such a way that it makes one of the $n-1$-cells not count towards the rank of the $n-1$st homology.

Another use of is to study groups. In particular, as it was shown in §1.B, the homotopy type of a $K(G, 1))$ (ie. a space X such that $\pi_1(X) \cong G$) is uniquely determined by the group G. From this, we can find the homology of a group G by taking $H_n(K(G, 1))$. The construction for such a space can be made with a CW complex, from which we can calculate its homology with cellular homology. This is a rather interesting application, as it shows us yet another example of the symbiotic relationship different fields of mathematics can have. In particular, while topology benefits from algebra via the fundamental (and upper homotopy) groups and homology groups, algebra benefits from topology through homological algebra (including the motivation for the snake lemma, five lemma, etc.) and group (co)homology.

Let us now recall from earlier all that we were able to compute using the long exact sequence of homology groups, given a pair (X, A). In particular, the main tool we leveraged was the fact that our sequence was exact - very rarely did we have to reference the chain complex of either X or A, nor even what the maps of our exact sequence were. Even though we can compute homology groups more directly now using cellular homology, let us not forget the power that comes from exact sequences.

Given a short exact sequence of groups $0 \to A \xrightarrow{i} B \xrightarrow{j} C \to 0$, we say that our short exact sequence splits if one of the following equivalent definitions hold:

1. There's a homomorphism $p : B \to A$ such that $pi = \mathbb{1}_A$.
2. There's a homomorphism $s : C \to B$ such that $js = \mathbb{1}_C$.
3. There's an isomorphism $\phi : B \to A \oplus C$ such that the following diagram commutes, where the lower maps are $a \mapsto (a, 0)$ and $(a, c) \mapsto c$.

$$\begin{tikzcd}
0 \arrow[r] & A \arrow[r, "i"] \arrow[dr] & B \arrow[r, "j"] \arrow[d, "\phi"] & C \arrow[r] & 0 \\
& & A \oplus C \arrow[ur] & &
\end{tikzcd}$$

Showing that these statements are equivalent is rather straightforward, and can even generalizes to nonabelian cases (with the exception of 2. implying 1. and 3.). It is not difficult to see how this theorem can be rather useful, in that it can simplify the computation of certain homology groups. To give a concrete example, we can use this theorem to show the nonexistence of certain retracts $r : X \to A$ for certain spaces, because if such existed, we would necessarily have that $H_n(X) \cong H_n(A) \oplus H_n(X, A)$,[6] which is not true in general.

We now introduce the Mayer-Vietoris sequence, which is, in a sense, the homology equivalent for van Kampen's theorem for the fundamental group. Just like how van Kampen's theorem gives us the fundamental groups of a space X given two fundamental group of two subspaces, the union of whose interiors give us all of X, the Mayer-Vietoris sequence gives us a long exact sequence relating the homology of X with the homology of two subspaces whose interiors[7], when unioned, give us all of X. Explicitly, the Mayer-Vietoris sequence is given below, where the maps will later be specified:

$$\cdots \to H_n(A \cap B) \overset{\Phi}{\to} H_n(A) \oplus H_n(B) \overset{\Psi}{\to} H_n(X) \overset{\partial}{\to} H_{n-1}(A \cap B) \to \cdots .$$

The construction of the Mayer-Vietoris sequence is in the same spirit as the long exact sequence of pairs. Let $C_n(A+B)$ be the set of n-chains in X that are the sum of n-chains of A and B. That is, $C_n(A+B) = C_n(A) + C_n(B)$ (note that this is NOT the direct sum!). We see that the boundary map takes elements of $C_n(A)$ to $C_{n-1}(A)$ and $C_n(H)$ to $C_{n-1}(B)$, so it follows that elements of $C_n(A+B)$ get mapped to $C_{n-1}(A+B)$. As such we see that we our set of $C_n(A+B)$ actually form a chain complex.

In fact, we see that $C_n(A+B)$ is, in a sense, $C_n(A) \oplus C_n(B)/C_n(A \cap B)$, since $C_n(A+B)$ count the chains in $C_n(A \cap B)$ once, while in $C_n(A) \oplus C_n(B)$, they are counted twice. From this, we have the short exact sequence

$$0 \to C_n(A \cap B) \overset{\phi}{\to} C_n(A) \oplus C_n(B) \overset{\psi}{\to} C_n(A+B) \to 0,$$

where $\phi(x) = (x, -x)$ and $\psi(x, y) = x + y$. Moreover, by the main proposition that was used in the proof of the excision theorem, since the interiors of A and B give X, we have that the inclusion $C_n(A+B) \to C_n(X)$ induces an isomorphism on the homologies. Since we have a short exact sequence of chain complexes, as well as the isomorphism $H_n(A+B) \cong H_n(X)$, we have an induced long exact sequence given by what we have above, where Φ and Ψ are the induced maps of ϕ and ψ respectively, and ∂ is the connecting map obtained using the Snake Lemma. By making a slight modification on the maps from the 0th chain groups, we also have the Mayer Vietoris sequence for reduced homology.

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[6] Since if r is a retract, then $i : A \hookrightarrow X$ must induce an injection $i_* : H_n(A) \hookrightarrow H_n(X)$.

[7] It should be noted that this condition is also that of the excision theorem. This is not a coincidence, as will be later mentioned.

As we can see, the Mayer Vietoris gives us a way to relate the homology of a space X by the homologies of two subspaces whose interiors give us X based on how they intersect. It should also be mentioned that we can actually leverage the sequence structure to for inductive arguments. For example, suppose $A_1, \cdots, A_n$ are open sets sets of X, such that $A_1 \cup \cdots \cup A_n = X$. Moreover, suppose any intersection of the A_i's is either empty or has trivial reduced homology. Using the (reduced) Mayer Vietoris sequence, we can induct on the number of open sets that make up X to show $H_i(X) \cong 0$ when $i \geq n-1$, by observing that

$$A_n \cap (A_1 \cup \cdots \cup A_{n-1}) = (A_n \cap A_1) \cup \cdots \cup (A_n \cap A_{n-1}),$$

which is itself a union of $n-1$ open sets[8].

Let us now discuss a generalization to the theory that we've developed. We recall from the beginning that the nth chain group of a topological space X, $C_n(X)$, is defined to be the free abelian group generated by the n-simplices of X. In other words, $C_n(X)$ consists of elements $\sum_i n_i \sigma_i$, where σ_i are the n simplices, and $n_i \in \mathbb{Z}$. But what's stopping us from using coefficients from another abelian[9] group G? The truth is, there's absolutely nothing holding us back from doing this. In fact, much of the theory would work exactly the same if we used coefficients from another abelian group. So, we let $C_n(X; G)$ be the elements $\sum_i n_i \sigma_i$ such that each $n_i \in G$. We note that the boundary maps ∂ would still work the same way as before, and that they actually give us a chain complex. From this, we have $H_n(X; G) = \ker \partial_n / Im(\partial_{n+1})$, which we refer to as the nth (singular) homology group with coefficients in G. We still have reduced homology groups $\tilde{H}_n(X; G)$, which are obtained by tacking on $\cdots \to C_0(X) \xrightarrow{\epsilon} G \to 0$ to our chain complex, where ϵ, as before, takes $\sum_i n_i \sigma_i \mapsto \sum_i n_i$. Similarly, we have relative homology as well, when we consider $C_n(X, A; G) = C_n(X; G)/C_n(A; G)$.

So just how much of the theory that we've built up for homology with $\mathbb{Z}$-coefficients transfers over for homology with G-coefficients? Turns out, pretty much all of it. This is because we didn't really use the fact that our coefficients were in $\mathbb{Z}$! Only when we had to do computations did the fact that we have $\mathbb{Z}$-coefficients come into play. As such the computation of homology groups with G-coefficients is where things differ. For example, just as we did the homology of a point, we see that if X is a point, $H_n(X; G) = 0$ when $n > 0$ and $H_0(X; G) \cong G$. From here, we can show that $\tilde{H}_n(S^k; G) \cong G$ when $n = k$ and 0 otherwise. However, despite the fact that these groups are not the same, we actually still have a notion of degree, since we can show that if we have a map $f : S^k \to S^k$, then its induced map $f_* : H_k(S^k) \to H_k(S^k)$ is actually multiplication by some $m \in \mathbb{Z}$. We can use this to develop cellular homology as we did before, except with coefficients in G, which (surprise surprise) agrees with singular homology with coefficients in G.

To see an example of homology with coefficients, consider our old friend $\mathbb{R}P^n$. We can show that the chain complex of $\mathbb{R}P^n$ with coefficients in G looks like

$$\cdots \xrightarrow{0} G \xrightarrow{2} G \xrightarrow{0} G \xrightarrow{2} G \xrightarrow{0} G.$$

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[8] This is problem 2.2.33 in Hatcher.

[9] Things would stop making sense if we allowed G to be nonabelian!

We now consider when $G = F$, where F is a field. If F has characteristic 2, then each boundary map is the 0 map, from which we see $H_k(\mathbb{R}P^n; F) \cong F$, for $0 \leq k \leq n$. However, if $\mathrm{char} F > 2$, then we see that each multiplication by 2 is an isomorphism, from which we have that $H_k(\mathbb{R}P^n; F) \cong F$ for $k = 0$ and k odd, and 0 otherwise (again, for $0 \leq k \leq n$).

Now that we've gone over quite a bit of the theory and computation of homology, let us further abstract what we've been doing. The reason for this is that when homology theory was first developed, there were multiple theories of homology, including simplicial homology, singular homology, cellular homology, and Cech homology, as well as various others. For a while, most of these theories seemed to agree, except, well, when they didn't[10]. What could be shown is that the various theories of homologies agreed when we had a CW complex. As a result, the following definition for homology theory developed.

We can formalize our notion of homology using the language of category theory. We define a *reduced* homology theory $\tilde{h}$ to be a functor between the category of topological spaces to the category of sequences of abelian groups such that the following hold:

1. If $f, g : X \to Y$ are homotopy equivalent, then $f_* = g_* : \tilde{h}_n(X) \to \tilde{h}_n(X)$.
2. For all CW pairs (X, A), there is a group homomorphism $\partial : \tilde{h}_n(X/A) \to \tilde{h}_{n-1}(A)$ such that the following sequence is long exact:

$$\cdots \to \tilde{h}_n(A) \xrightarrow{i_*} \tilde{h}_n(X) \xrightarrow{q_*} \tilde{h}_n(X/A) \xrightarrow{\partial} \tilde{h}_{n-1}(A) \xrightarrow{i_*} \tilde{h}_{n-1}(X) \to \cdots .$$

   Moreover, given a map $f : (X, A) \to (Y, B)$, there is an induced map $\bar{f} : X/A \to Y/B$ such that the following diagram commutes

$$\begin{tikzcd}
\tilde{h}_n(X/A) \arrow[r, "\partial"] \arrow[d, "\bar{f}_*"] & \tilde{h}_{n-1}(A) \arrow[d, "f_*"] \\
\tilde{h}_n(Y/B) \arrow[r, "\partial"] & \tilde{h}_{n-1}(B)
\end{tikzcd}$$

3. If $X = \bigvee_\alpha X_\alpha$ and $i_\alpha : X_\alpha \hookrightarrow X$ is the inclusion map for each α, then

$$\bigoplus_\alpha i_{\alpha *} : \bigoplus_\alpha \tilde{h}_n(X_\alpha) \to \tilde{h}_n(X) \text{ is an isomorphism.}$$

We notice that each of these statements have been shown to be true for (reduced) singular homology as we developed it. As such, the reason for choosing these axioms is none other than to "force" a homology theory to agree with singular homology for CW complexes. This, in a sense, makes singular homology our "model homology theory".

One thing to notice is that this construction is for reduced homologies. In the case of unreduced homology, we need to formalize the notion of relative homology groups $h_n(X, A)$ as a

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[10] See the Hawaiian Earring: Example 1.25 in Hatcher.

functor, where absolute homology groups are represented $h_n(X, \emptyset)$. Given the notion of relative homology, the axioms of unreduced homology is similar to that of reduced homology. The second axiom would need to be modified where the long exact sequence is that of the unreduced homology groups (with relative homology) as well as a word on excision, such as $h_n(X, A) \cong h_n(X/A, A/A)$, for CW pairs (X, A). We would also replace the third axiom with that of disjoint unions instead of wedge sums.

Let us now discuss some of the applications of homology theory as a whole. One result that we can show using homology theory is the famed Jordan Curve theorem, which tells us that a circle in $\mathbb{R}^2$ has an inside and outside. In more precise terms, if $h : S^1 \to S^2$ is an embedding, then $S^2 \setminus h(S^1)$ has exactly two connected components, each homeomorphic to open disks[11]. In fact, we can prove a more general version of this theorem, which goes as follows: If $h : D^k \to S^n$ $(k \leq n)$ is an embedding, then $\tilde{H}_i(S^n \setminus h(D^k)) = 0$. Moreover, if $h : S^k \to S^n$ is an embedding (again, $k \leq n$), then $\tilde{H}_i(S^n \setminus h(S^k)) \cong \mathbb{Z}$ when $i = n - k - 1$[12].

The first part of this can be proved by induction, by using the Mayer-Vietoris sequence, with $A = S^n \setminus h(I^{k-1} \times [0, 1/2])$ and $B = S^n \setminus h(I^{k-1} \times [1/2, 1])$. From this, we notice that $A \cup B = S^n \setminus h(I^{k-1} \times \{1/2\})$ and $A \cap B = S^n \setminus h(I^k)$, from which sets up our induction and (with some work) gives us the desired result. The second part of the theorem is also proved inductively with the (reduced) Mayer-Vietoris sequence, where the inductive step requires splitting up S^k into its northern and southern hemisphere D^k_+ and D^k_-, and letting $A = S^n \setminus h(D^k_+)$ and $B = S^n \setminus h(D^k_-)$, which gets us $\tilde{H}_i(S^n - h(S^k)) \cong \tilde{H}_{i+1}(S^n \setminus h(S^{k-1}))$.

Another result that we can obtain using homology theory is the Borsuk Ulam theorem, which tells us that an odd map $f : S^n \to S^n$ (ie. $f(-x) = -f(x)$) has odd degree. The proof of this[13] uses the induced map $\bar{f}$ on $\mathbb{R}P^n$, and as well as homology with coefficients (specifically we use coefficients from $\mathbb{Z}_2$), which shows that it's sometimes useful to consider coefficients outside of $\mathbb{Z}$. A corollary that follows from this is that any map $g : S^n \to \mathbb{R}^n$ has a point x such that $g(x) = g(-x)$.

Altogether, we see that homology theory is a rich theory readily available for use in a topological setting. It allows us to port over algebraic methods and ideas to prove and disprove statements about topological spaces. One thing that homology is especially good for is to prove the nonexistence of certain objects. For example, as it has been shown before, if we have $A \subset X$ such that there's a retract $r : X \to A$, then we necessarily have that $H_n(X) = H_n(A) \oplus H_n(X, A)$, which is not true in general.

One of the great advantages of homology theory, unlike homotopy theory, is that it's relatively easy to compute (especially with cellular homology). Even though homology is a bit tricky to define and the objects we're dealing with are rather nontrivial to wrap our heads around, it doesn't fail to give us a plethora of results. In other words, homology theory gives us a practical set of algebraic tools to utilize on our quest to further unlock the world of topology.

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[11] This result can be obtained through differential methods if we allow our embedding to be smooth. However, with algebraic techniques, we can show this for any embedding.

[12] We note that the Jordan Curve theorem is a special case of this specifically.

[13] See pg. 174 in Hatcher.