Math 971 Algebraic Topology

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Homology theory: Fundamental groups are a remarkably powerful tool for studying spaces; they capture a great deal of the global structure of a space, and so they are very good a distinguishing between homotopy-inequivalent spaces. In theory! But in practice, they suffer from the fact that deciding whether two groups are isomorphic or not is, in general, undecideable! Homology theory is designed to get around this deficiency; the theory builds (a sequence of) *abelian* groups $H_i(X)$ from a topological space. And deciding whether or not two abelian groups, at least if you're given a presentation for them, is, in the end, a matter of fairly routine linear algebra. Mostly because of the Fundamental Theorem of Finitely-generated Abelian groups; each such has a unique representation as $\mathbb{Z}^m \oplus \mathbb{Z}_{m_1} \oplus \cdots \oplus \mathbb{Z}_{m_n}$ with $m_{i+1}|m_i$ for every i .

There are also "higher" homotopy groups beyond the fundamental group π_1, (hence the name pi-*one*); elements are homtopy classes, rel boundary, of based maps $(I^n, \partial I^n) \to (X, x_0)$. Multiplication is again by concatenation. But unlike π_1, where we have a chance to compute it via Seifert-van Kampen, nobody, for example knows what all of the homotopy groups $\pi_n(S^2$ are (except that nearly all of them are non-trivial!). Like π_1, it describes, essentially, maps of S^n into X which don't extend to maps of D^{n+1}, i.e., it turns the "n-dimensional holes" of X into a group.

Homology theory does the exact same thing, counting n-dimensional holes. In the end we will find it to be extremely computable; but it will require building a fair bit of machinery before it will become so transparent to calculate. But the short version is that the homology groups compute "cycles mod boundaries", that is, n-dimesional objects/subsets that have no boundary (in the appropriate sense) modulo objects that are the boundary of $(n+1)$-dimensional ones. There are, in fact, probably as many ways to *define* homology groups as there are people actively working in the field; we will focus on two, simplicial homology and singular homology. The first is quick to define and compute, but hard to show is an invariant! The second is quick to see is an invariant, but, on the face of it, hard to compute! Luckily, for spaces where they are both defined, they are isomorphic. So, in the end, we get an invariant that is quick to compute. Of course, so is the invariant "4"; but this one will be a bit more informative....

First, simplicial homology. This is a sequence of groups defined for spaces for which they are easiest to define, which Hatcher calls Δ-complexes. Basically, they are spaces defined by gluing simplices together using nice enough maps. More precisely, the *standard n-simplex* Δ^n is the set of points $\{(x_1, \ldots x_{n+1}) \in \mathbb{R}^{n+1} : \sum x_i = 1, x_i \geq 0 \text{ for all } i\}$. This can also be expressed as convex linear combinations (literally, that's the conditions on the x_i's) of the points $e_i = (0, \ldots, 0, 1, 0, \ldots, 0)$, the *vertices* of the standard simplex. More generally, an n-simplex is the set $[v_0, \ldots v_n]$ of convex linear combinations of points $v_0, \ldots, v_n \in \mathbb{R}^k$ for which $v_1 - v_0, \ldots, v_n - v_0$ are linearly independent. Any bijection from the vertices of the standard simplex to the points $v_0, \ldots, v_n$ extends (linearly) to a homeomorphism of the simplices. The $n+1$ *faces* of a simplex, each sitting opposite a vertex v_i, are obtained by setting the corresponding coefficient x_i to 0. Each forms an $(n-1)$-simplex, which we denote $[v_0, \ldots, v_{i-1}, v_{i+1}, \ldots, v_n]$ or $[v_0, \ldots, \widehat{v_i}, \ldots, v_n]$. A *Δ-complex* X is a cell complex obtained by gluing simplices together, but we insist on an extra condition: the restriction of the attaching map to any face is equal to a (lower-dimensional) cell. As before, we use the weak topology on the space; a set is open iff it's inverse image under the induced map of a cell into the complex is open. Each n-cell comes equipped with a (continuous) map $\sigma : \Delta^n \to X$, which is one-to-one on its interior, whose restriction to the boundary is the attaching map, and whose restriction to each face is the associated map for that $(n-1)$-simplex. We will typically blur the distinction between the map σ (called the *characteristic map* of the simplex) and its image, and denote the image by σ (or σ^n), when this will cause no confusion, and call σ an n-simplex *in X*. When we feel the need for the distinction, we will use e^n for the image and σ^n for the map.

For example, taking our standard, identifications of the sides of a rectangle, cell structure for the 2-torus, and cutting the rectangle into two triangles (= 2-simplices) along a diagonal, we obtain a Δ-structure with 2 2-simplices, 3 1-simplices, and 1 0-simplex. A genus g surface can be built, by cutting the $2g$-gon into triangles, with $g+1$ 2-simplices, $3g$ 1-simplices, and 1 0-simplex.