cellular homology

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If X is a cell space, then let $(\mathcal{C}_*(X), \mathfrak{d})$ be the cell complex where the n-th group $\mathcal{C}_n(X)$ is the free abelian group on the cells of dimension n, and the boundary map is as follows: If e^n is an n-cell, then we can define a map $\varphi_f : \partial e^n \to f^{n-1}$, where f^{n-1} is any cell of dimension $n-1$ by the following rule: let $\varphi : e^n \to \mathrm{sk}_{n-1}X$ be the attaching map for e^n, where $\mathrm{sk}_{n-1}X$ is the $(n-1)$-skeleton of X. Then let π_f be the natural projection

$$\pi_f : \mathrm{sk}_{n-1}X \to \mathrm{sk}_{n-1}X/(\mathrm{sk}_{n-1}X - f) \cong f/\partial f.$$

Let $\varphi_f = \pi_f \circ \varphi$. Now, $f/\partial f$ is a (n-1)-sphere, so the map φ_f has a degree $\deg f$ which we use to define the boundary operator:

$$\mathfrak{d}([e^n]) = \sum_{\dim f = n-1} (\deg \varphi_f)[f^{n-1}].$$

The resulting chain complex is called the cellular chain complex.

Theorem 1 *The homology of the cellular complex is the same as the singular homology of the space. That is*

$$H_*(\mathcal{C}, \mathfrak{d}) = H_*(C, \partial).$$

Cellular homology is tremendously useful for computations because the groups involved are finitely generated.