Linear Time Recognition Algorithms for Topological Invariants in 3D

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Abstract

In this paper, we design linear time algorithms to recognize and determine topological invariants such as genus and homology groups in 3D. These invariants can be used to identify patterns in 3D image recognition and medical image analysis. Our method is based on cubical images with direct adjacency, also called (6,26)-connectivity images in discrete geometry. According to the fact that there are only six types of local surface points in 3D and a discrete version of the well-known Gauss-Bonnett Theorem in differential geometry, we first determine the genus of a closed 2D-connected component (a closed digital surface). Then, we use the Alexander duality to obtain the homology groups of a 3D object in 3D space. This idea can be extended to general simplicial decomposed manifolds or cell complexes in 3D.

1. Introduction

In recent years, there have been a great deal of new developments in applying topological tools to image analysis. In particular, computing topological invariants has been of great importance in understanding the shape of an arbitrary 2-dimensional (2D) or 3-dimensional (3D) object [8]. The most powerful invariant of these objects is the fundamental group [7]. Unfortunately, fundamental groups are highly non-commutative and therefore difficult to work with. In fact, the general problem in determining whether two given groups are isomorphic is undecidable. For fundamental groups of 3D objects, this problem is decidable but no practical algorithm has been found yet. As a result, homology groups have received the most attention because their computations are more feasible and they still provide significant information about the shape of the object [6] [9] [4]. This leads to the motivating problem addressed in this paper: Given a 3D object in 3-dimensional Euclidean space R^3, determine the homology groups of the object in the most effective way by only analyzing the digitization of the object.

The properties of homology groups have applications in many areas of bioinformatics and image processing [9]. Many researchers have made significant contributions in this area. For R^3, based on simplicial decomposition, Dey and Guha have developed an algorithm for computing the homology group (with generators) [6]. This algorithm has been improved by Damiand et al [4]. They used the boundary information to simplify the process.

In 2D, linear algorithms for both R^2 and the cubical complex (which is similar to that of digital spaces) are found to calculate Betti numbers, which are essentially the same as the genus [5] and [8]. Other algorithms for homology groups in cubical spaces are studies in 2D, these algorithms are either $O(nlog^2n)$ in [11] or $O(nlog^3n)$ in [8]. In general, the homology group can only be computed in $O(n^3)$ time for the cubical complex in [8]. More about computational homology is discussed in [9].

In this paper, we deal with the geometric and algebraic properties of manifolds and their optimal algorithms in 3D. We particularly look at a set of points in digital space, and our purpose is to find homology groups of the data set. We consider *digital manifolds* as defined in [3]. More information related to digital geometry and topology can be found in [10].

In this paper, we introduce optimal algorithms with time complexity $O(n)$ to compute the genus for close surfaces and homology groups for connected 3D manifolds in 3D digital space. In Section 2, we review some properties of digital surfaces and manifolds [3]. Based on the classical Gauss-Bonnet Theorem, we calculate the genus of a digital closed surface in 3D. Section 3 covers the necessary background in 3-manifold topology. Using Alexander duality, we relate homology groups of a 3D object to its 2-dimensional boundaries. In Section 4, we present our algorithm for homology groups.

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2 Gauss-Bonnet Theorem and Closed Digital Surfaces

Cubical space with direct adjacency, or (6,26)-connectivity space, has the simplest topology in 3D digital spaces. It is also believed to be sufficient for the topological property extraction of digital objects in 3D. Two points are said to be adjacent in (6,26)-connectivity space if the Euclidean distance of these two points is 1, i.e., direct adjacency.

Let M be a closed (orientable) digital surface in the 3D grid space in direct adjacency. We know that there are exactly 6-types of digital surface points [3][2]. Assume that M_i (M_3, M_4, M_5, M_6) is the set of digital points with i neighbors. We have the following result for a simply connected M [3]:

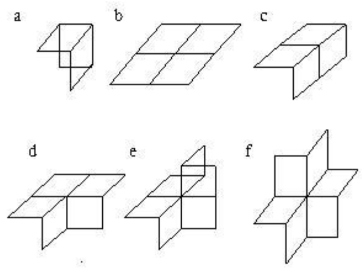

Figure 1. Six types of digital surfaces points in 3D

$$|M_3| = 8 + |M_5| + 2|M_6|. \quad (1)$$

M_4 and M_6 have two different types, respectively.

The Gauss-Bonnet theorem states that if M is a closed manifold, then

$$\int_M K_G dA = 2\pi\chi(M) \quad (2)$$

where dA is an element of area and K_G is the Gaussian curvature. Its discrete form is

$$\Sigma_{\{p \text{ is a point in } M\}} K(p) = 2\pi \cdot (2 - 2g) \quad (3)$$

where g is the genus of M. Assume that K_i is the curvature of elements in M_i, i = 3,4,5,6. We have

Lemma 2.1 *(a) $K_3 = \pi/2$, (b) $K_4 = 0$, for both types of digital surface points, (c) $K_5 = -\pi/2$, and (d) $K_6 = -\pi$, for both types of digital surface points.*

Lemma 2.1 can be calculated by using (3) directly with examples of simple digital closed surfaces or by the definition of discrete Gaussian curvature [12]. The curvature of the center vertex of the polyhedra is determined by

$$K_G = 2\pi - \Sigma_i \theta_i, \quad (4)$$

where $\Sigma_i \theta_i$ is the total angle around the center vertex.

Given a closed 2D manifold, we can calculate the genus g by counting the number of points in M_3, M_5, and M_6. According to (3), we have

$$\Sigma_{i=3}^{6} K_i \cdot |M_i| = 2\pi \cdot (2 - 2g),$$

$$\pi/2 \cdot |M_3| - \pi/2 \cdot |M_5| - \pi \cdot |M_6| = 2\pi \cdot (2 - 2g),$$

$$|M_3| - |M_5| - 2|M_6| = 4\pi \cdot (2 - 2g).$$

Therefore,

$$g = 1 + (|M_5| + 2 \cdot |M_6| - |M_3|)/8. \quad (5)$$

Algorithm 2.1 Let us assume that we have a connected M that is a closed digital surface in 3D. First, scan through all points (vertices) in M and count the neighbors of each point. We can see that a point in M has 4 neighbors indicating that it is in M_4 as are M_5 and M_6. Second, put points to each category of M_i. At last, use formula (5) to calculate the genus g.

Lemma 2.2 *Algorithm 2.1 can calculate the genus of M in linear time.*

The following example shows that the formula (5) is correct. The example shown in Fig. 2 is the simpliest case. In Fig.2 (a), there are 8 points in M_3 and no points in M_5 or M_6. According to (5), $g = 0$. Extend Fig. 2 (a) to a genus 1 surface as shown in Fig. 2 (b) where there are still 8 M_3 points but 8 M_5 points. We can extend it to Fig. 2 (c), it has 16 M_5 points and 8 M_3 points, so $g = 2$. Using the same method, one can insert more handles.

The above idea can be extended to simplicial cells (triangulation) or even general CW k-cells. This is because, for a closed discrete surface, we can calculate Gaussian curvature at each vertex point using formula (4). (The key is to calculate all angles separated by 1-cells at a vertex) Then use (3) to obtain the genus g. Since each line-cell (1-cell) is involved in exactly two 2-cells, it is only associated with four angles. Therefore the total complexity will be $O(|E|)$ where E is the set of 1-cells (edges). Thus,

Lemma 2.3 *There is an algorithm that can calculate the genus of a closed simplicial surface in $O(|E|)$ where E the set of 1-cells (edges).*

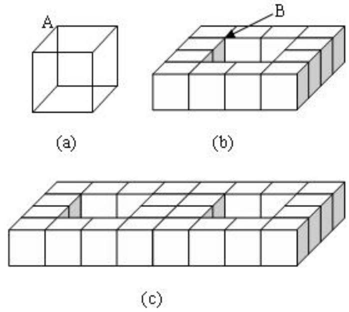

Figure 2. Simple examples with $g = 0, 1, 2$

3 Homology Groups of Manifolds in 3D Digital Space

Homology groups are invariants in topological classification. For a k-manifold , homology group H_i, $i = 0, ..., k$ indicates the number of holes in each i-skeleton of the manifold. Once we obtain the genus of a closed surface, we can then calculate the homology groups corresponding to its 3-dimensional manifold.

Consider a compact 3-dimensional manifold in R^3 whose boundary is represented by a surface. We show its homology groups can be expressed in terms of its boundary surface (Theorem 3.4). This result follows from standard results in algebraic topology [7]. Since it does not seem to be explicitly stated, we include all necessary results here. (The complete proofs can be found at http://arxiv.org/abs/0804.1982v2. It also appears in [6] in a somewhat different form.)

First, we recall some standard concepts and results in topology. Given a topological space M, its homology groups, $H_i(M)$, are certain measures of i-dimensional "holes" in M. For example, if M is the solid torus, its first homology group $H_1(M) \cong Z$, generated by its longitude, goes around the obvious hole. For a precise definition, see, e.g. [7]. Let $b_i = \text{rank} H_i(M, Z)$ be the ith Betti number of M. The Euler characteristic of M is defined by

$$\chi(M) = \sum_{i \geq 0} (-1)^i b_i$$

If M is a 3-dimensional manifold, $H_i(M) = 0$ for all $i > 3$ essentially because there are no i-dimensional holes. Therefore, $\chi(M) = b_o - b_1 + b_2 - b_3$. Furthermore, if M is in R^3, it must have nonempty boundary. This implies that $b_3 = 0$.

The following lemma is well known for 3-manifolds. It holds, with the same proof, for any odd dimensional manifolds.

Lemma 3.1 *Let M be a compact orientable 3-manifold (which may or may not be in R^3).*

(a) If M is closed (i.e. $\partial M = \emptyset$), then $\chi(M) = 0$.

(b) In general, $\chi(M) = \frac{1}{2}\chi(\partial M)$.

Next, we recall the Alexander duality.

Proposition 3.2 *Let $X \subset S^n$ be a compact, locally contractible subspace of S^n where S^n is the n-dimensional sphere. Then*
$\tilde{H}_i(S^n - X) \cong \tilde{H}^{n-i-1}(X)$ for all i where $\tilde{H}$ is the reduced homology.

We remark that S^n is the one point compactification of R^n. Therefore, a submanifold in R^n is automatically considered as a submanifold in S^n in a natural way. Conversely, a submanifold M in S^n is automatically a submanifold in S^n unless $M = S^n$.

Lemma 3.3 *Let S be a closed connected surface in S^3.*
(a) Its complement, $S^3 - S$, must have exactly two connected components. We denote them by M and M'.
(b) $H_1(M) \cong H_1(M') \cong Z^{\frac{1}{2}b_1(S)}$, $H_2(M) \cong H_2(M') = 0$.

Now we consider a general compact connected 3-manifold M in S^3. Its boundary, ∂M, is a closed orientable 2-dimensional manifold possibly with several components.

Theorem 3.4 *Let M be a compact connected 3-manifold in S^3. Then (a) $H_0(M) \cong Z$. (b) $H_1(M) \cong Z^{\frac{1}{2}b_1(\partial M)}$, i.e. $H_1(M)$ is torsion-free with rank being half of rank $H_1(\partial M)$. (c) $H_2(M) \cong Z^{n-1}$ where n is the number of components of ∂M. (d) $H_3(M) = 0$ unless $M = S^3$.*

4 A Linear Algorithm of finding Homology Groups in 3D

Based on the results we presented in Sections 2 and 3, we now describe a linear algorithm for computing the homology group of 3D objects in 3D digital space.

Assuming we only have a set of points in 3D. We can digitize this set into 3D digital spaces. There are two ways of doing so: (1) by treating each point as a cube-unit that is called the raster space, (2) by treating each point as a grid point. It is also called the point space. These two are dual spaces. Using the algorithm described in [3], we can determine whether the digitized set forms a 3D manifold in 3D space in direct adjacency for connectivity. The algorithm is in linear time. The more detailed considerations of recognition algorithms related to 3D manifolds can be found in [1].

Algorithm 4.1 Let us assume that we have a connected M that is a 3D digital manifold in 3D.

Step 1. Track the boundary of M, ∂M, which is a union of several closed surfaces. This algorithm only needs to scan though all the points in M to test if the point is linked to a point outside of M. If so, that point will be on boundary. (Separate ∂M into connected components using depth-first or breadth-first search.)

Step 2. Calculate the genus of each closed surface in ∂M using the method described in Section 2. We just need to count the number of neighbors on a surface. and put them in M_i, using the formula (5) to obtain g.

Step 3. Using the Theorem 3.4, we can get H_0, H_1, H_2, and H_3. H_0 is Z. For H_1, we need to get $b_1(\partial M)$, which is just the summation of the genus in all connected components in ∂M. (See [7] and [6].) H_2 is the number of components in ∂M. H_3 is trivial.

Lemma 4.1 *Algorithm 4.1 is a linear time algorithm.*

Proof. Step 1 uses linear time. We can first track all points in the object using breadth-first-search. We assume that the points in the object are marked as "1" and the others are marked as "0." Then, we test if a point in the object is adjacent to both "0" and "1" by using 26-adjacency for linking to "0." Such a point is called a boundary point. It takes linear time because the total number of adjacent points is only 26. Another algorithm is to test if each line cell on the boundary has exactly two parallel moves on the boundary [3]. This procedure only takes linear time for the total number of boundary points in most cases.

Step 2 is also in linear time by Lemma 2.2.

Step 3 is just a simple mathematics calculation. For H_0, H_2, and H_3, they can be computed in constant time. For H_1, the counting process is at most linear. ■

Therefore, we can use linear time algorithms to calculate g and all homology groups for digital manifolds in 3D based on Lemma 2.2 and Lemma 4.1.

Theorem 4.2 *There is a linear time algorithm to calculate all homology groups for each type of manifolds in 3D.*

To some extent, researchers are also interested in space complexity that is regarded as running space needed beyond the input data. Our new algorithm procedures do not need to store the past information, the algorithms presented in this paper are always $O(\log n)$. Here, $\log n$ is the bits needed to represent a number n.

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