

Volume Morphing Methods for Landmark Based 3D Image Deformation

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ABSTRACT

Volume morphing is a technique used for generating smooth 3D image transformations and deformations. In this paper, several algorithms are developed for morphing transformations that create new forms and simulate shape deformation and growth in biomedical applications. 3D biological point landmarks and their movements are defined to guide the morphing transformation using a scattered data interpolation algorithm. Two types of morphing algorithms, the Shepard-based interpolation and the radial basis function approach, are investigated in detail and applied for volume morphing in growth predictions of children and shape transformations between species.

Keywords – 3D morphing, shape deformation, landmark, scattered data interpolation.

1 INTRODUCTION

1.1 Volume morphing

Volume data of 3D arrays is the most commonly used data format in medical imaging data acquisition techniques, such as computed tomography (CT) and magnetic resonance (MR). In the past, research attention has been mostly focused on the visualization of such volume data.¹¹ Little work has been published in the area of manipulating the shape of the objects contained in the volume. This paper addresses one such shape manipulation operations — volume morphing.

Volume morphing is a technique used for generating smooth 3D volume transformations and deformations. It has widespread applications in creating new forms, and in analyzing and simulating shape deformation due to growth or surgical reconstruction in biomedical applications. In craniofacial surgery planning, for instance,

morphing techniques can be used to simulate the post-operative growth of the pediatric patient to provide information about the future appearance of the child and allow surgeons to better plan their surgery. Morphing between the heads of different people and species provides information and tools for studying the morphological relationships between people and across species. 3D volume morphing is also potentially very useful in 3D image registration, motion simulation and animation, flexible object modeling, and special-effect creation in entertainment applications.

1.2 Related work

Previous work in volume morphing includes the feature based volume morphing method by Lerios, Garfinkle and Levoy,¹³ the scheduled Fourier volume morphing by Hughes,¹⁰ and the wavelet based volume morphing by He, Wang and Kaufman.⁸ Hughes's method¹⁰ uses smooth interpolation between the Fourier transforms of two volume models, while He, Wang and Kaufman's method⁸ represents the two volume models in a wavelet domain and applies smooth interpolations between the corresponding subbands. Only the morphing of simple objects were shown in the above two methods, and non-smooth movements of isosurfaces have also been observed in the results from these two methods. Recent work by Lerios, Garfinkle and Levoy¹³ is a 3D extension of a 2D feature-based image morphing algorithm.² This method shows much more complicated and smooth morphing results for both the CT volume datasets and polygonal objects. It is a 3D extension of a 2D feature-based image morphing algorithm.² The quality of its morphing result, however, largely depends on the placement of the feature landmarks. The algorithm is not suitable for applications where only a relatively small number of point landmarks are available.

2D image level morphing, often called image warping, constructs image sequences showing a progressive transition from one image to another. The study of such 2D morphing techniques has been very extensive.^{4,2,12,17,20} Besides its visual drawbacks, such as the difficulties in handling viewing and lighting parameters and spatial relationships, 2D image warping cannot generate the morphed 3D models that are needed for non-visual applications as analysis and measurements. For 3D volume data, True 3D morphing technique is clearly a more appropriate solution.

Another related research topic is free-form deformation (FFD). FFD has been widely used in generating geometric deformations of geometric models.^{3,9,16,18} Most of these algorithms are control point based, that is, the deformation is controlled by a few external points. In practical applications, however, the control points are usually difficult to define and not very intuitive for manipulation. Scattered data interpolation based deformation approaches^{1,16} are currently receiving more attention, seem more intuitive and are easier to manipulate for practical purposes. The development of our volume morphing methods is based on this approach.

1.3 Overview

In this paper, we are mainly interested in landmark-based morphing, i. e. the morph is guided by the interpolation of a set of landmark points. In our cases, landmarks are biologically meaningful features that can be defined with high precision on objects of interest. Since the landmarks given are arbitrarily distributed across the volume, a scattered data interpolation problem has to be solved in building the morphing transformation. Unlike the warping and blending approach used by Lerios, Garfinkle and Levoy,¹³ our landmarks are all homologous between objects, and the morphing goes in one direction only without any blending. Our morphing approach is mainly based on two classes of scattered data interpolation methods, the Shepard-based methods and the radial basis function methods. Both methods have been successfully used in the fields of computer-aided geometric design and geometric modeling for constructing smooth surfaces to interpolate given data points. In the following paper, we first take a brief look at the landmark placement, matching and growth processes. It is part of the pre-processing needed for the volume morphing and growth algorithms. The two classes of the interpolation methods

are fully discussed in section 3. We describe the original interpolation methods and several improvements to fit them into the volume morphing problem. In section 4, the application of the interpolation methods to the volume morphing problem is presented. Finally, some remarks and future work are given in section 5.

2 LANDMARK PROCESSING

Given a set of landmark points $L^0 = \{L_i^0\}$ ($i = 1 \dots n$) in the source volume V_0 , and the target landmark set $L^1 = \{L_i^1\}$ ($i = 1 \dots n$), the landmark based volume morphing is defined as a mapping $F: R^3 \rightarrow R^3$ satisfying:

$$F(L_i^0) = L_i^1 \quad (i = 1 \dots n) \quad (1)$$

Applying such morphing transformation to the source volume will generate a new volume V_1 called the target volume.

It is clear that for a given interpolation algorithm, the morphing transformation F depends entirely on the two landmark sets L^0 and L^1 . Three dimensional coordinates of the source landmarks L^0 from the face, cranial base and neurocranium can be located directly on the 3D CT reconstruction of the source volume V_0 using a landmark placement tool. It is a manual process in which the landmark points are picked one by one from the volume or surface rendered image with an interactive visualization program. Since our morphing algorithm doesn't enforce any requirement on the number and distribution pattern of the landmark points (actually we so far only used biological landmarks), this landmark placement process can certainly be more automatic in the future.

The target landmark set, L^1 , can be obtained in two different ways:

1. If the target volume already exists, the target landmark set will be directly placed in the target volume. This is the same process as placing the source landmark set. Because the landmarks in source volume and target volume are obtained independently, and each time only a subset of all possible biological landmarks is placed, we may not have the same subset with the same order for both the source and target landmark sets. The interpolation algorithms, however, need a one-to-one correspondence between $\{L_i^0\}$ and $\{L_i^1\}$. Thus a matching needs to be done for the two sets of landmarks. In our implementation, all of our landmarks are biological landmarks, with known biological names and pre-assigned indices. So, building the correspondence becomes a straightforward string or index matching operation, and is easily automated.
2. If the target volume does not exist, for instance in growth prediction, a landmark growth process is then needed to compute the target landmarks from the source landmarks. As an example, the approach for craniofacial growth applications is briefly described here.

A growth model theory given by Richtsmeier and Lele¹⁵ was used in modeling the landmark growth for craniofacial patients. Based on this model, a growth matrix is first defined to represent the change in distances between landmarks after growth. Let $\{r_{ij}\}$ be the growth matrix. We have

$$r_{ij} = \|L_i^1 - L_j^1\| / \|L_i^0 - L_j^0\|$$

This growth matrix is usually derived from a database of previously recorded normal growth data sets using a statistical process. A growth prediction method based on a growth difference matrix analysis is then applied to obtain the coordinates of the grown landmark points. Details of this method can be found in Richtsmeier and Lele's paper.¹⁵

Using the same growth matrix, $\{r_{ij}\}$, we also experimented another landmark growth prediction algorithm using a pseudo-energy minimization process. A physical model assumes that a spring, with the rest length of $r_{ij}\|L_i^0 - L_j^0\|$, is attached to each pair of the original landmarks L_i^0 and L_j^0 . The algorithm then iteratively adjusts the coordinates of all the landmarks to try to reach an equilibrium. Mathematically, it is interpreted

as a numerical minimization process of the energy term:

$$E = \sum_{i \neq j} \left| \|L_i - L_j\| / \|L_i^0 - L_j^0\| - r_{ij} \right|^2$$

where $\{L_i\}$ are the landmark variables. This algorithm turned out to work equally well.

3 INTERPOLATION METHODS

The landmarks we obtained from section 2 have an arbitrary distribution across the whole volume, *i. e.* there is no regularity to be explored. Such a data set is often called *scattered data set*, and finding a smooth interpolation function over scattered data is called *scattered data interpolation*, *i. e.*

For given data pairs (also called interpolation points) (P_i, Q_i) , ($i = 1 \cdots n$, $P_i \in R^3$, $Q_i \in R^3$), find a function $G : R^3 \rightarrow R^3$ (also written as $G(P; \{P_i\}, \{Q_i\})$) and $G \in C^1$ so that

$$G(P_i) = Q_i \quad i = 1 \cdots n \quad (2)$$

The problem of scattered data interpolation has been extensively studied in computer aided geometric design (CAGD) and geometric modeling. Among the many methods proposed by researchers in these areas,^{6,5} we choose to investigate two classes of approaches, the Shepard approach and the radial basis function approach. The Shepard method is one of the oldest interpolation methods and the easiest to understand and implement, while radial basis function approach generates consistently good results. In the following we will take a look at both of these two approaches and try to improve and apply them to the volume morphing problem.

3.1 Shepard based methods

Shepard's approach¹⁹ constructs the interpolation function using a distance weighted average of the interpolation points. Directly applying this formula to the 3D scattered data interpolation problem gives:

$$G(P) = \sum_{i=1}^n \frac{Q_i}{d_i^r(P)} \bigg/ \sum_{i=1}^n \frac{1}{d_i^r(P)} \quad (3)$$

where $d_i(P)$ is the distance function from P_i and r is the exponent parameter, often set to 2 to avoid computing the square root. When $r > 1$, $G \in C^1$.

When the interpolation points are unevenly distributed, this straightforward use of Shepard formula causes the so called *remote points*, points that are not close to any of the interpolation points $\{P_i\}$, to be shifted towards the centroid of $\{Q_i\}$. This is because, in the extreme case, when all the distances are very large, the weights at all interpolation points are almost equal, and the result tends to be the average of $\{Q_i\}$. Images applied with Equation (3) can often be greatly distorted. In our experiment, it is virtually unusable for the biological landmarks can be very sparse and unevenly placed.

An easy fix to this problem is to use the displacements of the interpolation points, $\{Q_i - P_i\}$, instead of the actual points $\{Q_i\}$, *i. e.*

$$G_d(P) = P + \sum_{i=1}^n \frac{Q_i - P_i}{d_i^r(P)} \bigg/ \sum_{i=1}^n \frac{1}{d_i^r(P)} \quad (4)$$

Morphing generated from G_d is generally quite acceptable. But there are still two problems:

1. The remote points will now take the average displacement of all the interpolation points. The problem is in many applications, e. g. child growth, the displacements of the interpolation points often offset each other and average to zero or close to zero, resulting in zero or very small displacement for the remote points, which is clearly incorrect for such applications. An example is shown in Figure 1(b) where points at the upper portion of the skull grow very little. Another example given in Figure 2(b) shows distortion at the top of the head. Both instances occur because of the lack of landmarks in the top portion of the skull.
2. The transformation (4) is not affine invariant, i. e. \exists affine transformations $g : R^3 \rightarrow R^3$, for which

$$G_d(P; \{P_i\}, \{g(Q_i)\}) \neq g(G_d(P; \{P_i\}, \{Q_i\}))$$

Affine invariance is very desirable since the source and the target landmark sets can be in totally different coordinate systems when they are placed independently. A degenerate case is that if $\{Q_i = g(P_i)\}$, G_d is generally not the same as g .

The above two problems can be solved by a more general extension to the Shepard formula. Assuming a local interpolant function, $g_i : R^3 \rightarrow R^3$, exists for each interpolation point P_i , and g_i is an affine transformation interpolating P_i , i. e. $g_i(P_i) = Q_i$, the interpolation function is then defined as:

$$G_a(P) = \sum_{i=1}^n \frac{g_i(P)}{d_i^r(P)} \Bigg/ \sum_{i=1}^n \frac{1}{d_i^r(P)} \quad (5)$$

To construct the local interpolants $\{g_i\}$, ($i = 1 \dots n$), a pseudo-energy minimization process is employed.

Let

$$g_i = A_i(x - x_i) + B_i(y - y_i) + C_i(z - z_i) + Q_i \quad (6)$$

where $P_i = (x_i, y_i, z_i)$, and $A_i, B_i, C_i \in R^3$ are 3D coefficients of g_i . We define an energy term at each interpolation point as:

$$E_i(A_i, B_i, C_i) = \sum_{j \neq i} \frac{(g_i(P_j) - Q_j)^2}{d_i^2(P_j)} \Bigg/ \sum_{j \neq i} \frac{1}{d_i^2(P_j)} \quad (7)$$

(A_i, B_i, C_i) can then be solved with a numerical minimization process. From the above, it is easy to verify:

1. Interpolation condition is satisfied, i. e. $G_a(P_i) = Q_i$
2. When $r > 1$, the first derivatives of G_a at all the interpolation points interpolate the first derivatives of the local interpolants, i. e.

$$\frac{\partial G_a(P_i)}{\partial x} = \frac{\partial g_i(P_i)}{\partial x} = A_i; \quad \frac{\partial G_a(P_i)}{\partial y} = \frac{\partial g_i(P_i)}{\partial y} = B_i; \quad \frac{\partial G_a(P_i)}{\partial z} = \frac{\partial g_i(P_i)}{\partial z} = C_i \quad (8)$$

3. G_a is affine invariant, i. e. \forall affine transformation $g()$,

$$G_a(P; \{P_i\}, \{g(Q_i)\}) = g(G_a(P; \{P_i\}, \{Q_i\}))$$

In Figure 1(c) the growth using G_a looks a lot more natural than the one in Figure 1(b). The problem in Figure 2(b) also gets largely corrected by using G_a in Figure 1(c).

If in the above formula we assume $A_i = B_i = C_i = s_i$, where s_i is called the local scaling factor, we get:

$$G_s(P) = \sum_{i=1}^n \frac{s_i \cdot (P - P_i) + Q_i}{d_i^r(P)} \Bigg/ \sum_{i=1}^n \frac{1}{d_i^r(P)} \quad (9)$$

Figure 1: (a) The skull of a craniofacial patient; (b) Growth with the displacement-Shepard method; (c) Growth with the affine-Shepard method; (d) Growth with the scaling-Shepard method.

This simplification is very useful in such cases as growth simulation where the deformation demonstrates certain degree of local scaling. Figure 1(d) shows a growth result using this simplified method. It looks as good as Figure 1(c) in this case. It also greatly simplifies the numerical computation because the energy minimization is no longer needed in this case for the local scaling factor is simply a weighted average of the scaling factors of the landmark points (elements in the growth matrix r_{ij}), i. e.

$$s_i = \frac{\sum_{j \neq i} \frac{r_{ij}}{d_i^2(P_j)}}{\sum_{j \neq i} \frac{1}{d_i^2(P_j)}} \quad (10)$$

We now call the morphing method using G_d the displacement-Shepard method, the one using G_a the affine-Shepard method, and the one using G_s the scaling-Shepard method. They are all called Shepard-based methods.

3.2 Radial basis function methods

One common problem of all the Shepard based methods is that the global smoothness of the deformation is not always satisfactory. For example, valleys or peaks can often be seen around the landmark points in the morphed image, particularly when the landmark points are very unevenly distributed (see Figure 2(b)(c)). A radial basis function approach can effectively overcome this problem and is globally much smoother.

A radial basis function is loosely defined as a basis function whose value depends only on the distance from the data point. A radial basis function interpolation method is simply the linear combination of such basis functions:

$$G(P) = \sum_{i=1}^n c_i R_i(P) \quad (11)$$

where $\{c_i\}$ are 3D coefficients, and $\{R_i\}$ are the radial basis functions.

The most well known and very effective radial basis function is the Hardy multiquadrics.⁷ It is defined as

$$R_i(P) = (d_i^2(P) + r_i^2)^\alpha$$

Figure 2: (a) The translucent rendering of a human head; (b) The human head morphed to a cebus using the displacement-Shepard method; (c) morphing with the affine-Shepard method; (d) morphing with the Hardy method.

where d_i is the distance function from P_i , r_i is the stiffness radius controlling the stiffness of the deformation around P_i , and $\alpha > 0$ is an exponent parameter. It was also noted that Equation 11 does not have affine precision, i. e. when $\{Q_i\}$ are merely affine transformed from $\{P_i\}$, G cannot recover this affine transformation. A solution suggested and used by many researchers is to add a linear term in the equation to absorb the linear part of the morphing transformation. Thus the radial basis function method using Hardy's multiquadrics, also called Hardy method, can be written as:

$$G_h(P) = \sum_{i=1}^n h_i \cdot (d_i^2(P) + r_i^2)^\alpha + \mathcal{L}(P) \quad (12)$$

where $\mathcal{L}(P) = h_{n+1} \cdot x + h_{n+2} \cdot y + h_{n+3} \cdot z + h_{n+4}$ is the affine transformation, $\{h_i\}$ ($h_i \in R^3$, $i = 1 \dots n + 4$) are called Hardy coefficients. In principle, though rarely used, $\mathcal{L}(P)$ can be polynomials of higher degrees as well. The parameters $\{r_i\}$ can be arbitrary. But for smooth results, they are normally set to:

$$r_i = \min_{j \neq i} d_i(P_j)$$

This ensures that the morphing is soft in the area where $\{P_i\}$ are sparse, and stiff in the area where $\{P_i\}$ are dense. For the exponent parameter α , our experiments show best results with $\alpha = 0.5$, and less robust but still very smooth results with $\alpha = -1$. The former is, however, more costly because of the square root computation.

Computation of the Hardy coefficients is quite straightforward. If we substitute condition $G_h(P_j) = Q_j$ ($j = 1 \dots n$) into Equation 12, we get the following linear system of n equations:

$$\sum_{i=1}^n h_i \cdot (d_i^2(P_j) + r_i^2)^\alpha + \mathcal{L}(P_j) \quad (j = 1 \dots n) \quad (13)$$

For linear precision, we also require:

$$\sum_{i=1}^n h_i \cdot x_i = 0 \quad (14)$$

$$\sum_{i=1}^n h_i \cdot y_i = 0 \quad (15)$$

$$\sum_{i=1}^n h_i \cdot z_i = 0 \quad (16)$$

$$\sum_{i=1}^n h_i = 0 \quad (17)$$

This results in a linear system of $n+4$ equations with $n+4$ unknowns $\{h_i\}$ ($i = 1 \dots n+4$). As shown in Micchelli’s paper,¹⁴ such linear systems are usually very stable and the interpolant exists and is unique under normal data sets. This is perhaps one of the main reasons why Hardy method works remarkably well. One example is shown in Figure 2(d) using the Hardy method. It demonstrates a much smoother result than the Shepard-based methods. We will show more examples of the Hardy morph in next section.

The volume morphing transformation using Hardy interpolation is generally fairly smooth. But since the linear system in Equation 13 to 17 leave no additional degrees of freedom, Hardy method does not allow for control of slight modifications of results while keeping the interpolation points unchanged. The obvious parameters for such control, aside from the interpolation point itself, are the first derivatives at the interpolation points. The Hardy method doesn’t attempt to interpolate any estimate of the first derivatives at $\{P_i\}$. It can, however, be modified to do so. The modification we attempted is to add an affine-Shepard term to the the Hardy interpolation. The result is a modified Hardy method:

$$G_H(P) = G_h + G_a \quad (18)$$

Here G_a is the affine-Shepard interpolation, as described in Equation 5, with local interpolants:

$$g_i = dx_i \cdot x + dy_i \cdot y + dz_i \cdot z$$

where $dx_i, dy_i, dz_i \in R^3$ are the first derivatives, as local control parameters, at the interpolation point P_i .

For more user control of the morphing, dx_i, dy_i, dz_i can be used as an interactive tool to fine-tune the result. Alternatively dx_i, dy_i, dz_i can also be estimated, similarly to the affine-Shepard method, from the interpolation points $\{P_i\}$ using the energy minimization process as shown in Equation 7. In this case, the result will fit the data better than the original Hardy method because it takes account of their derivatives as well. Overall, since the spatial interpolation is still done by the Hardy method, the morphing result still has the smoothness of the Hardy interpolation and the desired slopes at the interpolation points.

4 VOLUME MORPHING

Volume morphing is concerned usually with mapping the values of a function from one domain to another in 3D space. To simplify our description, let us define a volume as a scalar valued function, often known as the intensity value function, and represent it discretely as its values at a 3D array of grid points, or voxels. The source volume V_0 can then be considered as a scalar function I_0 , with only the values at voxel points $I_0(i, j, k)$ known. The purpose of volume morphing is to obtain the target volume V_1 , represented as its intensity values at voxel points $I_1(i, j, k)$ ($i, j, k = 1 \dots N$), so that:

$$I_1(i, j, k) = I_0(F^{-1}(i, j, k))$$

where F is the morphing transformation with interpolation condition $F(L_i^0) = L_i^1$ ($i = 1 \dots n$).

If we simply take F as one of the scattered data interpolation methods described in section 3, i. e. $F = G$ (G is one of the G_d, G_a, G_s, G_h or G_H), with $P_i = L_i^0$ and $Q_i = L_i^1$, we will have to compute the inverse of G in order to get the intensity values for V_1 , for $I_1(i, j, k) = I_0(G^{-1}(i, j, k))$. Unfortunately such inverse computation is very difficult and may not even be unique if the interpolation function is not a one-to-one mapping.

Figure 3: (a) A human skull is morphed using the landmarks from four different non-human primates; (b) A higher resolution rendering of one of the morphing results.

To avoid computing the inverse of G , we take an reversed interpolation approach. Instead of interpolating from L^0 to L^1 , we do it the other way around. In this approach, F is set to be the inverse of G , i. e. $F = G^{-1}$, and in computing the interpolation function G , we assume:

$$P_i = L_i^1 \quad (i = 1 \cdots n)$$

$$Q_i = L_i^0 \quad (i = 1 \cdots n)$$

We now have:

$$I_1(i, j, k) = I_0(F^{-1}(i, j, k)) = I_0(G(i, j, k))$$

$G(i, j, k) \in R^3$, computed directly from the interpolation function, is generally not at one of the voxel points in V_0 , and a trilinear interpolation needs to be done for $I_0(G(i, j, k))$ from the values of its neighboring eight voxel points.

The above approach for volume morphing is, however, very expensive. For every grid point (i, j, k) in V_1 , $G(i, j, k)$ needs to be computed and the result then has to be trilinearly interpolated in the source volume. For a typical 256^3 volume, there are over 16 million such points, taking sometimes hours to compute. There are many approaches to speed this up so as to make such volume morphing more practical. Lierios, Garfinkle and Levoy gave several such measures in their 1995 paper.¹³ All of them can be easily used in our volume morphing approach.

From section 3 we can also see that the cost of computing G is linearly proportional to the number of landmarks. Therefore, it is not practical to rely entirely on selecting a large number of landmarks to achieve a desired morphing effect - such a practice is not only tedious and difficult for the users but also very computationally costly. We think that it is more natural and efficient to use simple point landmarks and rely on better mathematical interpolation functions and perhaps physical or biological properties to obtain good results.

We have implemented all five interpolation methods given in section 3, including the displacement-Shepard, the affine-Shepard, the scale-Shepard, the Hardy and the modified Hardy methods. High resolution CT scans of the heads of human and animals were used for two applications: (1) growth prediction of children, (2) shape transformations between animals or between human and non-human primates. All the morphing results were based on biological landmarks placed by workers at the Johns Hopkins University School of Medicine. We show

Figure 4: A visualization sequence of the morph from human to macaque.

Figure 5: A visualization sequence showing the surgical correction and growth of a craniofacial patient.

some of the morphing cases here. In Figure 3(a), a human skull is morphed to four different modern primates. Figure 3(b) shows a higher resolution image of the morphing result. A visualization sequence of one of the morphs, from human to macaque is given in Figure 4. Around forty to fifty common landmarks for the human and monkeys were used. Hardy interpolation method was used for both Figure 3 and Figure 4. In Figure 5, we show a sequence of the surgical correction and the post-operative growth prediction for a craniofacial patient. The affine-Shepard method was used for the growth simulation with 41 landmarks, and the growth is from one month to 55 month age. SGI's 3D texture mapping hardware was used for the volume rendering of all the images in Figure 1, Figure 2 and Figure 5. The images in Figure 3 and Figure 4 are generated using a raycasting volume rendering algorithm on an SGI Indigo 2 workstation.

5 CONCLUSION

We have presented a landmark-based volume morphing approach using various scattered data interpolation methods. Only a relatively small number of biological landmarks are used. The morphing results depend, to a large extent, on the behavior of the mathematical interpolation functions. Both Shepard-based interpolation methods and radial basis function methods are discussed. Some modifications to the interpolation functions are also made to utilize the first derivative information of the landmark data set. These 3D morphing algorithms have been applied to real CT datasets in applications of growth prediction and shape transformation between species. Our experiments show that: (1) The Shepard-based method is useful for growth problems; and (2) For large deformation, such as the morphing between different species, Shepard-based methods are generally less effective when landmarks are scarce, but Hardy and the modified Hardy methods work very well.

Volume morphing is a potentially powerful tool for many applications in both research and clinical medicine, as well as in other areas such as education and entertainment industry. Future work includes:

- Better mathematical interpolation functions to fill the large gaps caused by very sparse landmark placement, and more computationally efficient interpolation functions to reduce the cost in morphing each point.
- Better speed-up strategy in the volume morphing process to take full advantages of object coherences and interpolation function coherence for achieving interactive morphing rate.
- 3D image processing technique for semi-automatic placement of landmarks, and graphical and visualization tools for interactive free-morphing techniques.

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