A METHOD FOR 3D MORPHING USING SLICES

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Abstract: 3-D morphing, in its simplest definition, is shape transformation between a pair of objects i.e. source and target, by gradual, continuous and simultaneous dissolvement of the shape of source object to its target and vice versa resulting in a number of intermediate shapes. Many algorithms have been developed for this purpose with each one having its own speciality. In this paper, a novel algorithm is presented which is based on slices. The technique originates from the concept of reducing a 3-D object to a number of slices in 2D plane. In the algorithm, all of the 2D slices may not be oriented in either x, y, z or in a particular direction. Orientation and rotation of the slices within a single body can be varied from one slice to another based on the alignment of the object. Oriented Bounding Box (OBB) is used to determine the orientation of the object. The advantages of the proposed method i.e. minimal user input, flexibility, dynamism and ease of implementing over other 3D morphing algorithms are also discussed.

1 INTRODUCTION

Starting from the late eighties until the end of nineties numerous algorithms on 3D morphing have been developed. Now morphing has become an indispensable tool in 3D animation industry. Not just for the purpose of transforming from one shape to another, morphing is also useful in incorporating characteristics of different bodies in different proportions to the morphed output.

In this paper a morphing algorithm which takes into account of orientation and distortion of the object is presented. Object is cut into slices along its alignment. Oriented Bounding Box (OBB) is used to determine the initial alignment of the object. The more dense the slices, the more accurate is the alignment (though there is an optimal limit on how dense the slices could be). For all kind of objects, this method works with minimal user input. The simplicity, accuracy, versatility, flexibility and extendibility of the algorithm meet all the criteria of a good and efficient morphing algorithm based on our survey on a number of morphing algorithms.

2 BACKGROUND

Depending on the various approaches, existing morphing algorithms can be classified into the

following categories: a) Surface-based morphing: consists of continuous mapping of small pieces of polygonal surfaces of source object to those of target object; b) Volume-based morphing: modifies voxel values of a volume data set for smooth transition between source and target shapes.

Surface-based approach uses user-defined control fields such as point fields, line fields etc. during morphing to map key features of source and target objects ((Hong, 1988), (Parent, 1992), (Lazarous, 1994), (Turk, 1999), (Lee, 1999)). Surface-based methods are important because of its ability to morph between objects of different types of genus, but these methods also require a significant amount of user input. Another troubling feature of surface-based method is the problem of selfintersection. It cannot guarantee that polygonal surfaces will not pass through themselves, creating self-intersecting intermediate result as found in (Hong, 88).

Volume-based approach alleviates some of the problems mentioned above. Among them, the simplest approach is the cross-dissolving method (Hughes, 1992) which at first transforms volume data from spatial domain to frequency domain by Fourier transform, then linearly interpolates volume in frequency domain and again transforms back to spatial domain. To enhance the smoothness of the in-between volumes, Fourier transform has been used by gradually removing high frequencies of source model, interpolating over to the low frequencies of the second model and smoothly adding in the high frequencies of the second model. But Fourier transform does not localize in spatial domain. In order to have a smooth transition, voxel values of the entire volume are modified according to the distance of the nearest iso-surface. This problem can be solved by Wavelet transformation (He, 1994), which localizes both in frequency and spatial domain resulting in a multi-resolution fashion so that high frequency distortion can be adjusted at the desired level.

Both of the above mentioned methods have difficulties in specifying slightly complex geometric transformations such as object rotation. By relying on the frequency information, the methods would also have difficulties while associating with some scalars such as colors, opacities and texture. This problem can be alleviated by applying warping before interpolation as found in (Lerois, 1995). Here user-defined warp is applied on source and target objects to resemble each other. Warped source object and target object are then interpolated.

Instead of using point and line control fields in 3-D volume morphing, user-specified disk field (Chen, 1996) can be used. Equal number of disks are applied on both source and target to establish correspondence between them. Each disk has its own normal direction which helps in considering distortion of the body.

Payne et al. introduces 'Distance Volume' measured by computing the shortest distance of each voxel within the volume to the surface of the object. Distance field is transformed to a function to meet greater, equal or lesser "blobbiness" between the source and target objects. Once the distance field for the input surfaces are computed, interpolation is performed in between the surfaces.

In (Breen, 2001), the way in which points on the surface moves is used to establish connection between source and target. Every point on the source surface moves in the direction of the normal at that point with a velocity proportional to the signed distance at that point in 3-D space from target surface and vice-versa. Those parts of source which are outside the target contract whereas inside parts move in the direction of surface normals and expand.

Shape transformation using implicit function (Turk, 1999) is constructed by reducing a 3-D volume to a stack of 2-D slices along any of the major axes. Implicit functions of each pair of 2-D slices are determined using a set of constraints i.e. location, weight, scalar values etc. The resultant 2-D

contour is established by interpolating each pair of implicit functions and this is repeated for each pair of slices between source and target objects along the third axis.

From the above discussion, it is obvious that volume-based approach has got some advantages over surface-based approach though each approach has its own advantages. It is imperative that we strive to develop a new volume-based morphing algorithm which optimizes user input, considers rotation/orientation of rigid body during morphing and preserves smooth transition between source and target.

3 ALGORITHM OVERVIEW

The algorithm mainly consists of the following major steps :

- Data Traversal and Slicing of Data;
- Boundary Extraction;
- Boundary Projection and Boundary Interpolation;
- Orientation and Translation of Boundaries;
- Surface Reconstruction.

3.1 Data Traversal and Slicing of Data

Source and target data are collected. The initial orientation along which the data are subdivided in the first step of the binary subdivision is defined along any of the directions of the Oriented Bounding Box (OBB) (Gottschalk, 1996). An Oriented Bounding Box (OBB) is a bounding box that does not necessarily align itself along the coordinate axes. OBB is constructed from the mean and covariance matrix of the cells and their vertices that define the dataset. The eigen vectors of the covariance matrix are extracted, giving a set of three orthogonal vectors that define the alignment of the dataset. Figure 1 shows the difference between a normal bounding box and an oriented bounding box. No doubt, an oriented bounding box more closely fits the data than a normal bounding box. The purpose of choosing the oriented bounding box is to allow checking of the longitudinal direction of dataset from its oriented bounding box rather than from normal bounding box. The OBB only bounds the "geometry" attached to the cells if the convex hull of the cells bounds the geometry. This is done in order to negate the effects of the extreme distribution of the points.



Figure 1: (a) Normal Bounding Box and (b) Oriented Bounding Box.

Eigen vectors describe the maximum, medium and minimum variance of concentration of point clouds. Usually either maximum or medium direc tion of the eigen vectors are used as the direction of the initial alignment. The 'maximum' direction shows the maximum amount of concentration of the cells of the data along that direction, whereas the 'medium' direction exhibits less amount of concen tration than maximum direction and the 'minimum' direction shows the least amount of concentration or the least alignment of the cells along that direction. The first subdivision takes place along a plane centered at the center of the Oriented Bounding Box (OBB) of the object with normal along the initial alignment. This step, called 'step 0', divides the data into two end parts. In each of the subsequent steps, the number of slices is doubled.

In the next step i.e. 'step 1', each of the two end pieces found from 'step 0' is wrapped with OBB and tested whether the longitudinal direction of the alignment of the sliced end is still within the maximum or medium direction of the OBB. If the alignment is still within maximum/ medium direction, a line joining the center of the previous cut plane and the center of the OBB is used as the direction of the cut plane normal for the ends in that step (Figure 2). Otherwise ends are sliced along the cut plane normal found in the previous step which is used for any further subdivision of the ends and in the subsequent steps no further checking on the alignment is done. At the end of 'step 1', the data is divided into four parts i.e. two end parts and two middle parts.

Before further subdivision of the ends, if necessary, checking is done for the alignment of the two sliced ends. The procedure described in 'step 1' is followed for further subdivision of the two ends. For the middle parts, data is sliced along the plane with center as the center of the OBB and normal directed along the resultant normals of the two ends of the middle data (Figure 2(a)). Slicing is continued along the longitudinal direction until the desired number of steps is reached. In each subsequent step, the number of slices is doubled at each step. The default longitudinal direction is the 'maximum' direction of the eigen vectors and the default number of steps for binary subdivision of the data is 'four'. To provide more flexibility, the initial longitudinal direction as well as the number of steps can be defined by the user. We indicate the maximum alignment as '0', the medium alignment as '1' and the minimum as '2'. Therefore, the users are allowed to vary the morphed output based on the initial alignment. Subdivision can also be forced to happen along any particular direction or along any of the axes i.e. x, y or z to generate parallel slices.



Figure 2: Division of (a) the End Data and (b) the Middle Data.

The steps involved in slicing a given data with default initial settings are depicted in Figure 3. After reaching the desired number of steps, cut edges of the ends are usually still a bit far from the tip. In order to extract a proper outline of the object, ends near the tip need to be extracted. For this purpose, two ends are traversed along the tip. Usually no fur ther checking for the alignments of the two ends are needed now as the current alignments of the sliced ends are usually not along the maximum or the medium direction of the OBB of the two sliced ends. So for any further subdivision, the normal is usually along the direction which was found at the step before the last checking step and traversing towards the tip is continued along that direction until it is close enough to the tip. Now the ends are again divided into two parts. At this stage, each of the two end slices which were found at the end of the last step consists of two end parts with very thin top ends near the tips as shown at the bottom of Figure 3.



Figure 3: Traversal and Slicing of a Given Data.

3.2 Boundary Extraction

Only boundaries of the slices are extracted (Figure 4). As discussed above, in 'step 0', data is divided into two parts. In each of the subsequent steps, the number of slices are doubled. Hence in 'step 4', there are $2^{(4+1)}$ i.e. 32 slices. From 32 slices 31 boundaries can be extracted. Then boundaries at the ends which are determined after the specified number of steps is reached are also added. Two such boundaries each. Hence in 'step 4', the number of extracted boundaries (for each source and target) is computed as follows:

$$2^{(\text{step}+1)} + 1 = 2^{(4+1)} + 1 = 2^5 + 1 = 33$$



Figure 4: Extraction of Source and Target Boundaries.

3.3 Boundary Projection and Boundary Interpolation

Both source and target boundaries are projected onto the XZ plane and centered at the origin. Each of the source and target boundaries are traversed along the direction of their minimum $X(X_{min})$ to maximum X (X_{max}) with a traversal plane defined as (1,0,0). For each source and target boundaries, traversal spacings are determined separately. Equal number of traversals is performed for both source and target data. Traversal spacing is determined as follows:

Spacing = $(X_{max} - X_{min})$ /Number of Traversals

Source and target boundary points are extracted from the traversals. If the number of extracted points in any cut plane happens to be odd, it is made to be even. Next interpolation is performed onto the XZ plane. For simplicity linear interpolation is used in our implementation. Here it should be noted that only one normal is extracted per boundary regardless of whether any particular boundary consists of multiple holes or empty spaces. Also each boundary has one center irrespective of the irregular geometric configuration of that particular boundary.

Three special cases need to be considered during interpolation. They are as follows:

Case 1: Both Source and Target Boundaries Contain no Empty Spaces. Source points are just interpolated with target points. Enhancement of the interpolation process can be carried out when both source and target have equal number of regions and there are more than one region in both. Region is an area where the number of points extracted by the cut plane is the same while traversing along the X axis. In Figure 5, both source and target boundaries consist of equal number of regions i.e. 3 (two 2point region and one 4-point region). Hence the interpolated point clouds also have three regions.

Case 2: Only One of the Source and Target Boundaries Contains Empty Spaces. The number of empty spaces is calculated for the boundary which contains empty spaces. Then equal number of empty spaces are inserted into the other boundary so that empty space will appear in the interpolated point clouds.

Case 3: Both Source and Target Boundaries Contain Empty Space. When there are equal number of empty spaces in both source and target boundaries, we have equal number of regions. Thus corresponding regions from both source and target can be interpolated. However when there are unequal number of empty spaces/ regions, rightward and leftward traversals are carried out until either one of source or target is exhausted (Figure 6). Corresponding regions during the traver -sal are just mapped and interpolated while the remaining regions can just be mapped if the exhausted side ends with an empty space. Otherwise a process similar to Case 2 above is applied by inserting into the region of the exhausted side the same number of empty spaces left in the non-exhausted side.



Figure 5: Interpolation of Points after Region Separation.

3.4 Orientation and Translation of Interpolated Boundaries

Each of the interpolated boundary already projected onto the XZ plane is oriented along the resultant normal of each of the source and target boundaries and translated to the average center of each of source and target boundaries (Figure 7). When all the interpolated boundaries are oriented as well as translated, we get the outline of the morphed output. Figure 8 describes this sequence.

3.5 Surface Reconstruction

From the stack of oriented and translated bounda ries, surface of the morphed object is constructed. Each of the boundaries merges with the next boundary by dividing the in-between space of the two consecutive boundaries into a number of cells and each cell is connected to its neighboring cells. Sur face construction is performed by only considering each of the two consecutive boundaries.



Figure 6: Interpolation case when there are unequal number of empty spaces between source and target.



Figure 7: Orientation and Translation of a Single Interpolated Boundary.



Figure 8: Orientation and Translation of All Interpolated Boundaries.

This simplifies the overall surface reconstruction process as where data is highly irregular, necessary modification among cell coordinates is limited to only two consecutive boundaries. Surface reconstruction in detail is discussed next.

3.5.1 Separating Disconnected Region

Each consecutive boundary may have regions which are disconnected from one another (Figure 9(a)). Nearest neighbor searching is carried out to find this kind of regions. The disconnected regions are horizontally mapped (for better effect) and the other regions are to be vertically mapped (Figure 9(b)). The details of the vertical mapping are discussed in the next sub section.



Figure 9: Separating Disconnecting Regions between Two Consecutive Boundaries.

3.5.2 Basic Cell Construction

After region separation, two consecutive point/ cell arrays (representing two consecutive slices) are obtained and vertically mapped. The two arrays which contain the number of interpolated points at each index need to be compressed so that the process of mapping can be carried out in an easier and straightforward manner.



Figure 10: Basic Cell Construction between Two Consecutive Interpolated Boundaries.

Figure 10 shows the process of compressing two consecutive arrays. In the compression, the arrays are transformed into two new arrays each: region number array (where region numbers are stored) and number of occurrences array (where the number of occurrences of each region number are stored). Firstly, the size of both arrays should be made equal using a heuristic approach. Sometimes some index values are dissolved and some are omitted in order to make the size of both arrays equal. Corresponding values of the number of occurrences arrays should also be made equal so that they are ready to be vertically mapped. In the case of unequal values, the larger of the two values is made equal to the smaller number by removing excess number of that particular number of occurrences value. Corresponding numbers in the two region number arrays should also be equal for the purpose of vertical mapping. If they are not equal, a further processing needs to be done. The process starts with finding the nearest matched index values of the region number arrays by traversing to the left and the right. The nearest matched values will ensure continuity between different-numbered hetter regions. Next the corresponding region numbers are split into two portions where the values of the region number of the first portion is derived from the

continuous mapping of the nearest matched index values to the corresponding region number values and the values of the region number of the second portion are the remaining region numbers resulting from the split. In the example (Figure 10), the first discrepancy occurs at index number '2' and the nearest matched values are at index number '1' with a value of '4' and '4'. The current values (i.e. 8 and 6) need to be split into two portions. The first portions are made equal to '4' and the second portions are assigned the remaining values (8-4 = 4)and 6-4 = 2). At the end of the entire processing, two sets of region number arrays are obtained. The top set (Figure 10(a)) now consists of equal region number and can therefore be vertically mapped whereas each of the bottom set (Figure 10(b)) is to be horizontally mapped separately. Enhancement is carried out in surface reconstruction when empty space is met or at the transition point between two different-numbered regions.

4 IMPLEMENTATION AND RESULTS

The algorithm has been implemented using C++ with Visualization Tool Kit (VTK) as graphics plat form. In Figure 11(a), a sequence of three intermediate stages is generated using '5' as the number of steps with the initial direction of traversal for source as well as target along the maximum direction of the eigen vector i.e. 'alignment = 0'. Using '4' as the number of steps, the same sequence is generated without producing major distortion to the eye. As the number of step increases, the number of slices is doubled which also increases the overall run time.

Figure 11(b) shows the morphing sequence between two tori each with different radius with the initial direction of traversal along the minimum direction of eigen vector i.e. 'alignment = 2' for both source and target. In Figure 11(c), a morphing sequence between a complex object and a bent pipe has been generated. Here the initial direction of traversal for the source is along the minimum direction of eigen vector i.e. 'alignment = 2' whereas the initial direction of traversal for the target is along the maximum direction of eigen vector i.e. 'alignment = 0'. Figure 11(d) shows the morphing sequence between a conic spiral and a torus with the initial directions of traversal for both source and target along the maximum direction of eigen vector i.e. 'alignment = 0'.



Figure 11: Morphing Sequence between Source (left most) and Target (right most) for Different Eigen Vectors as Initial Direction of Traversal.

As highlighted in Section 3.1, the initial direction of traversal can also be forced to happen along the principal axis. In Figure 12(a), morphing sequence between a teapot and a parametric surface 'dini' has been generated. Here the initial directions of traversal for both source and target are along the Yaxis. Figure 12(b) shows the morphing sequence between a cow and a cylindrical object. Here the initial direction of traversal for the source is along the X-axis and the initial direction of traversal for the target is along the Y-axis.



Figure 12: Morphing Sequence between Source (left most) and Target (right most) for Different Principal Axis as Initial Direction of Traversal.

Figure 13 compares the gradual morphing sequence between the same source and target as used in Figure 11(a) when initial direction of tra - versal for source/ target changes. Figure 13(a) shows the gradual transformation between source and target when the initial directions of traversal for source and target are along medium and maximum direction of the eigen vector i.e. 'alignment = 1' and 'alignment = 0' respectively. Figure 13(b) shows the morphing sequence when the initial directions of traversal for both source and target are along the minimum direction of eigen vector i.e. 'alignment = 2'.



Figure 13: Morphing Sequence between the Same Source (left most) and Target (right most) for Different Eigen Vectors as Initial Direction of Traversal.

Instead of principal axis, if morphing sequence is generated along the longitudinal direc -tion, warping in rigid body is also considered when it is needed. Figure 14 compares this situation. In Figure 14(a), the morphing sequence is generated with initial direction of traversal along the principal axis X and Y for source and target respectively whereas in Figure 14(b), the morphing sequence is generated with the initial direction of traversal for both source and target along the maximum direction of eigen vector i.e. 'alignment = 0'.



Figure 14: Morphing Sequence between the Same Source (leftmost) and Target (rightmost) with (a) Principal Axis and (b) Eigen Vector as Initial Direction of Traversal.

5 DISCUSSION

This section compares the proposed algorithm with some other existing morphing algorithms on the basis of a number of criteria for good morphing. Most surface-based methods consider the distortion/rotation of the rigid body, but division of both source/ target into a number of morphing patches or meshes is needed at the expense of a large number of user input and longer pre-processing stage ((Kent, -1992), (Lazarous, 1994), (Gregory, 1998), (Breen, 2001)). The proposed algorithm works without any user input with default initial settings ('number of steps = 4' and 'alignment = max'). If variations in the number of steps and alignments are desired, the user just needs to specify these two variables. The number of slices can also be reduced by varying the number of steps. This automated method of reducing the number of slices as well as run time is absent in the most other algorithms. In most other existing algorithms, specific number of user-defined disk fields (Chen, 1996) or point/line fields ((Kent, 1992), (Lazarous, 1994), (Gregory, 1998), (Breen, 2001)) are used. Varying these fields involves a considerable amount

of user intervention and longer pre-processing time: minor variation in these fields can generate a major variation in the output. The proposed algorithm automatically traverses the data along its alignment and is free from any inaccurate user intervention and at the same time if needed allows user to specify the initial direction of traversal.

Simplicity is one of the major characteristics of the proposed algorithm. Some early surface-based algorithm preserves this feature but at the same time fails when the object is a bit complex producing selfintersecting intermediate objects (Hong, 1988). In the proposed algorithm, aligned slices are extracted from data traversal and before interpolation, slices of the corresponding source and target slices are projected onto the XZ plane. Hence chances of selfintersection are very slim as that can happen when triangulated surfaces are interpolated or extracted slices are not properly aligned.

Another important feature of a good morphing is that intermediate outputs should be confined to the geometric features of source and target only. However sometimes unnecessary fea -tures are also seen among the intermediate morphed objects ((Gregory, 1998), (Kent, 1992)). In the pro -posed algorithm smooth transition takes place bet -ween source and target. Orientation as well as rota -tion of a rigid body are preserved while morphing.

Some volume-based methods use discrete mathematical function in morphing between complex objects ((Hughes, 92), (He, 1994), (Turk, 1999)) generating smooth output using sophisticated interpolation technique. But interpolation is only one facet of morphing. The major shortcoming of these methods is that they overlook the curvature of rigid body while morphing, which is one of the most important properties needed to be considered for morphing between curved objects. The proposed algorithm nicely fills in the gap. Some volume-based algorithms alleviate this problems ((Payne, 1992), (Breen, 2001)). However they are highly sensitive to the user-specified initial overlapping of source and target. These methods have weakness around the regions of high curvature: accuracy of intermediate objects also depends on the accuracy of user-defined overlapping of source and target. This sometimes results in incomplete morphed output in case of curved objects. The proposed algorithm shows more consistency than these methods.

In the proposed algorithm, instead of traversing along the longitudinal direction of data, traversal can also take place along any particular direction producing different morphing sequences. This flexibility may be difficult to achieve in surfacebased algorithms or in some volume-based algorithms which exhibit characteristics like surfacebased algorithms (Lerois, 1995). Some volumebased algorithms can consider this but may involve considerable user intervention ((Payne, 1992), (Chen, 1996), (Breen, 2001)). Morphing involving discrete mathematical functions for interpolation ((Hughes, 1992), (He, 1994), (Turk, 1999)) is capable of traversing along only a specified direction.

Now let us analyze the algorithm in terms of efficiency. In field morphing, control data sets are used to specify coordinate mapping hence time complexity is usually $\Theta(nm)$ as all coordinates of a single dataset are more or less influenced by all control fields (Chen, 1995). Here 'n' is the size of volume and 'm' is the number of control fields. In the proposed method, control fields i.e. slices are automatically determined during data traversal and these control fields have little influence or control in coordinate mapping: only coordinates of respective boundaries are influenced. Hence if the number of extracted coordinates from each boundary is 'p' and the number of automatically defined slices ('m') are considered as control fields, then time complexity is $\Theta(mp + m)$. Here 'mp' can be equated with the volume size 'n' hence time complexity for the proposed algorithm is $\Theta(n + m)$ which is much less than volume morphing using disk field $\Theta(nm)$ (Chen, 1996).

6 CONCLUSIONS

Simplicity and flexibility are two major characteris tics of the proposed algorithm which have made it more dynamic and extendible than other existing morphing algorithms. Future work includes exten ding the algorithm in order to show the extendibility of the method by incorporating influence shape while morphing including multiple influences and exploitation of the method in parallel/distributed computing environment as simple data structure of sliced body and binary subdivision is suitable for both data as well as functional partitioning.

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