Inferring shape evolution

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Abstract

Dynamic shapes represent an important issue in several scientific and technological contexts. The current article presents a model-based mathematic-computational approach for inferring the processes of neural evolution, including analytical mappings, convolution models and normal wavefront propagation, illustrated with respect to stationary and non-stationary evolutions along time and space.

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1. Introduction

Most processes in science and nature involve objects whose shapes change with time. The growth of a leaf, a cell, an organ or a crystal, as well as the erosion of a rock, provide just a few examples of such dynamical shapes. The geometrical study of such processes can therefore yield valuable information for understanding the related physical or biological phenomena. For instance, as the evolution of a neural cell is known to be defined by intrinsic factors, such as the genetic content, as well as extrinsic effects (influence fields such as gravity, electric fields, neurotrophic gradients, etc.; Lasek and Black, 1986), the identification and geometrical characterization of the processes acting over the shape can provide valuable indication about the biochemical processes underlying the development of the nervous system. However, in spite of its promising potential, the systematic investigation of shape development has proven to be particularly challenging given the infinite variety of possible morphing processes. For instance, a shape can inflate or deflate, and even exhibit drastic changes over short time periods (a popcorn, for instance), involving local and/or global modifications. Mathematically, there is no limit to the number of theoretically possible morphing processes, which can even include bizarre situations unlikely to be verified in nature. Indeed, most of the natural morphing processes are characterized by a relatively smooth evolution of the shapes, which restricts our attention to a reduced number of particular processes, such as

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those involving evolution along the direction normal to the object surface (dilations, progressive accumulation of material around objects, and wavefront propagation presented in (Sethian, 1999) as well as convolutions). Such relatively restricted classes of natural shape evolutions have motivated the approach reported in this paper, namely a model-based methodology for identifying and characterizing morphing processes in nature, with special attention given to biology and physics. More specifically, a limited number of processes are considered and some tests are devised in order to verify if a given situation is possibly governed by any of them and, if so, what are the involved parametric settings. The critical issue of the correspondence between seriated sections is also discussed, thus justifying the adopted alternative of using curvature singularities as control points. Non-stationary situations (i.e. involving different settings along time or the shape position), which are likely to occur in nature, are also addressed.

The article starts by presenting the basic concepts and reviewing the main related literature, and proceeds by describing the proposed model-based methodology and the main considered morphing processes, which are illustrated with respect to synthetic and real examples. Given a sequence of images representing the development of a neural cell, our approach includes the verification of coincidences between the mathematical models and the experimental data. Such knowledge is essential not only for better understanding neural cell evolution, but also as a means for implementing realistic neural growth models and simulations. Although the paper focuses on two dimensional (2D) shapes, the reported results can be extended to higher dimensional shapes.

2. Basic concepts in shape evolution

As suggested in (Costa and Cesar, 2000), a 2D shape is henceforth understood as a connected set of points (in both continuous and discrete image spaces, implying suitable respective definitions of connectivity), and a morphing process is henceforth understood as the mathematic characterization of the evolution of a shape along a given period of time. Fig. 1 shows the basic representation of an evolving 2D binary shape, where the original contour \( c(s,t_0) = (x(s,t_0), y(s,t_0)) \), i.e. a time dependent curve parameterized along \( s \), undergoes a continuous series of transformations (of which just a few are presented in the figure) along the time \( t \). Each instance of such a process is henceforth represented in terms of the contour \( c(s,t) = (x(s,t), y(s,t)) \). Filled shapes can be addressed in terms of their borders, which can be obtained by applying conventional edge detection approaches (Costa and Cesar, 2000).

Observe that \( \hat{c}(s,t) = (\hat{x}(s,t), \hat{y}(s,t)) \) is the velocity of the shape along time, i.e. a vector field defined along \( s \) for each time instant \( t \), in such a way that \( \hat{c}(s,t + \Delta t) \cong \hat{c}(s,t) + \hat{c}(s,t)\Delta t \). Mathematically, a 2D morphing process can be defined in several ways, such as by using differential equations, analytical mappings, 3D surfaces, and convolution models. An example of the former situation is the equation \( \hat{c}(s,t) = a\tilde{n}(s,t) \), where \( a \) is a real constant and \( \tilde{n}(s,t) \) is the unit normal field to the curve oriented with respect to the inside and outside of the shape, i.e. the curve evolves along its normal with speed magnitude \( a \). The normal model is particularly suitable for treating situations where the shape is uniformly dilated, such as by internal pressure, by deposition of material along its surface, or where the shape evolves as a propagating front (Sethian, 1999). In the case of analytical mappings, the next instance of the curve (considering time step \( \Delta t \)) is represented as a vector function of the previous shape instance, i.e. \( \hat{c}(s,t + \Delta t) = f(\hat{c}(s,t)) \). The 3D surface approach involves the surface defined by \( \hat{c}(s,t) \) as time varies.

Finally, convolution models involve expressing the shape changes in terms of the convolution, described as \( \hat{c}(s,t + \Delta t) = \hat{c}(s,t) \times h(s,t) \), where \( h(s,t) \) is the considered convolution kernel. This
model nicely reflects several situations where the shape speed is defined by the weighted linear combination of values of some physical property around a neighborhood in each of the shape elements. Fig. 1 presents examples of such a type of evolution considering a Gaussian convolution kernel (low-pass filtering or blurring).

3. Correspondence

Given any two instances \( \bar{c}(s, t_1) \) and \( \bar{c}(s, t_2) \) of a morphing sequence, a critical issue is the association of correspondences between each of the elements of these two curves. In other words, such associations indicate where a point in the first curve has been mapped along the second curve. Observe that such a mapping is not always one-to-one and onto, since some points may be created and others eliminated. This association problem, commonly known as correspondence or registration between the shapes, which is closely related to the shape velocity, is not easily solved since it ultimately involves the knowledge of the respective morphing process governing the specific shape dynamics, which is the very objective of the investigation.

To cope with this problem, a possible solution is somehow to mark reference points, henceforth called control points, along the natural shapes. However, as this is rarely possible, especially at microscopic scales, some alternative scheme is necessary in order to define at least some reliable correspondences along the subsequent shape instances. In the present work, the landmark or control points, discussed in (Bookstein, 1978; Leyton, 1992), are obtained using peaks of curvature (i.e. curvature singularities) along the contour of each shape instance, which may demand human intervention.

The procedure for curvature peak detection adopted is based on the spectral approach described in (Costa and Cesar, 1995), which involves the following three steps: (i) calculation of the curvature modulus, (ii) detection of zero-crossings in the first derivative of the curvature modulus, and (iii) identification of negative points of the second derivative of the curvature.

A correspondence can therefore be established by associating curvature peaks that are closest along the curve parameter values. Fig. 2 illustrates the correspondences obtained through this strategy with respect to a specific pair of shape instances. Although this approach can fail in some circumstances (e.g. when curvature peaks disappear during the process), it provides a reasonable approach to the correspondence problem in many cases.

In order to address the many problems related to the correspondence of control points of shapes, a semi-automated process has been developed, which involves a graphic-interactive interface. Such a process allows a human operator either to remove or to add control points whenever necessary (which, in practice, has been done only for about 10% of the control points), and to select similar points in successive images, therefore producing the correspondence pairs. The correspondence task has been greatly improved by an automatic pre-assignment of control points while taking into account the smallest Euclidean Distance between successive shape instances. Despite the simplicity of the adopted approach, the obtained correspondences were found to be of good quality. Another possibility being currently considered involves the use of optical flow (Barron et al., 1994), over the original gray-level images in order to obtain the shape velocity.

4. Shape trajectory

An important aspect to be considered during the shape evolution is the characterization of the
properties exhibited by the morphing process. For instance, they may imply conservation of the information along the shape, in the sense that any previous instance can be recovered from one of the posterior instances (the inverse of the morphing along that time interval). Such processes will be said to preserve information. In case the type and parametric setting of a process does not change along some time interval, the process is henceforth said to be time stationary in that interval. Otherwise it is called non-stationary. The stationary classification can also be extended to the process characterization along the space, e.g. the shape contour, in which case it is said to be space stationary or non-stationary. Observe that some processes can be non-stationary in both time and space. Another interesting characterization of morphing processes is in terms of their continuity and smoothness (i.e. existence and continuity of derivatives) along the spatial and time domain, which can be stated in terms of classical mathematical analysis concepts (e.g. Apostol, 1967).

At the most comprehensive side, the properties and evolution of a morphing process involve mapping the shape state (a vector in the phase space) considering as state variables its x- and y-coordinates parameterized along time, therefore defining a shape trajectory, where specific behaviors of the morphing process can be identified from the analysis of such trajectories. Less comprehensive characterizations of morphing processes are however obtained by using global measures such as the shape perimeter, area, fractal dimension or bending energy, to name but a few, as state variables. Such a possibility, which is typically degenerated (i.e. involves information loss), is more amenable for proper visualization and can still provide valuable insights about general properties of the morphing processes. Fig. 3 shows an example of such a trajectory considering perimeter, radius to maximum value of fractal dimension and fractal dimension for a real sequence of image during growth process.

The estimation of fractal dimension was achieved by using Minkowsky sausages obtained through exact dilations of the shape along the radius scale ($R$), as presented in (Costa and Estrozi, 1999; Costa and Cesar, 2000). The interpolation of non-uniformly spaced points in the loglog plot (area vs. radii) was performed through Gaussian smoothing and the differentiation by using Fourier-based properties. The chosen features were the maximum value of the fractal dimension and the radius for which the maximum fractal dimension is verified.

5. Related works

Although the specific problem of mathematic-computational modeling of shape evolution, at least as far as a more formal and unified approach is concerned, has not received substantial attention from the scientific community at large, several related issues have been independently pursued in a variety of related areas. Among those more closely connected to image analysis and computer vision, we highlight the areas of morphology and pattern formation in (Murray, 1993; Thompson, 1994; Ascoli and Krichmar, 2000), statistical shape analysis in (Bookstein, 1978; Mardia and Dryden, 1998), morphing in (Wolberg, 1998), dynamical contours presented in (Kass et al., 1987; Cootes et al., 1995; Lanitis et al., 1997; Blake and Isard, 1999), registration in (Brown, 1992; Maintz and Viegever, 1998; Van den Elsen and
Viegever, 1993), seriated reconstruction in (Levinthal and Ware, 1972), and biological growth process by Alt et al. (1997) and Oldenbourg et al. (2000).

As far as shape evolution and pattern formation are concerned, a number of approaches have been developed in the literature. For instance, Thompson (1994) describes a 2D discrete growth model using probabilistic and deterministic methodologies, capable of producing anisotropic growth allowing compact, elongated and concave morphologies, and used to describe multiple sclerosis morphology in the brain. Another methodology related to shape evolution is in terms of seriated reconstruction in (Levinthal and Ware, 1972) of images, where each section can be related to a shape instance. Registration approaches have been surveyed in (Brown, 1992; Maintz and Viegever, 1998), and Van den Elsen and Viegever (1993) presents a systematic classification of the existing techniques. Registration is strictly related to obtaining markers from images, which may be extrinsic or intrinsic, and automatic or semi-automatic. One of the most commonly considered techniques involve deformable models (such as snakes or active contours (Kass et al., 1987; Cootes et al., 1995) that are based in a set of intrinsic markers in a semi-automatic way. Morphing is a transformation process where an image is modified until approaching another image. The whole process, discussed in (Wolberg, 1998), can be divided into three steps: definition of a set of correspondences (features) that may be points or lines, the interpolation function (using bicubic spline interpolation, thin plate spline and snakes), and transition.

As far as biological morphing processes are concerned, Alt et al. (1997) provides a comprehensive treatment of cell and tissue dynamics including cell division, aggregation and cooperative motion, as well as morphogenesis processes. As discussed in (Lasek and Black, 1986; Oldenbourg et al., 2000), cell motility and shape formation are believed to be directly related to the polymerization dynamics of actin and actin-associated proteins. The latter encompasses proteins that regulate actin polymerization and establish cross-links between actin filaments inside the meshwork as well as cross-links between the meshwork and integrins, allowing the cell to generate traction forces.

6. Neural culture cells and image acquisition and processing

This section describes the methodology through which the experimental data, related to neural cell development, has been prepared and obtained. Culture ware was purchased from Corning Glass Works (Corning, NY), and medium and other cell culture reagents were obtained from Gibco (Grand Island, NY) and Sigma (St. Louis, MO). The cells used for culture were obtained in Rio de Janeiro Cell Bank (#CR098), the Neuro-2A cell line (mouse neuroblastoma cells). The Cells were grown in a humidified, 37°C incubator in an atmosphere of 95%air–5%CO2. The medium consisted of Dulbecco’s Modified Eagle’s Medium containing 25 mM glucose and supplemented with 10% fetal bovine serum plus 100 units of penicillin, 100 µg of streptomycin sulfate and 0.29 mg of L-Glutamine/ml. For the experiments, cells were plated at 1.0 × 10^5 cells/35 mm treated-Petri dish and grown for two days in the same medium. At this low density, individual cells and neurites could be traced.

A microscope workstation from cell robotics was used for image acquisition of neural cell during growth in the Petri dish. The equipment was coupled to a microcomputer with TV/Video acquisition board and a microscopy Zeiss Axiovert 100/135 enabling real time image acquisition. The cell was placed over a Smart Stage platform, capable of moving in eight directions, that linked with a tool called Cell Selector, allows store positions of visited cell making possible the return in the same cell after a time period. In a Petri dish it was chosen a neural cell, whose images were acquired (amplification of 40×) after nearly 30 s, during 7 min. Despite the relatively short time interval, great modifications of the neural shape can occur from one image to the next, raising difficulties to model the neuron evolution and implying a problem of uncertainty in the registry and in the correspondence of images. For example,
a neuron termination can branch at the next time period, implying one curvature peak to break into two peaks.

7. Methodology and results

This section presents the main morphing processes considered in the present work, the respective tests for identifying their possible participation in a specific shape evolution, as well as their exemplification in a neural cell sequence.

7.1. Segmentation and correspondence

Once the neural cell image sequence has been obtained, a segmentation procedure is necessary in order to separate the cells from the background and other secondary structures. This represents a critical task because the transparency and noise from illumination and immersion environment characterizing the microscopic images can not be properly dealt with automatically by using standard linear filters as discussed in (Costa and Cesar, 2000). Such problems have been minimized in the current approach by performing edge detection under human assistance. The inherent advantage of this approach, at the expense of speed, is that humans are experts in edge detection even in presence of strong distortions and noise, and also acquainted with the types of neural cells under consideration. Thus, segmentation was done manually considering not only the current image in the sequence, but also the previous and next instances. Once the segmented image contours is obtained, the next step involves the identification of the control points and respective correspondences. As mentioned before in Section 3, control points were obtained from the curvature peaks (negative and positive) of the sequence of contours.

7.2. Analytical mappings

In this approach, the next instance of the shape evolution is specified as an analytical function $f$ of one of its previous instances, i.e., $c_x(s, t + \Delta t) = f_x(\tilde{c}(s, t))$ and $c_y(s, t + \Delta t) = f_y(\tilde{c}(s, t))$.

A straightforward approach to this problem is to represent the functions $f_x$ and $f_y$ in terms of polynomials or orthogonal series defined on the coordinates of the previous shape instances. This is followed by interpolation, such as in minimum squared methods, which minimizes the differences between the estimated and real values of the coordinates along the second shape instance (Kay, 1993). An alternative approach that allows the incorporation of general knowledge about the morphing process is to consider a variational solution taking into account additional restrictions such as several degrees of smoothness. In such situations, it is interesting to identify some of the most relevant points along the two shape instances (i.e. the control points, as mentioned in Section 3) and to obtain the remaining points by using the variational approach. One such a possibility is to use 2D thin-plate splines presented in (Costa and Cesar, 2000), which impose minimal energy restrictions, to interpolate between the shape control points. Fig. 4(a) presents the previous (in black) and next (in gray) shape instances, and Fig. 4(b) illustrates the latter (in gray) and its reconstruction obtained from the control points by using thin-plate splines (in black).

7.3. Differential equations

As outlined in Section 2, several morphing processes can be properly modeled in terms of
differentialequations. At present we are especially interested in the two following situations: (a) where the speed is oriented along the normal to the shape contour and (b) the differential evolution is modeled in terms of convolutions involving the respective Green function (Boas, 1983). These possibilities are covered in more detail in the following sections.

7.3.1. Normal evolution

In this case, the shape velocity \( \hat{\mathbf{c}}(s,t) \) at instant \( t \) is oriented along the normal \( \vec{n}(s,t) \) to the shape contour, i.e., \( \hat{\mathbf{c}}(s,t) = f(s,t)\vec{n}(s,t) \), where \( f(s,t) \) is a general function of \( s \) and \( t \) corresponding to the speed magnitude. In case \( f(s,t) = a > 0 \), the shape dilates with constant speed \( a \). If \( a < 0 \) the shape shrinks with constant speed.

The procedure of normal evolution investigation consists in examine if a specific instance of a shape has evolved along the normal with respect to a previous configuration; this hypothesis is tested by comparing the velocity field with the normal to the previous instance. Therefore, provided we have the correspondences, the velocity field and a means to estimate the original normal, for instance by using the Fourier transform derivative property described in (Costa and Cesar, 1995), normal evolution can be tested for each of the shape portions.

Since curvature peaks have been assumed as control points, unwanted sensitivity of the normal vectors near sharp contour extremities (see Fig. 4) tends to deteriorate the above proposed test for normal evolution. Therefore, it is interesting to

Fig. 5. Sequence of an evolving neural shape and the velocity (gray) and normal fields (black) at the control points.
avoid defining control points at particularly sharp curvature peaks. Given the sequence of real images obtained during the considered neuron growth sequence, Fig. 5 presents some results of the normal test considering two subsequent shape instances. For the sake of better graphical representation, the sequence is zoomed at a specific branch of the cell. At each control point (in gray), the shape velocity is presented as gray vectors and the normal as black vectors.

The shape speed provides an interesting local measure of the changes taking place along the shape. As with the general problem of shape dynamics identification, the magnitude inference can be done based on a model approach considering the most common schemes verified in natural processes. Currently we are particularly interested in situations where the speed magnitude is constant or proportional to the contour curvature. In order to better quantify the adherence of the normal evolution model with respect to the obtained image sequence, histograms of the signed angles between the control point speed vectors and the respective normal directions have been calculated and shown in Fig. 6(a), for termination points, and (b), for branching points. Other features in such a histogram can also be very helpful. For example, a clear peak in this histogram would indicate that a portion (or even the whole) of the shape is being translated as a consequence of some external influence.

Another particularly interesting approach for description of normal evolution in contours can be done in terms of dilations of first instance contour. Given two consecutive contours, dilation in normal direction is performed over the first one and hit and miss values are obtained by considering the first contour and its dilated version. The value used for dilation is obtained from the median value of the Euclidean distance between control points. The results presented in Fig. 6(d) and (e) indicate a higher number of non-coincidences between the vectors at successive images, thus suggesting that the studied process does not follow evolution through normal dilation.

7.3.2. Convolutive processes

The more general case of time non-stationary convolution (the convolution kernel is a function

![Fig. 6. Angles between the control point speed vector and contour normal vector at positive (a) and negative (b) curvature points, and the distribution of the angles between the speed and the horizontal direction (c). Hit (d) and miss (e) obtained for normal evolution considering all pairs of images in the experimented neural development sequence.](image-url)
of $\xi$) in a continuous domain can be represented in terms of the following expression:

$$c_x(\xi, t + \Delta t) = \int_0^L c_x(\xi - s, t) h_x(\xi, s, t) ds$$

where $h_x(\xi, s, t)$ is the convolution kernel acting at the neighborhood of the parameter position $\xi$. The non-stationarity along space arises from the fact that different kernels are verified at different positions. Fig. 7 illustrates a spatial non-stationary convolutive morphing process characterized by two Gaussians with different standard deviations adopted as convolution kernels ($\sigma = 1$ and 7, respectively).

The currently considered approach for checking if a specific morphing processes involves a spatial non-stationary convolutive model consists in obtaining a system of linear equations defined by the internal product between the several convolution kernels (the unknowns) and the shape contour, which are taken as extending $L$ positions to both sides along the curve parameter domain. Each sought convolution kernel is applied to $Q$ points along both sides of the parameter domain, yielding $2Q + 1$ equations for each point of the shape contour, and $2L + 1$ variables. After obtaining such a set of equations, the convolution kernels can be estimated by applying the pseudoinverse approach (Jennings, 1980). In order to cope with instabilities, the ridge regression approach discussed in (Hoerl and Kennard, 1970), a kind of first order regularization (Tikhonov and Arsenin, 1977) has been adopted. Fig. 7(c) presents some of the convolution kernels obtained by using the approach described above over the pair of subsequent shape instances. The noisier recovered kernel at the lower left corner of the figure is a consequence of the fact that it was estimated near one of the transition regions of the convolution, i.e. a position affected by the proximity of two different convolution kernels.

8. Conclusions

A novel model-based approach to identify and characterize natural morphing processes has been reported, discussed, and illustrated with respect to several synthetic and natural shapes. The methodology involves testing for several of the most plausible shape evolutions found in nature, including non-stationary situations along time and space. The obtained results have substantiated the potential of the approach, which is being currently applied in order to investigate the development of neural cells as well as embryos.

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