

INFERRING SHAPE EVOLUTION

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Abstract: Dynamic shapes, namely shapes that change with time, represent an important issue in several scientific and technological contexts. The current article presents a model-based mathematic-computational approach for inferring the processes governing some of the most representative types of shape evolution, with special attention given to biological shapes. The considered models include functional mappings, convolution-based evolution and normal wavefront propagation. The methods are illustrated with respect to stationary (global) and non-stationary (local) dynamic evolutions, and the obtained results substantiate the potential of the presented methodology. Although concentrating on 2D shapes, the reported results can be extended to higher dimensional objects.

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 changing shapes. The geometrical study of such dynamical processes can yield valuable information for understanding the related physical or biological phenomena. For instance, as the evolution of a neural cell is known [1] to be defined by internal factors, such as gene expression and external effects (influence fields such as gravity, electric fields, neurotrophic gradients, etc.), the identification and quantitative geometrical characterization of the processes acting over the shape can provide valuable indication about the biochemical processes underlying the nervous system. However, in spite of its potential, the endeavor of investigating the processes involved in shape evolution has been particularly challenging given the infinite variety of possible morphing processes. For instance, a shape can grow while being attracted by an external field. In other circumstances, 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. Other evolutions may be governed by the physical properties at each neighborhood of the shape, and it is also common to verify combinations of the above possibilities. Mathematically, there is no limit to the number of 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, and restricted to some particular classes of processes, such as those involving evolution along the normal surface (dilations, progressive accumulation of material around objects, and wavefront propagation) as well as convolutions (solutions of differential equations in terms of Green functions).

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 specific morphing processes are considered and specific tests are devised in order to verify if a given morphing sequence 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, 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) are also considered.

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 several synthetic and real examples. Although the paper focus 2D shapes, the reported results can be extended to higher dimensional shapes.

2 Basic Concepts

As suggested in [2], a 2D shape is henceforth understood as any connected set of points (in both continuous and discrete image spaces). A *morphing process* is henceforth understood as the mathematic-computational characterization of the evolution of a shape along a time period. Figure 1 shows the basic mathematical representation of an evolving two-dimensional binary shape, where the original contour $\vec{c}(s, t_0) = (x(s, t_0), y(s, t_0))$, 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 its contour $\vec{c}(s,t)=(x(s,t),y(s,t))$, which can be obtained by applying conventional edge detection approaches [2].

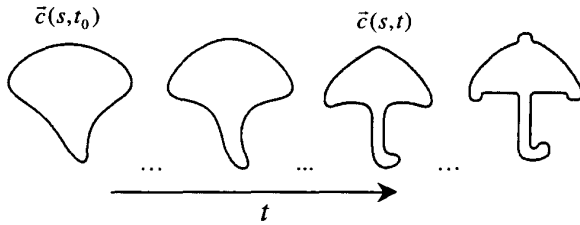


Figure 1 The basic representation of a morphing process in terms of the parametric contour of the involved shape.

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

Finally, *convolution models* involve expressing the shape in terms of the convolution $\vec{c}(s,t+\Delta t)=\vec{c}(s,t)*h(s,t)$, where $h(s,t)$ is the considered convolution kernel. This model nicely reflects several situations where the shape speed is defined by the weighted combination of the values of physical properties around a neighborhood of each of the shape elements. Figures 1 and 2 present examples of such a type of evolution considering a Gaussian convolution kernel (low-pass filtering or blurring).

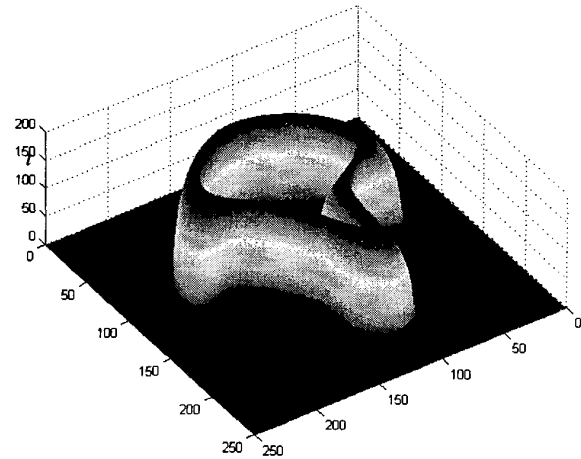


Figure 2 3D Surface representation of a 2D morphing process.

Given any two instances $\vec{c}(s,t_1)$ and $\vec{c}(s,t_2)$ of a morphing process, an important 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 as it ultimately involves the knowledge of the respective morphing process governing the specific shape dynamics. A possibility to cope with this problem is to mark in some way reference points, henceforth called *control points*, along the natural shapes (for instance painting points along the surface of a growing apple). However, as this is rarely possible, some alternative scheme is necessary in order to define at least some reliable correspondences along the subsequent shape instances. In the present work, the correspondences are established between landmark points [3, 4] defined by peaks of curvature (i.e. curvature singularities) along the contour of each shape instance, which may demand human intervention [5,6]. The procedure for curvature peak detection adopted in the present work involves three steps, according [7]: (i) calculation of curvature modulus, (ii) detection of zero-crossing of first derivative of curvature modulus, and (iii) identification of negative points of second derivative of curvature. Figure 3(a) presents a contour and its respective detected curvature peaks, 3(b) shows the curvature modulus along contour ($\sigma=20$), (c) and (d) its first and second derivatives, respectively, and (e) the curvature along the contour with marked peaks, for a curvature modulus threshold equal to 0.03.

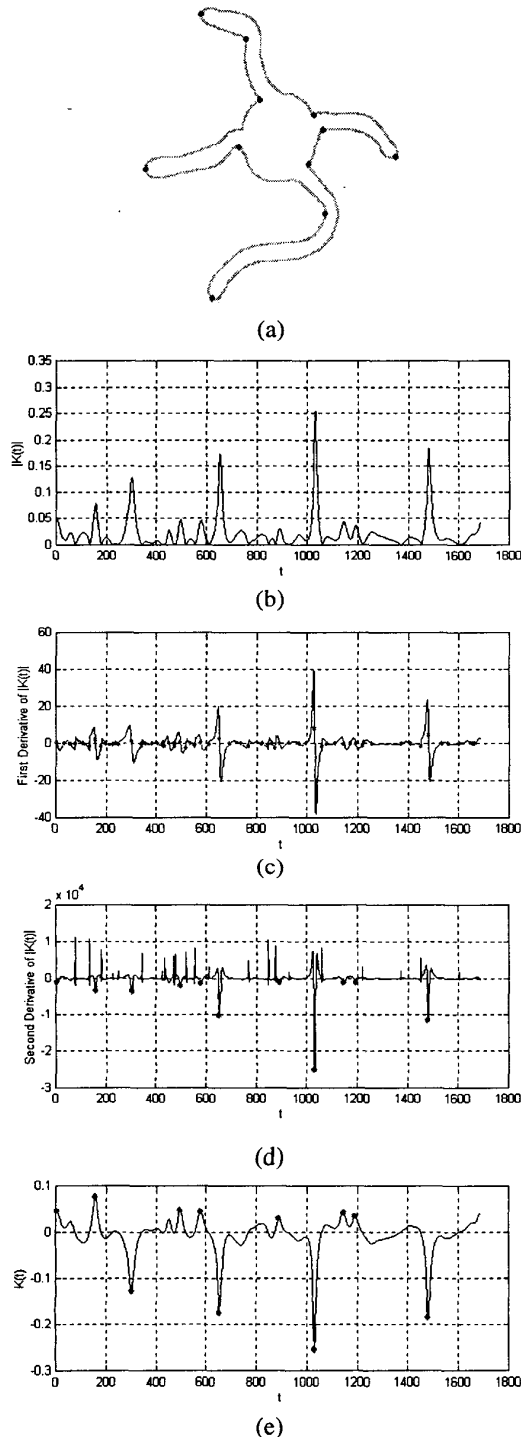


Figure 3 (a) Original Contour, (b) curvature modulus, (c) first derivative, (d) second derivative, and (e) curvature with detected peaks.

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, while being unavoidably biased. Figure 4 illustrates this strategy with respect to a specific pair of shape instances.

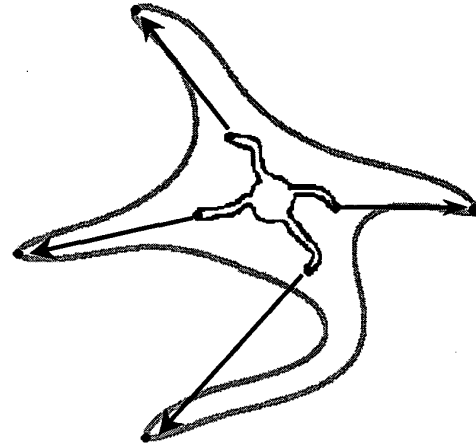


Figure 4 Correspondence between two shape instances in terms of curvature peaks.

At this point it is interesting to characterize some of the properties exhibited by morphing processes. For instance, they may occur so as to preserve 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 in that time interval, the process is henceforth said to be *time stationary*, otherwise it is called *non-stationary*. The stationary classification can also be extended to the process characterization along the shape contour, in which case it is said to be *spatial 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. [8]).

The representation of a morphing process can be done according to several levels of detail and abstraction. 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*. Specific behaviors of the morphing process, such as discontinuities and conservation of specific properties (e.g. energy or

area), can be identified from the analysis of such trajectories. Less comprehensive characterizations of morphing processes are however obtained by the use of global measures such as the shape perimeter, area, fractal dimension or elastic 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 the morphing processes. Figure 5 illustrates the trajectory of a dynamic shape (Gaussian smoothing) in terms of the perimeter, area and elastic energy of the shape instances, and the reconstructed shapes for $\sigma = 2, 3, 5, 8, 50$.

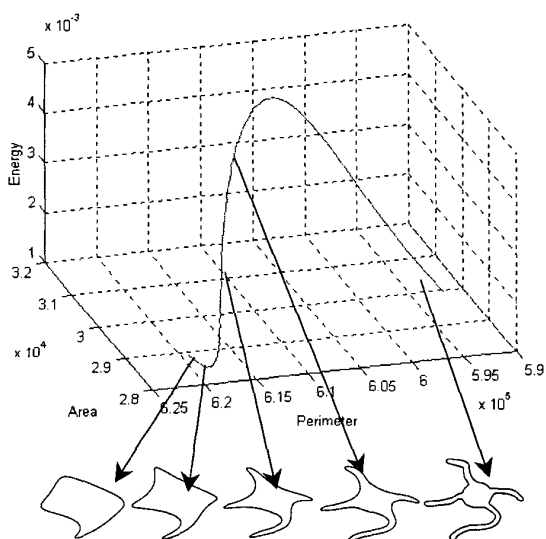


Figure 5 Representation of a Gaussian smoothing morphing process in the perimeter-area-elastic energy phase space for $\sigma = 2, 3, 5, 8, 50$.

3 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 research areas. Among those more closely related to image analysis and computer vision, we highlight the areas of morphology and pattern formation [9,10,11,12,13,14], statistical shape analysis [3,6], morphing [15], dynamical contours [16,17], registration [18,19,20], seriated reconstruction [21,22], and biological growth process [23,24].

As far as shape evolution and pattern formation [9] are concerned, a number of approaches have been developed. For instance, [10] describes a 2D discrete growth model using probabilistic and deterministic anisotropic growth, where the latter is capable of producing compact, elongated and concave morphologies. The model is used to describe multiple sclerosis morphology in the brain. In [11] an approach is reported to investigate the processes governing the growth of human mandibles. Another methodology related to shape evolution is in terms of seriated reconstruction [21,22] of images, where each section can be related to a shape instance. Registration approaches have been surveyed in [18,19], and [20] 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 [17]) 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 [15] is divided into 3 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, [23] provides a comprehensive treatment of cell and tissue dynamics including cell division, aggregation and cooperative motion, as well as morphogenesis processes. As discussed in [1, 24] 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.

4 Methodology

This section presents the main morphing processes considered in the present work, as well as the respective tests for identifying their possible participation in specific shape evolutions.

4.1 Functional Mappings

In this approach, the next instance of the shape evolution is specified as a function f of one of its previous instances, i.e. $\bar{c}(s, t + \Delta t) = f(\bar{c}(s, t))$. In particular, it is possible to define each point in the new instance as a function of the previous one, i.e.

$$c_x(s, t + \Delta t) = f_x(\bar{c}(s, t))$$

and

$$c_y(s, t + \Delta t) = f_y(\bar{c}(s, t))$$

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 instance. 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 [25].

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) and to obtain the remaining points by using the variational approach. One such a possibility is to use two-dimensional thin-plate splines [2, 3], which impose minimal energy restrictions, to interpolate between the shape control points, Figure 5(a) presents the previous (in black) and next (in gray) shape instances, and Figure 6(b) illustrates the latter (in gray) and its reconstruction obtained from the control points in Figure 3(a) by using thin-plate splines (in black).

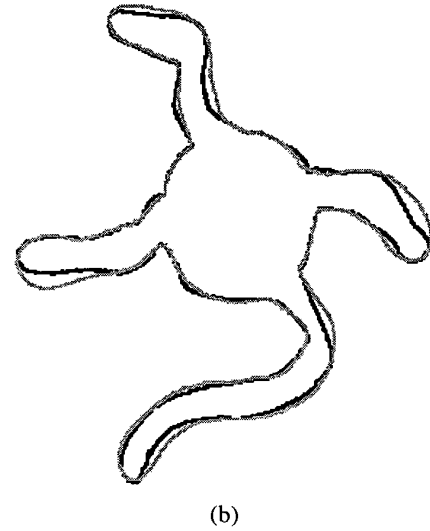
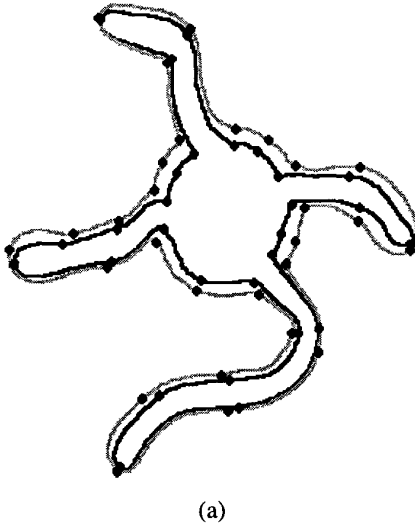


Figure 6 Thin-plate based interpolation as a means of checking for morphing mechanisms.

4.2 Differential Equations

As outlined in Section 2, several morphing processes can be properly modeled in terms of differential equations. At present we are especially interested in the two following situations: (a) 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 [26]. These possibilities are covered in more detail in the following subsections.

4.2.1 Normal Evolution

In this case, the shape speed $\dot{\bar{c}}(s, t)$ at instant t is oriented along the normal $\bar{n}(s, t)$ to the shape border, i.e.:

$$\dot{\bar{c}}(s, t) = f(s, t)\bar{n}(s, t)$$

where $f(s, t)$ is a general function of s and t . In case $f(s, t) = a > 0$, the shape dilates (or expands) with constant speed a . If $a < 0$ the shape shrinks with constant speed.

A possible natural means for investigating if a specific instance of a shape has evolved along the normal with respect to a previous configuration is to compare the shape velocity field with the normal to the previous instance. Therefore, provided we have the correspondences (or velocity field) and a means to estimate the original normal, for instance by using the Fourier transform derivative property [7], normal evolution can be tested for each of the shape elements. Figure 7 illustrates this possibility with respect to a neural

shape undergoing normal evolution along most of its contour, except at its upper portion.

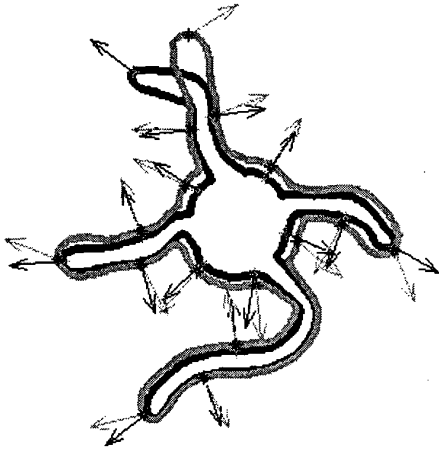


Figure 7 Two instances of a neuronal shape undergoing normal evolution along most of its contour.

Since curvature peaks have been assumed as control points, unwanted sensitivity of the normal near sharp shape extremities (see the previous figure) tends to deteriorate the above proposed test for normal evolution. Therefore, it is interesting to avoid defining control points at particularly sharp curvature peaks.

While the above test allows us to identify portions along the shape contour undergoing normal evolution, the magnitude of such a process has to be inferred by

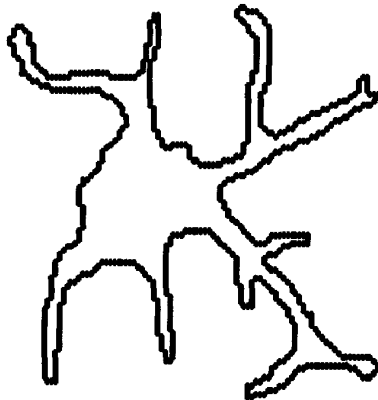
alternative means, which should take into account a wide variety of possibilities (for instance, it can be defined in term of the local curvature magnitude). As with the general problem of shape dynamics identification, the magnitude inference can be done based on a model approach considering the most common schemes verified in natural process. Currently we are particularly interested in situations where the speed magnitude is constant or proportional to the contour curvature.

4.2.2 Convolutional Processes

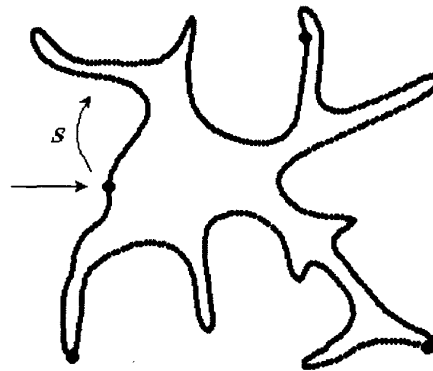
The more general case of time *non-stationary* convolution (the convolution kernel is a function of ξ) in continuous domain can be represented in terms of the following expression:

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

where $h_x(\xi, s, t)$ is the convolution kernel acting at the neighborhood of the parameter position ξ . The non-stationarity arises from the fact that different kernels are verified at different positions. Figure 8 (a,b) illustrates a spatial non-stationary convolutional morphing processes characterized by Gaussians with different standard deviations as convolution kernels.



(a)



(b)

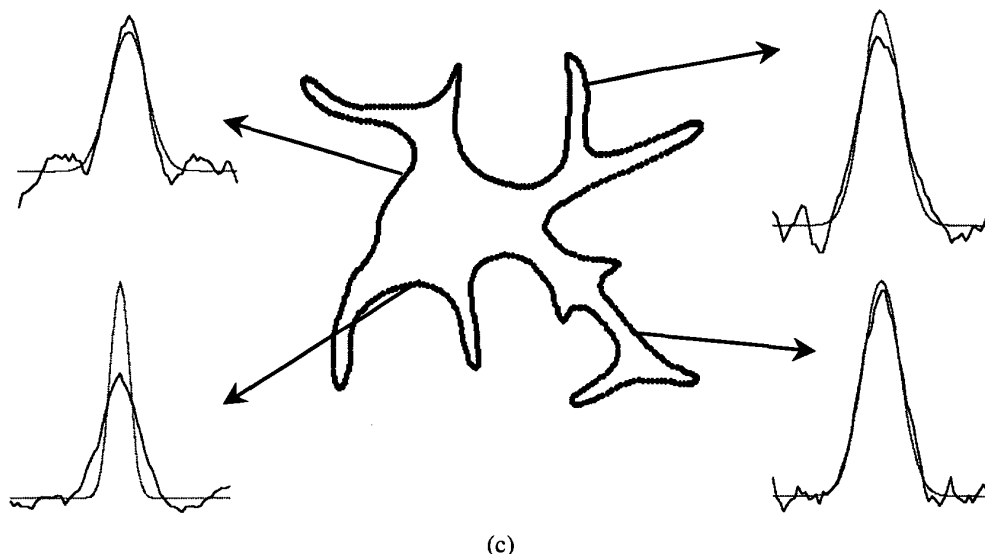


Figure 8 A pair of subsequent shape instances (a and b) produced by spatial non-stationary morphing process (a). Some of the inferred convolution kernels (in black), including also the original kernels (in gray), are identified in (c).

The currently considered approach for testing 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 problem variables) 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. After obtaining such set of equations, the convolution kernels can be estimated by applying the pseudoinverse approach [27]. In order to cope with instabilities, the ridge regression approach [28], a kind of first order regularization [29], has been adopted. Figure 6 presents some of the convolution kernels obtained by using the above described approach over the pair of subsequent shape instances in Figure 7(c).

6 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. 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 of embryos.

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7 References

- [1] R. J. Lasek. and M. M. Black, "Intrinsic Determinants of Neuronal Form and Function", *Proc. Of a Meeting on Intrinsic Determinants of Neuronal Form and Function*, Case Western Reserve University, Cleveland, Ohio, 1986.
- [2] L. da F. Costa and R. M. Cesar Jr., "*Shape Analysis and Classification: Theory and Practice*", CRC Press, Florida, 2000.
- [3] F. L. Bookstein, *The Measurement of Biological Shape and Shape Change*, Vol 24 of Lectures Notes on BioMathematics, Springer Verlag, NY, 1978.
- [4] F. L. Bookstein, *Morphometric Tools for Landmark Data: Geometry and Biology*, Cambridge University Press, Cambridge, 1991.
- [5] M. Leyton, *Symetry, Causality, Mind*, MIT Press, 1992.

- [6] K. V. Mardia and I. Dryden, *Statistical Shape Analysis*, John Wiley & Sons, 1988.
- [7] L. da F. Costa, and R. M. Cesar Jr., "Piecewise linear segmentation of digital contours in $O(N \cdot \log(N))$ through a technique based on effective digital curvature estimation", *Real-Time Imag*, Vol 1, N 6, 1995.
- [8] T. M. Apostol, *Calculus*, John Wiley and Sons, 1967.
- [9] J. D. Murray, *Mathematical Biology*, Berlin, Springer Verlag, 1993.
- [10] S. F. Thompson, *Growth Model for Shapes*, Thesis presented to University of Maryland, 1994.
- [11] P. R. Andresen, *Surface-Bounded Growth Modeling Applied to Human Mandibles (3D)*, Ph.D. Thesis presented to Technical University of Denmark, 1999.
- [12] G. Ascoli, J.L. Krichmar, "L-Neuron, a modeling tool for the efficient generation and parsimonious description of dendritic morphology", *Neurocomputing*, Vol 32-33, 2000, pp.1003-1011.
- [13] R. Scorcioni, G. Ascoli, "Algorithmic extraction of morphological statistics from electronic archives of neuroanatomy", *Lect. Notes Comp. Sci.*, In Press 2001.
- [14] G. Ascoli, J.L. Krichmar, S J. Nasuto, S.L. Senft, "Generation, description, and storage of dendritic morphology data", *Phil. Trans. R. Acad. Sci. B*, In Press 2001.
- [15] G. Wolberg, "Image Morphing: A Survey", *The Visual Computer*, Vol 14, 1998, pp 360-372.
- [16] M. Kass, A. Witkin, and D. Terzopoulos, "Snakes: active contour models". In *First International Conference on Computer Vision*, 1987, pp 259-268.
- [17] W. Blake, and M. Isard, *Active Contours: The Application of Techniques from Graphics, Vision, Control Theory and Statistics to Visual Tracking of Shapes in Motion*, Springer Verlag, 1999.
- [18] G. L. Brown, "A Survey of Image Registration Techniques", *ACM Computing Surveys*, Vol 24, N 4, 1992.
- [19] J. B. A. Maintz, and M. A. Viergever, "A Survey of Medical Image Registration, Medical Image Analysis", Vol 2, N 1, 1998, pp 1-37.
- [20] P. E. Van den Elsen, P. E. and M. Viergever, "Medical Image Matching - A Review with Classification", *IEEE Engineering In Medicine and Biology*, Vol 12, N 1, 26-39, 1993.
- [21] C. Levinthal, and R. Ware, "Three Dimensional Reconstruction from Serial Sections," *Nature*, Vol. 236, 1972, pp. 207-211.
- [22] V. A. Moss, D. M. Jenkinson, and Y. H. Elder, "Automated Image Segmentation and Serial Section Reconstruction in Microscopy," *Journal of Microscopy*, Vol. 158, N 56, 1990, pp. 187-196.
- [23] W. Alt, A. Deutsch, and D. Dunn, *Dynamics of Cell and Tissue Motion*, Birkhauser, 1997.
- [24] R. Oldenbourg, K. Katoh, and G. Danuser, "Mechanism of lateral motility of filopodia and actin bundles in lamellipodia of neuronal growth cones", *Biophysical Journal*, Vol 78, N^o 3, 2000, pp. 1176 - 1182.
- [25] Kay, S. M. R., *Statistical Signal Processing*, Prentice Hall, New Jersey, 1993.
- [26] Boas, M. L., *Mathematical Methods in the Physical Science*, John Wiley and Sons, Singapore, 1983.
- [27] A. Jennings, *Matrix computation for engineers and scientists*, John Wiley & Sons, 1980.
- [28] A. Hoerl, and R. Kennard, "Ridge Regression: Applications to Nonorthogonal Problems," *Technometrics*, Vol. 12, N 1, 1970, pp. 69-82.
- [29] A. N. Tikhonov, and V. Y. Arsenin, *Solutions of ill-posed problem*, W. H. Winston, Washington DC, 1977.