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Low-level grouping mechanisms for contour completion

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Abstract

The human visual system achieves effective segmentation in situations where many computational methods fail. This study seeks to demonstrate how methods based on low-level models of early visual processing can be adapted to perform this task in the difficult domain of muscle histology. Through analysis of typical images of muscle tissue we have identified basic features likely to be of importance in human perception. Considering these in the light of current neurological and psychophysical research, we have concluded that the manner of boundary completion is, in this case, akin to that underlying amodal completion of occluded surfaces in normal situations. The issue of contrast polarity is discussed, and a model for the completion of fragmented line figures, incorporating both polarity-sensitivity and the concept of partial closure, is presented. This has been adapted into a computational system, aimed at the segmentation of muscle cell images, that attempts to exploit useful features of low-level processing in combination with knowledge of the domain. © 2000 Elsevier Science Inc. All rights reserved.

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1. Introduction

The continued emergence of increasingly sophisticated microscopic tools and techniques has led to a tide of interest in the development of methods for computerised analysis of microbiological data. It is now possible to obtain very high resolution digital images of tissue samples and many quantitative analysis techniques have already been developed in response to the needs of the industry.

A major stumbling block to the development of *fully* automated analysis systems, however, is the ability to automatically delineate the boundaries of objects of interest in an image. An image must first be segmented into meaningful regions before measurements or classification can be performed on them. Due to the nature of soft tissue, even with very high resolution, the boundaries of objects may be difficult to detect using current computational methods and the task of grouping fragmented boundaries into complete contours, in what are, sometimes, very cluttered images, is daunting. Human beings do not appear to experience the same level of difficulty when faced with this task. This research is motivated by the relative ease with which the human visual system segments a scene when presented with, frequently, incomplete or degraded data.

The focus of the work is the analysis of images of histological sections of striated muscle tissue. Physiologists investigating pathological changes associated with diseases such as diabetes and hypertension, and others studying the development of muscle tissue in response to exercise, are interested in deriving quantitative descriptions of the tissue structure from histological data accumulated over recent years. Recent computational methods (e.g. [14]) still fail to cope with realistically complex images and, currently, the manual effort involved in processing the data – each image of a transverse section may contain of the order of 200 fibres which must be delineated by hand – is prohibitive.

Through analysis of the elements that characterise the structures observed in such images, we have tried to isolate the basic features and mechanisms likely to be of importance in early visual processing of these images, and seek to exploit useful techniques derived from our knowledge of human vision in the development of an engineering solution to our problem.

We see this study as presenting an opportunity for a two-way flow of ideas between studies of visual perception and neuroscience on one hand, and computational sciences, aimed at the development of real applications, on the other. In visual sciences, where many studies focus on understanding carefully structured synthetic data, the analysis of natural images, performed with a view to understanding the biological processes underlying their perception, serves to highlight the infinite variety of even simple features such as lines, edges and junctions found in combinations not seen in artificial situations. Such work, therefore poses interesting questions on which to found further research. On

the engineering side, biologically plausible models are frequently dismissed as being either too complex or too inefficient for practical purposes. We do not aim to develop a *biologically-plausible* system but, rather, seek to demonstrate how *biologically-inspired* computing can lead to robust solutions for real-life images.

2. Feature analysis

Variations in the nature of histological images of muscle tissue (shown in Fig. 1) are, largely, due to the use of different stains in the preparation process. However, the main problem generally associated with the segmentation of these images is the fragmentation of cell contours due to poor image contrast, with the additional problems of noise and irregularity of cell shape and size. Typical images of stained transverse sections of striated muscle tissue were analysed with the aim of (1) determining the main featural composition of the images in terms of visual primitives such as line-and edge-based boundary fragments, and junctions of these features and, (2) relating the results of the analysis to our knowledge of human vision, particularly with regard to (data-driven) theories of low-level visual processing.

In general, the analysis revealed a number of elementary features likely to be of importance to the segmentation process. (The results are summarised in Fig. 2.) The boundaries of cells within a given image are defined by either line or edge fragments. Lines may vary in thickness, and the contrast polarity may differ between features. Line terminations occur both at junctions between cells and where boundary fragmentation has occurred due to poor contrast. The cell bodies themselves, of course, can be regarded as roughly homogeneous surface regions.

The most important points to be noted, however, relate mainly to the arrangements of junctions in the images and the manner in which their grouping may be interpreted, perceptually. Junctions play a crucial role where contour information is scant. Indeed, the structure can largely be defined by linking together suitably matched pairs of junctions across an image. Clearly, although instances of all types of junction occur in the images, Y-like junctions were found to be, by far, the most common. However, the number of boundaries co-terminating at a junction does not appear to be important. Rather, grouping is signalled by an occurrence of collinearity between boundary fragments associated with two junctions. Indeed, boundary ownership is only defined if we reduce junctions between multiple cells to a series of V-like junctions and group together only those boundary fragments that enclose the surface of an individual cell (e.g. Fig. 3).

Another notable factor is the presence of small fragments of boundary information along a line between matched junctions. These have a dramatic

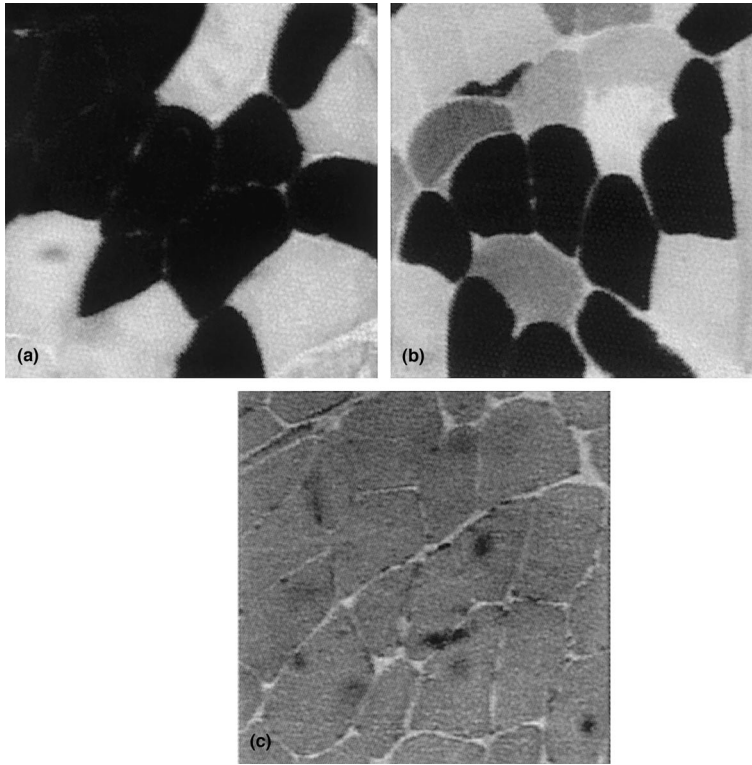


Fig. 1. Stained histological sections: (a) ATP stain ($\text{pH} = 4.35$), highlighting two different types of muscle fibre. (b) ATP stain ($\text{pH} = 4.6$), highlighting three different types of muscle fibre. (c) Haematoxylin and Eosin stain, displaying no differentiation according to fibre type. The ATPase stains tend to cause shrinkage of the tissue, resulting in clumping together of cells of the same type. This is most apparent in (a), where the boundaries of clumps of cells are defined by strong contrast discontinuities within which only very few fragments of individual cell boundaries can be seen. Within clumps, boundary fragments are line-like in appearance. The Haematoxylin and Eosin (H&E) stain does not cause tissue shrinkage. Here, all cell types have the same grey-level value, and boundaries are delimited by thin lines of interstitial space between cells. Significant noise is also apparent, caused by slicing of the tissue during the histological preparation process.

affect on our ability to determine the exact location of cell boundaries. We expect that the mechanism underlying the perceptual grouping of these features in human vision is likely to take this factor into account.

Obviously, we recognise that knowledge of the domain and the context in which we see individual features have a role to play in our ability to correctly segment these images. However, we are interested in developing our system as far as possible on data-driven methods, with the exception of any knowledge that may be implicitly incorporated through operators that make up the process. A great deal of research in the fields of neurophysiology and psycho-

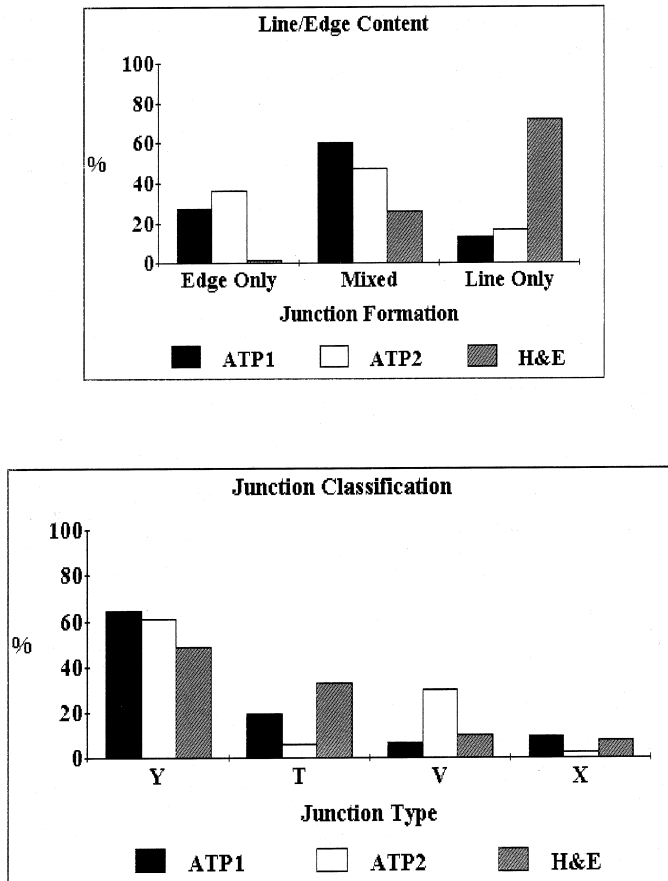


Fig. 2. Feature analysis. As a guide to line width, we took the limits suggested by neurological data on simple cell receptive fields preferring a line width of 1–9 min of arc (equivalent, at maximum, to 1.5 mm at 57 cm from the eye) [1]. Junctions were coarsely classified into four general types (Y, T, V or X) and were further classified within these categories according to the nature (line or edge) of each of their components. We see that H&E images are clearly dominated by line-like boundary information, while in ATPase images, the boundaries are defined by a mixture of both lines and edges.

physics has been carried out in recent years aimed at increasing our understanding of low-level grouping processes and, based on their findings, a number of neurally-based computational models [4,5,7,12] have attempted to explain boundary completion by simulating the activity of neurons in V1 and V2 of the visual cortex. These models have shown success in the, so-called, modal (or foreground) completion of illusory contours such as those perceived in the Kanizsa square in Fig. 5(a). This is achieved by combining features similar to

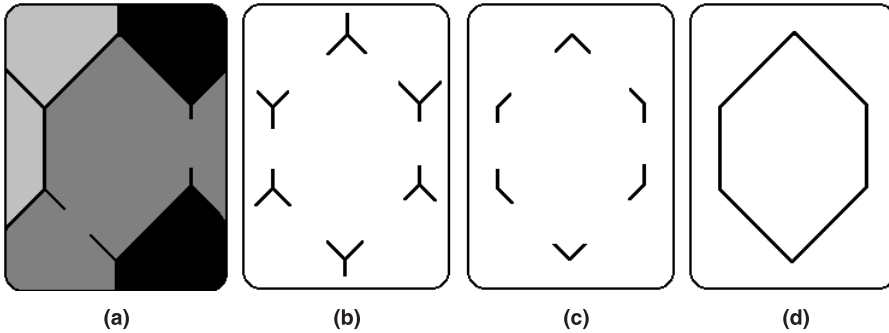


Fig. 3. The completion of cell contours: (a) possible cell structure, (b) junction formation, (c) junction information necessary for contour completion, and (d) contour completion.

those we observe in this domain, and would appear to be a good basis on which to found our segmentation system.

However, if we attempt to apply their methods to the problem addressed here, we encounter a number of difficulties. These are associated with the main assumption on which the models are founded, namely, that the human visual system is strongly tuned to the recovery information regarding depth and occlusion. Due to the physical structure of muscle tissue, the images we are dealing with are inherently two-dimensional in nature. Despite this, the feature analysis revealed a number of T-junctions and line terminations, normally indicative of occlusion in a three-dimensional world. We also see a number of incomplete junctions where there is severe fragmentation of the contours, often within dark clumps of cells. In these cases, the point of intersection can only be inferred from the orientation of the boundary fragments co-terminating at the junction. Such arrangements resemble the classical Ehrenstein figure (shown in Fig. 4), normally interpreted in terms of an arrangement of lines, partially

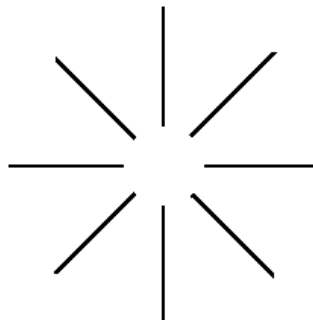


Fig. 4. Ehrenstein figure.

occluded by an illusory surface. Faced with this, illusory contour mechanisms will attempt to complete the boundary of the occluding surface, while the correct segmentation here would appear to require completion of the, apparently, occluded junction.

Our postulate is, therefore, that a process of amodal (or background) completion could be responsible for the, effortless, correct visual segmentation of these images by even naive human observers. To this end we re-examine neurological and psychophysical evidence with a view to establishing the nature of this process.

3. Modal and amodal completion

An instance of so-called modal completion is classically demonstrated by the Kanizsa square in Fig. 5(a). Here, we generally perceive a surface occluding four small squares, with an illusory contour filling in the gaps where no contrast-defined boundary exists, and the models discussed above all attempt to establish the boundaries of the foreground surface in such a case (i.e., those of the illusory square). We believe that a mechanism aimed at the completion of cell boundaries in muscle images is more akin to that which would amodally complete the inducing elements in Fig. 5(a) or the square in Fig. 5(b). Whilst a square is also perceived in Fig. 5(b), the sensation is somewhat different to that of the Kanizsa figure, and we consider this to be a special case of amodal completion, as we will explain later. Although it may be tempting to assume that the completions of Figs. 5(a) and (b) are products of the same perceptual mechanism, we suggest that various pieces of evidence point to the conclusion that two similar, but essentially different processes, are involved.

Von der Heydt et al. [13] showed that a number of neurons in area V2 of the visual cortex of monkeys responded not only to contrast-defined boundary features, such as bars and edges, but also to illusory contours, such as perceived in Figs. 4 and 5(a). This was taken as evidence that some grouping of features takes place at a very early stage in visual processing, without a priori knowledge of the scene, and the models discussed above attempt to simulate this. Our first difference is this. It would appear that these same neurons do not respond in a similar way to stimuli such as shown in Fig. 5(b) [11]. So, although the features group well together to form a square, an illusory contour is not formed in this case. This difference in the activity of V2 contour cells could suggest that either the completion takes place at a different cortical location, or that the completion is the result of activity within a different set of cells at the same site. This may, or may not, be the case. However, work examining the perceptual grouping of line-like boundary fragments [8] found significant pop-out effects for closed arrangements of such features. We feel this suggests that a low-level mechanism is also responsible for the grouping seen in Fig. 5(b).

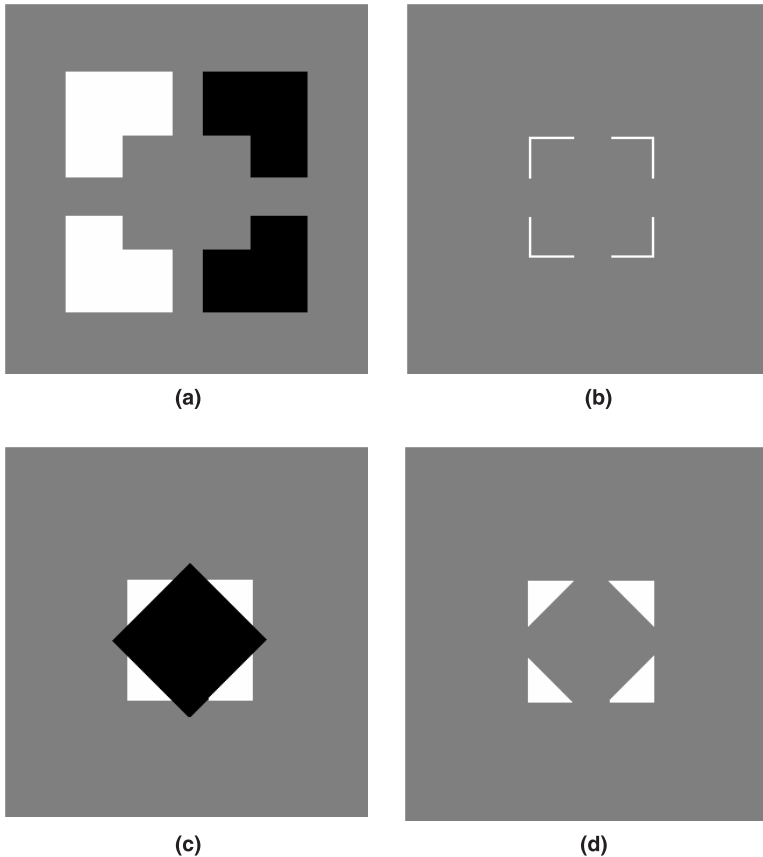


Fig. 5. Modal and amodal completion: (a) Kanizsa figure, (b) perceptually closed line figure, (c) occlusion by a solid surface, and (d) occlusion by an illusory surface.

Our second reason for claiming differences in mechanisms for modal and amodal completion stems from Elder and Zucker's visual search experiments [2], investigating the perceptual closure of fragmented line figures such as shown in Fig. 8. They found considerable differences in the measured response times of subjects depending on whether the contrast polarity of the figures used in the display remained constant, or changed along part of the boundary of a figure. McIlhagga and Mullen [9], too, found contrast polarity-dependent effects in the grouping of line-like features. If a single mechanism underlies the completion of both Figs. 5(a) and (b), this evidence would appear to be in conflict with our knowledge of illusory contours, which emerge regardless of the contrast polarity of the inducing elements.

The illusory square in Fig. 5(a) is, clearly, an *occluding* surface. Ecologically speaking, we might expect the background of an object to change frequently,

leading to variations in contrast polarity along its boundary. A process seeking to establish foreground surfaces through the integration of occlusion cues, such as line terminations orthogonal to the surface, is unlikely, therefore, to be influenced by the sign of contrast of boundary features. A process seeking to complete *occluded* surfaces may be governed by different constraints.

We claim that a possible interpretation of Fig. 5(b) is that of a square, partially occluded by an illusory surface. In this case, the line fragments represent contour information remaining after the removal of all the boundaries belonging to the occluding surface. Note that the remaining boundaries will be the same regardless of whether the underlying figure is a solid surface, or a line drawing, or whether the occluding surface is real or illusory (as in Figs. 5(c) and (d)). Such an interpretation is not unreasonable, given that in nature, the fragmentation of a contour is frequently due to occlusion. On this basis, we propose that the mechanism underlying the perception of a square in Fig. 5(b) is a special case of amodal completion and is therefore akin to that governing the completion of partially occluded surfaces in normal circumstances. Hence, Elder and Zucker's results may be explained as resulting from a polarity-sensitive grouping mechanism seeking the amodal completion of occluded surfaces, and we have constructed our model with this in mind.

4. The model

We have developed a neurally-based system, using receptive field models of cortical cells in area V1 and other operators thought to play a role in the early stages of biological vision, linked in a feed-forward manner. Focusing, initially, on the completion of fragmented line figures, we attempt to capture the concept of partial closure and sensitivity to contrast polarity proposed by Elder and Zucker in [2]. Their findings suggest that matched junctions, or points of significant curvature have a principal part to play in bringing about figural completion. In agreement with our own observations of small, but very salient, boundary fragments in muscle images, they also found that the distribution of line segments between junctions was of significant importance. We have interpreted their results as pointing towards a mechanism combining the responses of a relatively long-range grouping process between suitably matched points of high curvature with a short-range grouping process between roughly collinear line segments. Hence, boundary completion is achieved by integrating contour and junction evidence in a polarity-sensitive manner, and the strength of closure is estimated from a surface that emerges as the result of a diffusion of 'binding' activity from these boundaries. The steps involved in the process are as follows.

Firstly, in order to preserve contrast polarity information, oriented line detection is performed through convolution of the original image with a simple

cell model of even symmetry (Fig. 6(a)). The receptive field model used here is that developed by Heitger et al. [7], based on the one-dimensional gabor-type function

$$G(x) = e^{-x^2/(2\sigma^2)} \cos(2\pi v_0 x \zeta(x)),$$

where σ gives the width of the Gaussian envelope, v_0 is the frequency at the origin and $\zeta(x)$ determines the relative weight of the negative side-lobes of the function.

$$\zeta(x) = k e^{-\lambda x^2/\sigma^2} + (1 - k).$$

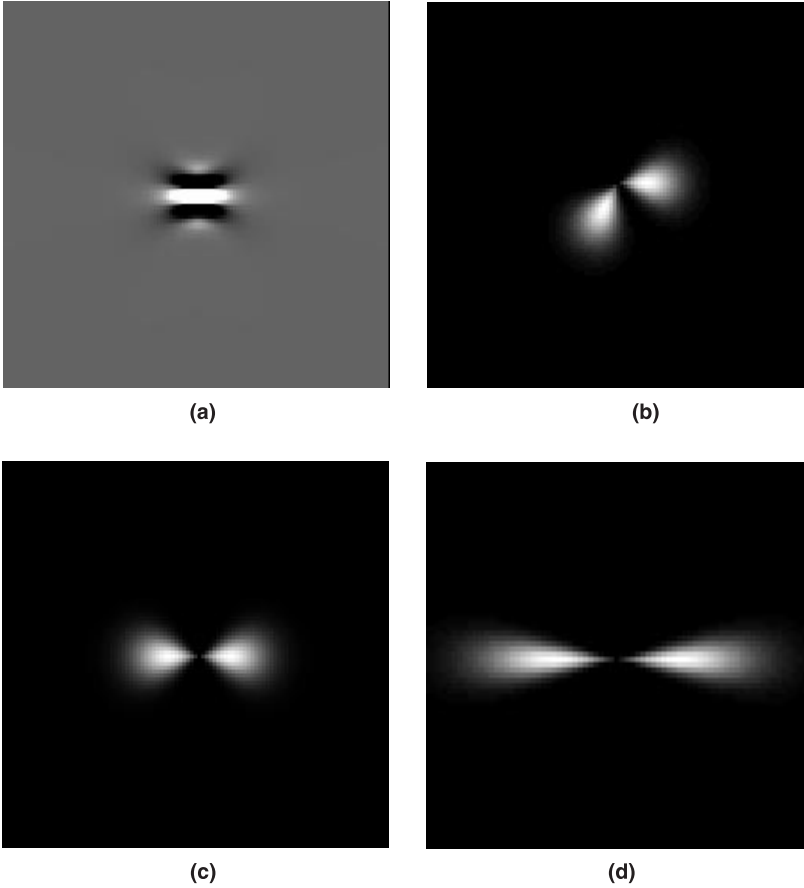


Fig. 6. Model operators: (a) simple cell ($k = 0.5$, $v_0 = 0.2$, $\sigma = 2.0$, $\lambda = 0.334$), (b) junction detector for a 120° junction at orientation 0° ($\sigma = 4.0$, $m = 4.0$, $b = 1.0$), (c) short-range grouping field ($\sigma = 4.0$, $m = 4.0$, and $b = 1.0$), and (d) long-range grouping field ($\sigma = 12.0$, $m = 25.0$, and $b = 1.0$).

This is transformed into a two-dimensional operator in the frequency domain by a rotation with angular variation such that

$$F(r, \varphi) = R(r) \cos^{2m}(\varphi_0 - \varphi),$$

where $R(r)$ is the one-dimensional spatial filter, $F(r, \varphi)$ is the two-dimensional Fourier filter, φ_0 determines the orientation preference of the resulting filter and m determines its degree of orientational tuning. The polar form is then transformed into a Cartesian frame of reference for further processing.

Points of high curvature are detected in the resulting oriented line maps by the application of a series of bi-directional filters (e.g. Fig. 6(b)). This mechanism is similar, in principle, to that proposed by Neumann and Stiehl [10] as a possible method for the detection of n th order junctions in images. By weighting the relative influence of neurons spatially shifted from the central point of the operator, we achieve effective completion of the, apparently, occluded junctions shown to be present in muscle tissue images. These operators are not only orientationally selective, but also sensitive to both degree of curvature and contrast polarity. A single lobe of the detector is defined as

$$J(r, \varphi) = r^b e^{-r^2/(2\sigma^2)} \cos^{2m}(\varphi_0 - \varphi),$$

where $0 \leq b \leq 1$ varies the weighting function. Corner responses will occur when lines are detected in a pair of such lobes. We require, only, junctions subtending an angle of $<180^\circ$ and these are retained in oriented corner maps, feeding into the directional matching of the grouping stage.

Grouping is then performed over a short range between roughly collinear line segments, and over a long range between suitably matched points of curvature. Both short and long-range grouping fields (Figs. 6(c) and (d)) are of the same general form as the junction detectors, differing only in their parameterisation. A multiplicative gating mechanism ensures that completion only takes place between features of like contrast polarity. In each case, grouping between elements of a like polarity leads to an excitatory grouping response, while grouping between elements of opposite polarity leads to an inhibitory grouping response. The completed contour is the rectified sum of the grouping and corner responses. i.e.

$$C(x, y) = [G_{\text{short}}(x, y) + G_{\text{long}}(x, y) + J(x, y)]^+.$$

We assert that boundary completion, itself, does not model the concept of perceptual closure. Closure requires the emergence of a *surface*. We simulate this using a non-linear diffusion of ‘binding’ activity, based on the mechanism used by Grossberg et al. [6] to model the spread of brightness within boundaries completed by the BCS. Note here that the combined grouping response forms the input to this self-limiting diffusion process. The resulting surface does not reflect brightness perception as in the case of the Grossberg model but,

rather, gives a measure of the likelihood that spatially separated boundary fragments belong together. The binding activity, S , is evaluated iteratively, with

$$\frac{dS}{dt} = -kS_{xy} + \sum_N (S_{pq} - S_{xy}) P_{pqxy} + C_{xy},$$

where

$$P_{pqxy} = \frac{\delta}{1 + \varepsilon (C_{pq} + C_{xy})}$$

and N_{xy} are nearest neighbours of (x, y) .

5. Results

Fig. 7 shows the completed contours and binding activity obtained for a number of fragmented line figures displaying varying degrees of closure. In accordance with the aims of the model we expect to obtain contour completion only between suitably matched features of like polarity. Also, the degree of perceived closure should be reflected in the surface representing the level of binding activity for a figure.

Grouping was performed over eight equally spaced orientations, with simple cell parameters ($k = 0.5$, $v_0 = 0.2$, $\sigma = 2.0$, $\lambda = 0.334$) constant throughout all trials. For all square figures the short-range grouping field had $\sigma = 4.0$, $m = 4.0$, and $b = 1.0$ and the long-range grouping field had $\sigma = 8.0$, $m = 25.0$, and $b = 1.0$. For the fragmented circle, the size of the short- and long-range grouping fields were increased to $\sigma = 8.0$ and $\sigma = 12.0$, respectively, with all other parameters remaining the same.

With the closed square in Fig. 7(a), it can be seen that the gaps in the contour are bridged, and the surface is completely filled. In Fig. 7(b), however, although we perceive a partial square, the figure is not closed. Here, the contour is not completed and the surface falls away at the ill-matched corner. An interesting effect is induced by a change in the polarity of one of the corners of the square. In this case, the model does not complete the contour, and a ring of lower intensity in the binding activity around the corner reflects a degree of uncertainty about the closure at this point. It should be noted that although the model favours convexity, sharp corners are not required for figural closure, as demonstrated by the closure of the fragmented circle in Fig. 7(d).

Based on their psychophysical results, Elder and Zucker [3] proposed the existence of a closure continuum, and developed a measure of closure based on a sum of squares of contour gaps (the L_2 norm). We compared the average binding activity (the average brightness of the surface) for the series of figures shown in Fig. 8 with the corresponding L_2 norms calculated by Elder and

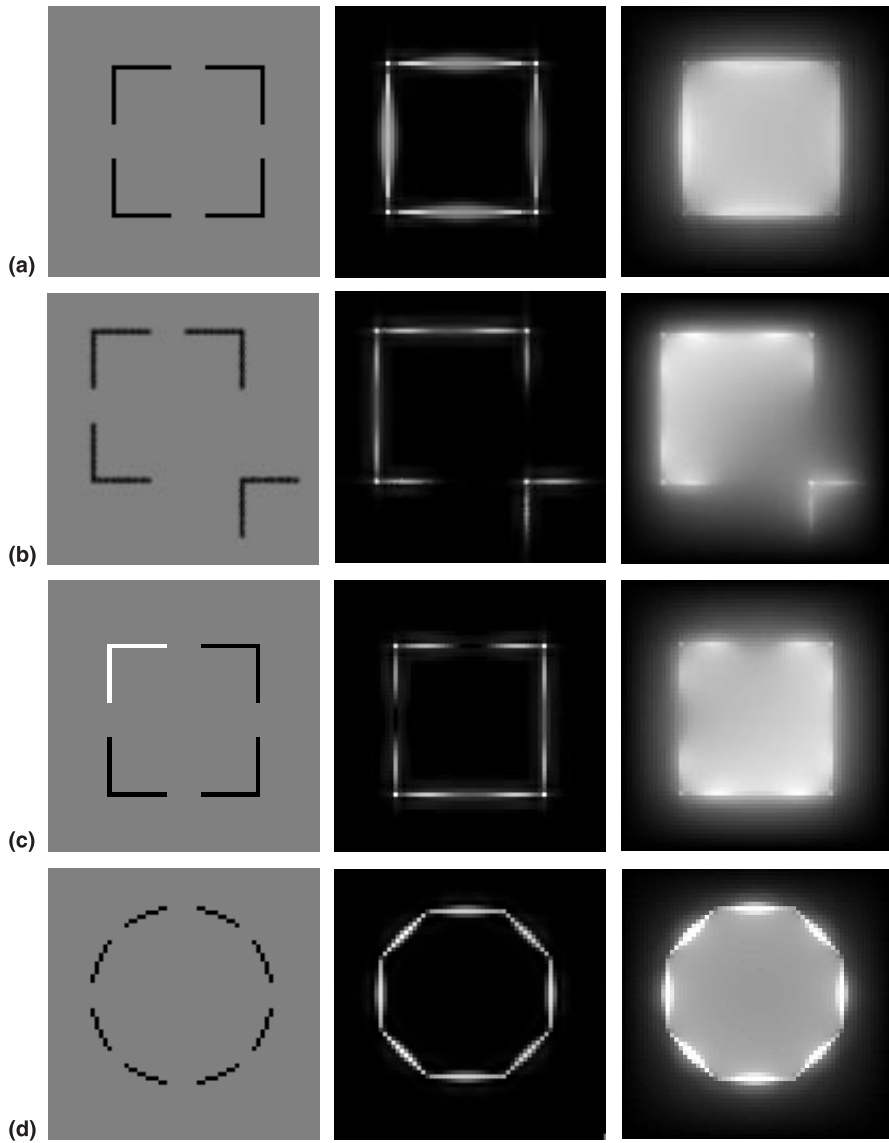


Fig. 7. Synthetic data. The three columns show the input image, completed contour and binding activity, respectively: (a) closed square, (b) partially closed square, (c) mixed polarity figure, and (d) fragmented circle.

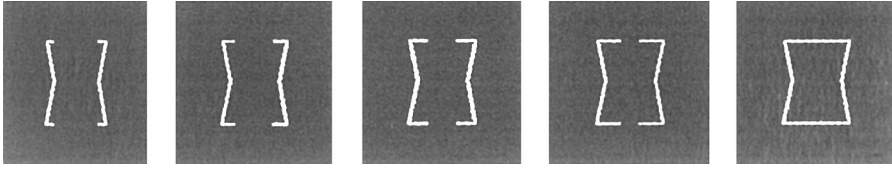


Fig. 8. Series of Elder and Zucker figures with increasing degrees of closure.

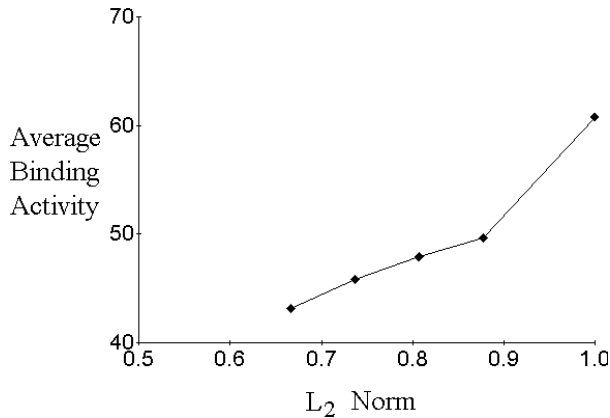


Fig. 9. Relationship between the measure of closure derived from the mean binding activity and the L_2 norm calculated by Elder and Zucker. The monotonically increasing function suggests qualitative agreement in our results.

Zucker. The graph in Fig. 9 would suggest that the measure of perceptual closure obtained by our model is in fair agreement with their results.

As regards contrast polarity, our model is also in agreement with their findings. However, unfortunately, neurological and psychophysical studies exploring, in detail, the role of contrast polarity in low-level grouping mechanisms are few, and we would like to have further empirical data on which to test our model.

6. Histological data

In our system for the segmentation of histological images of muscle tissue, we exploit the nature of receptive field models for boundary detection and the grouping principles developed in our model for closure. In addition, however, we recognise the value of domain-based knowledge in this process.

As noted in the feature analysis, the working system must deal with both edge and line-like boundary features and the use of the energy model for a complex cell, capable of localising both in an image at the same time, is used for feature detection. The response of such a cell can be modelled as

$$CC(x, y) = \sqrt{E_{\text{even}}^2(x, y) + E_{\text{odd}}^2(x, y)},$$

where E_{even} represents the response of a symmetrical (line-detecting) simple cell, and E_{odd} represents the corresponding asymmetrical (edge-detecting) cell response in quadrature. However, a feature of the complex cell is its insensitivity to contrast polarity. Whilst it would appear that low-level mechanisms underlying amodal completion in the human visual system may be sensitive to contrast polarity, we believe that top-down effects such as context and knowledge of tissue structure must also be considered here. Lines of opposite polarity to those formed by interstitial space sometimes occur due to tissue compression. In such cases, this nearly always happens at a cell boundary. Therefore, although it would be possible to retrieve polarity information from the simple cell responses, we have chosen to base our grouping simply on the complex cell response. In addition to this, we have knowledge of the approximate size of cells in an image. Hence, we apply a form of non-maximum suppression across each orientation that selects the maximum ridge point within a neighbourhood related to the expected cell size, suppressing all others. This not only locates the most probable boundary points for a given orientation, but also allows us to enhance the contribution of weak line-like responses in salient locations.

As can be seen from the results in Fig. 10, the grouping mechanism completes cell boundaries in many instances where actual boundary information is scant. This is particularly true within the dark clumps of cells commonly found in ATPase images. The problem of parameterisation is commonly considered an undesirable feature of neural network systems such as this. We hope to show that, despite the large number of parameters required by the system, these can all be related to a single scale parameter that defines the average size of cells seen in the image. The ATP results were both obtained using identical parameters to those closing the circle in Fig. 7. H&E images present even more of a challenge, yet despite considerable problems of noise and poor contrast, we are able to complete many cell boundaries correctly. We hope, in future, to improve segmentation of these images by introducing a recursive loop, feeding a first estimate of the boundary back to the grouping mechanism in order to reaffirm correct responses. Once having obtained closed contours, it is a relatively straightforward task to locate cell centres. This can be achieved using existing methods and the subsequent labelling of boundaries performed by searching outwards from such points for ridges in the contour responses.

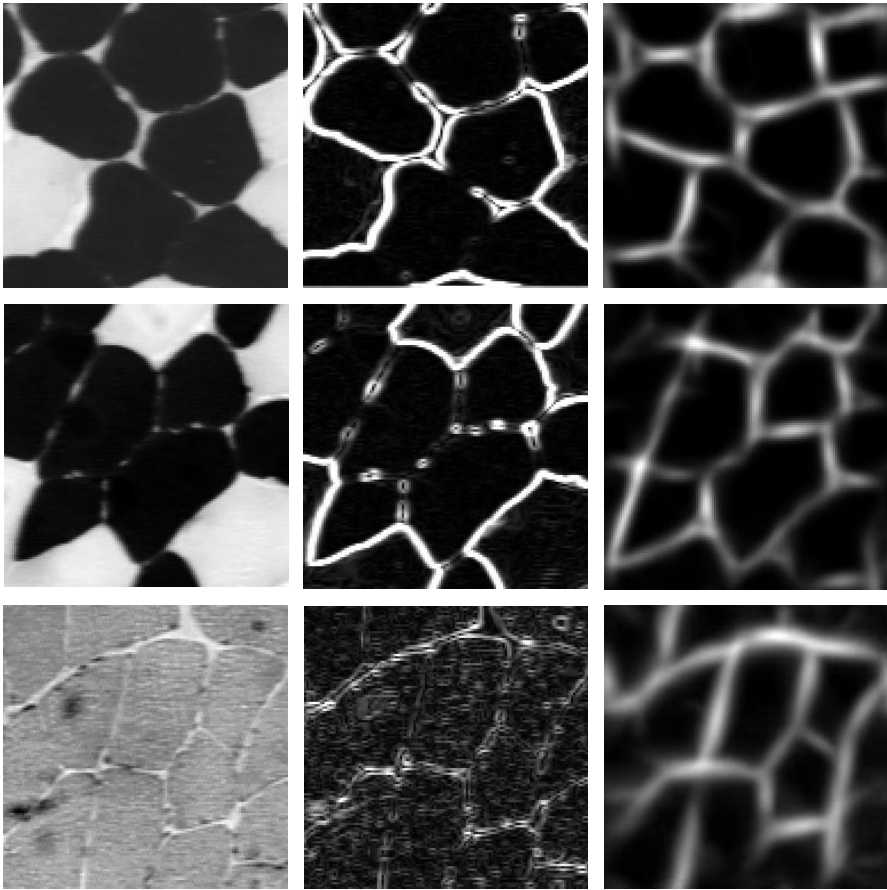


Fig. 10. Histological data. The three columns show the input data, boundaries detected using standard edge detection techniques and the contour responses computed by the new system, respectively, for two ATPase and one H&E section.

7. Conclusions

In summary, we conclude that a great deal can be learned about the nature of visual processing through detailed analysis of natural images. Similarly, computational methods may be improved by exploiting our knowledge of early visual processes, particularly through the use of neurally-based, data-driven methods. We have demonstrated that these may be incorporated into working systems, and tuned to a particular domain, through the development of a system aimed at the segmentation of histological images, where current com-

putational segmentation methods still fail to produce satisfactory results in difficult situations.

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