

## **Cell segmentation in histological images of striated muscle tissue – a perceptual grouping approach**

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# Cell Segmentation in Histological Images of Striated Muscle Tissue - A Perceptual Grouping Approach

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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 visual 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 circumstances, and have simulated this through a neurally-based system incorporating receptive field models of cells found in area V1 of the visual cortex and grouping mechanisms based on human perception. This has been adapted into a system aimed at the segmentation of muscle cell images, that attempts to exploit useful features of low-level visual processing in combination with our knowledge of the image domain.

## 1 Introduction

This research was motivated by a need to solve the problem of muscle cell segmentation in stained histological images. Existing computational methods (e.g. [8]) are unable to cope with realistically complex situations although the task is performed with apparent ease by the human eye. A solution has been sought through investigation of the mechanisms underlying segmentation in the human visual system, which displays an outstanding ability to rapidly group fragmented contours into closed contours bounding surface regions.

Variations in the nature of histological images of muscle tissue are, largely, due to the use of different stains in the preparation process. However, the main problem generally associated with segmentation in this case is the fragmentation of cell contours due to poor image contrast, with additional problems of noise and irregularity of cell shape and size. Typical images were analysed with the aim of 1) determining their main featural composition 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.

The analysis identified a number of elementary features considered to be of importance to the segmentation process. 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.

A great deal of research in the fields of neurophysiology and psychophysics 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 ([3], [2], [4]) have attempted to explain boundary completion by simulating the activity of neurons in areas V1 and V2 of the visual cortex. These models have shown success in the modal completion of so-called illusory contours, perceived in certain circumstances despite the absence of physical brightness contrast. This is

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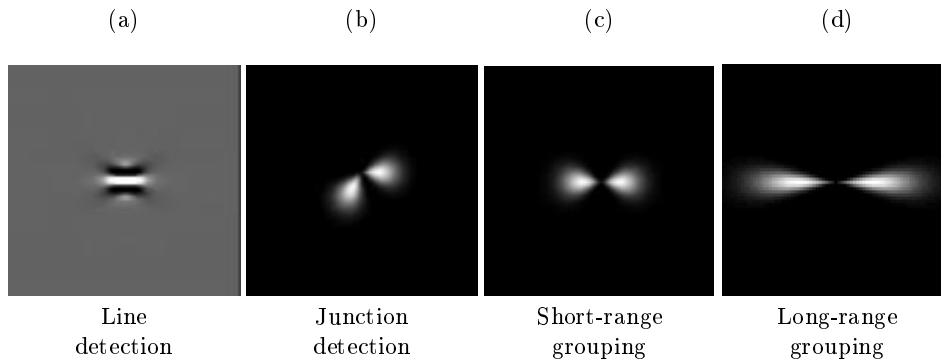
achieved by combining features similar to those we observe in this domain, and would therefore appear to be a good basis on which to found our segmentation system.

However, if we attempt to apply their methods directly to the problem addressed here, we encounter a number of difficulties. The reason for this is that the models rely on the assumption that the human visual system is strongly tuned to the recovery of information regarding depth and occlusion. Due to the physical structure of muscle tissue and the manner of sectioning, we know that these muscle images are inherently 2-dimensional in nature. Yet, despite this, the feature analysis revealed a number of T-junctions and line terminations, normally indicative of occlusion in a 3-dimensional world. In the case of illusory contours, the contour formed represents the boundary of an (illusory) occluding surface. We feel that the correct segmentation here results, instead, from a mechanism aimed at the completion of *occluded* line contours, i.e. those remaining after the removal of an occluding surface. Our postulate is, therefore, that a process of amodal completion may be the mechanism underlying the, effortless, correct visual segmentation of these images by even naive human observers [7].

Hence, building on models of illusory contour mechanisms, we have developed a system aimed at the completion of fragmented background contours. Recent psychophysical research ([1], [5]) has suggested that contrast polarity may affect such grouping, in particular, with regard to the grouping of line fragments. Therefore, unlike the original neural architectures, our model takes into account the contrast polarity of all elementary features. In this way, boundary completion is achieved by integrating contour and junction evidence in a polarity-sensitive manner and the emerging surface is estimated through a diffusive binding activity from these boundaries.

Biological plausibility is not our aim here, and the requirements for a working image analysis system differ in a number of ways from those of a system attempting to model human perception. 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 aspects of the new model in the development of an engineering solution to our problem. The final system combines these with our knowledge of the domain to achieve effective segmentation of difficult real images.

## 2 The Model



**Fig. 1.** Receptive field operators

The model makes use of receptive field models of cortical cells found in area V1 and other operators thought to play a role in the early stages of biological vision, linked in a feed-forward network, with neuronal interactions being simulated by convolution of the image with the receptive field operator at each stage of the process. Psychophysical evidence points towards a grouping mechanism for amodal completion that is sensitive to contrast polarity and combines the response of a relatively short-range grouping mechanisms between roughly collinear boundary fragments with that of a long-range grouping mechanism between suitably matched junctions.

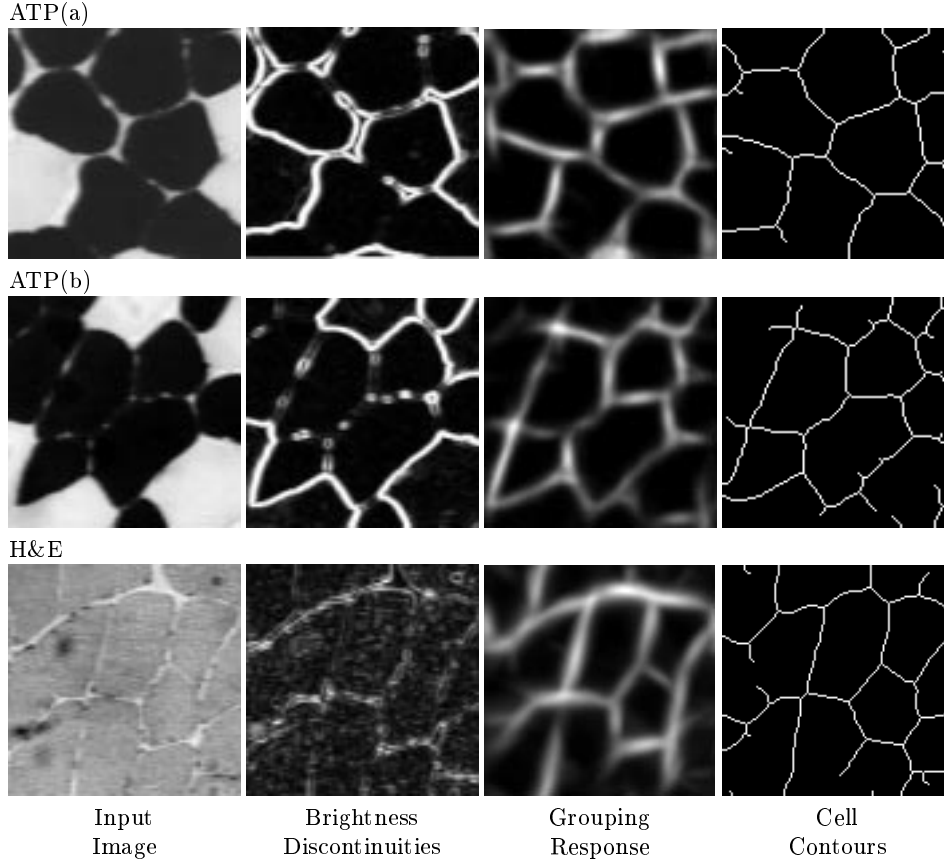
In our perceptual model, oriented line detection is first performed using a Gabor-type simple cell model [4], such as shown in Figure 1a. This simple cell response feeds into a set of bi-directional

filters (Figure 1b), similar to those used by Neumann & Steihl [6] for the detection of N-th order junctions, that detect significant points of curvature in the image. By weighting the relative influence of neurons spatially shifted from the central point of the operator, we achieve effective completion of, apparently, occluded junctions observed in some muscle tissue images. These operators are not only orientationally selective, but also sensitive to both contrast polarity and degree of curvature (detecting only angles of less than  $180^\circ$ ).

Grouping is then performed over a short range between roughly collinear line segments within each orientation, and over a long range between suitably matched points of curvature. Both short and long-range grouping fields (Figure 1c and d) have 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.

### 3 Application to Muscle Images

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 to this, however, we recognise the value of domain-based knowledge in the process.



**Fig. 2.** Contour completion with histological data. The four columns show the input data, major brightness discontinuities, grouping responses and completed contours computed by the new system, respectively, for two ATPase and one Haematoxin & Eosin section.

Given that we know the approximate size of cells, we apply non-maximum suppression within a specified range across each orientation. This not only sharpens the grouping responses, but also allows us to enhance the contribution of weak line-like responses in salient locations, while suppressing unlikely ones.

Also, although the model as it stands is suitable for stains giving rise to many line-like features (such as the H&E image in Figure 2) it must also cope, in many instances, with a combination of both edge and line-like boundary features. Here, the energy model for a complex cell, capable of localising both edges and lines in an image at the same time, is used for feature detection. The response of such a cell can be modelled by combining the response of a symmetrical (line-detecting) simple cell response with the corresponding asymmetrical (edge-detecting) cell response in quadrature. A feature of the complex cell, however, is its insensitivity to contrast polarity. While 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. Features of opposing polarity sometimes arise in this type of image due to tissue compression, but this nearly always occurs 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.

As can be seen in Figure 2, 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 images of ATPase stained sections. Images where a Haematoxin & Eosin stain has been used 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.

## 4 Conclusions

In summary, we conclude that computational methods may be improved by exploiting our knowledge of early visual processes, particularly through the use of neurally-based, data-driven methods. Biologically-based models of visual perception are frequently dismissed as being impractical for use in real computer vision applications. We claim that they may, indeed, be incorporated into working systems, and have demonstrated this through the development of a system aimed at the segmentation of histological images where current computational methods still fail to produce satisfactory results in difficult situations.

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