Evaluation of serial sections using Gabor pyramid matching

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Introduction

The evaluation of electron microscopic (EM) images of serial sections is a tedious process demanding high expertise. Here we present an algorithm to ease and accelerate this process. It is a modification of an algorithm successfully applied in computer vision for object recognition (Würtz, 1997). However, instead of recognising individual structures a transformation is computed mapping a whole section on the consecutive one. This mapping can be used to transfer labelled information from one section to the next, e.g. a classification of visible structures by a human expert. We evaluate its performance quantitatively on an artificial benchmark and qualitatively on real sections taken in primary visual cortex. The high accuracy of the obtained transformation and the fast computation times give this algorithm the potential to greatly speed up and facilitate the evaluation of serial sections.

The electron microscopic photographs were used for a different study, kindly provided by J.C. Anderson and K.A.C. Martin. The tissue was taken from cat primary visual cortex (area 17, layer 3) and processed according to standard protocols (Anderson et al., 1994).

The Algorithm

The presented algorithm is based on the dynamical link matching approach, a method successfully used for object recognition (von der Marlsburg, 1988, Lades et al., 1993, Würtz, 1997). A mapping between two images is computed in the following way. Local features are extracted from each image by convolution with Gabor wavelets of different preferred orientation and different spatial frequencies. This is done efficiently in the Fourier domain and only evaluated on a grid of points whose number depends on the spatial frequency of the wavelet (Fig.1). This results in a complex number for each grid point, whose amplitude is then used to compute the phase of thecomplex of the first image with the complex conjugate of the second image. The best match then determines a local shift for the patch. The transformation of the whole image is computed by interpolation of these local shifts.

The algorithm starts with the lowest specified frequency and correspondsingly large grid. The computed transformation is taken as a startpoint for the next matching process, which uses a higher frequency and a correspondingly finer grid to extract smaller features from the image. This process can be iterated till a satisfactory mapping is achieved (pyramidal algorithm).

A benchmark test

To quantitatively the quality of the mappings an artificial benchmark was created. A pair of EM images with known transformation was distorted by stretching an image from a real section (Fig. 2) on average by 60 pixels. The left 40% of the image was squashed horizontally, the next 40% were stretched (both by 20%) and the right 20% of the image were not modified in horizontal direction. The distorted image is shown in B and differs from the original on average by 60 pixels.

We applied the algorithm with 3 different frequencies, corresponding to 64, 32 and 16 pixels wavelength and 8 different orientations (spaced by 22.5 degrees). The sampling grids had a size of 25*25, 59*59 and 129*129 points for the 3 different frequencies.

The average deviations reduced from 60 pixels to 53.4 after the first, 26 after the second and 12.7 pixels after the third frequency. However in the central half of the image, where enough information is present for matching, the average error reduced to 5.3 pixel.

The figure shows the mapping for a number of selected points. Most points are mapped accurately, except those marked by a small square. Points near the left border were systematically shifted to the left, which can be understood since not enough information is available near the boundary.

A real world test

The above figure shows that most labels are transferred correctly over several consecutive sections. Larger deviations occur near the boundary of two adjacent sections. This results from a smaller amount of information in the image near these points. Nevertheless a satisfactory mapping of more than 80% of the labelled points is reached and this can further be improved by choosing points clear off the boundary.

Conclusion

The presented algorithm computes a transformation between electron microscopic images of serial sections and transfers labels from the first to consecutive images of the section. However, the algorithm does not recognize anatomical structures, a duty left to the scientist. We did not systematically analyze the effect of different parameters settings, which leaves room for further optimization. The accuracy of the transformation together with a fast implementation give this algorithm the potential of greatly facilitating and speeding up the evaluation of serial sections.

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References