Computational and Structural Biotechnology Journal 15 (2017) 56–67

ELSEVIER

COMPUTATIONAL AND STRUCTURAL BIOTECHNOLOGY JOURNAL

journal homepage: www.elsevier.com/locate/csbj

Mining textural knowledge in biological images: Applications, methods and trends

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ARTICLE INFO

Article history:
Received 25 August 2016
Received in revised form 14 November 2016
Accepted 15 November 2016
Available online 24 November 2016

Keywords:
Textural analysis
Bioimaging
Textural features extraction
Texture classification
Feature encoding
Deep learning

ABSTRACT

Texture analysis is a major task in many areas of computer vision and pattern recognition, including biological imaging. Indeed, visual textures can be exploited to distinguish specific tissues or cells in a biological sample, to highlight chemical reactions between molecules, as well as to detect subcellular patterns that can be evidence of certain pathologies. This makes automated texture analysis fundamental in many applications of biomedicine, such as the accurate detection and grading of multiple types of cancer, the differential diagnosis of autoimmune diseases, or the study of physiological processes. Due to their specific characteristics and challenges, the design of texture analysis systems for biological images has attracted ever-growing attention in the last few years. In this paper, we perform a critical review of this important topic. First, we provide a general definition of texture analysis and discuss its role in the context of bioimaging, with examples of applications from the recent literature. Then, we review the main approaches to automated texture analysis, with special attention to the methods of feature extraction and encoding that can be successfully applied to microscopy images of cells or tissues. Our aim is to provide an overview of the state of the art, as well as a glimpse into the latest and future trends of research in this area.

Contents

1. Texture analysis: definition and main application areas

Texture analysis attempts at the formalisation of an inherently informal concept, that is the appearance and feel of visual textures in an image. Generally speaking, visual textures are non-random arrangement of entities (*subpatterns* [1]) with a certain distribution of brightness, colours, shapes, etc. (see Fig. 1). The fine aggregation of the subpatterns in the observer's eye generates the perception of texture as a whole, even in absence of well-defined boundaries.

Texture analysis has received attention from the research community since the early 70s, and over the years it has been successfully

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http://dx.doi.org/10.1016/j.csbj.2016.11.002

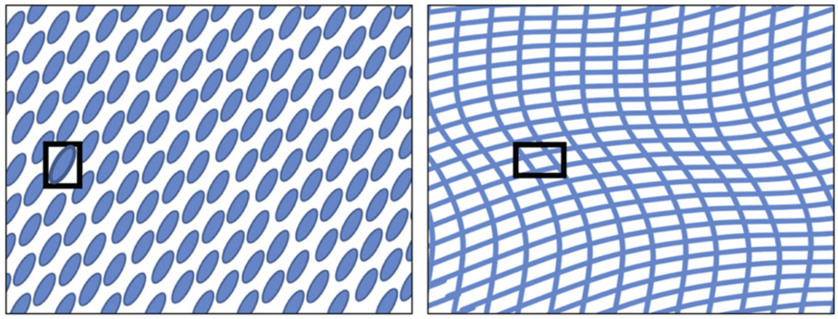

Fig. 1. Visual textures with corresponding subpatterns.

applied to a large number of tasks in computer vision. Among the others:

– *Image segmentation.* Leveraging on the variation of textures with respect to the background, it is possible to identify objects or regions of interest, even though their boundaries are poorly defined or non-existent. For example, a traditional application in computer vision is the segmentation of natural scene images, especially from remote sensing devices [2, 3].
– *Object classification.* Textural characteristics allow to infer physical or chemical properties of the imaged objects. This allows, for example, to classify objects' materials [4] or, in case of medical images, to categorise a patient into a specific range of diseases [5].
– *Image and video compression.* Robust texture representations are essential to achieve efficient and loss-less compressions of digital images [6].
– *Content-based image retrieval.* Texture descriptors provide compact characterisations of the image content, allowing the automatic retrieval of images from databases without need of metadata indexing [7].
– *3D scene reconstruction and rendering.* 3D shape information about objects can be inferred from two-dimensional texture using cameras from specific viewpoints (*shape-from-texture* [8, 9]).

The perception and segregation of different textures in an image has much to do with the way the visual patterns are processed and aggregated by the human visual cortex. Even for the simplest forms of textures, the formalisation of this process into compact mathematical definitions can be very challenging, and may require a-priori assumptions about the distribution of intensities in subregions of the image. Such assumptions are unavoidably context-specific, as they depend on the unique characteristics of the targeted images.

General approaches of texture analysis can be shared among different applications and types of images. Nevertheless, specific imaging contexts, such as bioimage processing, need textural descriptors able to reflect their peculiar characteristics and challenges [10].

In this paper, we will go deeper into the role and fundamentals of textural analysis in bioimage informatics.

2. Texture analysis in biological imaging

The automated analysis of textures has always been a topic of importance in biomedical imaging and especially in the radiology sector, involving different imaging techniques such as X-ray radiography, ultrasound (US), computed tomography (CT), positron emission tomography (PET) and magnetic resonance imaging (MRI) [11]. Due to its superior characteristics in terms of image definition and soft tissues discrimination capabilities, MRI is by far the one where texture analysis has found the highest variety of applications, which include the segmentation of different anatomical areas, the differentiation between normal and pathological subjects as well as the classification and grading of a large number of pathological conditions. For example, widely referenced studies on brain MRI leverage on automated texture analysis to segment the cerebellum, the hippocampus or the corpus callosum, to aid the automated diagnosis of encephalopathy, multiple sclerosis or Alzheimer's disease, as well as to classify hippocampal alterations into different grades [12].

While the automated analysis of textures in medical images (e.g. MRI) has a quite consolidated tradition, microscopy-based bioimaging is a context where the human evaluation of the images has prevailed for a long time. Indeed, the interpretation of the biological specimens is traditionally considered a very complicated task, requiring experienced and well-trained operators. This complication is a consequence of the extreme variability affecting the images, where a "biological" noise, due to different types of cells and corpuscles of variable morphology coexisting in the same specimens, is added to a "technological" noise, due to the general lack of standards in the image generation and acquisition process [13].

Nonetheless, the considerable technological advance of microscopy and the increased availability of computational power at a lower cost have recently determined a growing interest of pathologists and biotechnologists for quantitative analysis systems, where the interpretation of the biological specimens is not left to the subjective evaluation of a human operator but based on analytic features automatically extracted from the digital images [14]. The reason of this interest is two-fold. First, higher accuracy and repeatability of the analysis' outcome. Second, reduced need for highly specialised operators, and hence much lower costs for the health system [15]. Hence, in the last few years the automated analysis of biological textures has become increasingly popular among computer scientists.

In the biological images, we can call "texture" any special spatial arrangements of the biological components appearing in the image, which may have some relevance to a clinical or biological application. Depending on the scale of this spatial arrangement, we can roughly group these textures into two categories:

– In *tissue textures*, texture is a property of a tissue, or in general of a large area of the sample, and it is generated by a specific spatial arrangement of the cells in such area. In other words, the way the cells are positioned within the tissue have some kind of ordered structure, which can be defined as a texture (see two examples in Fig. 2).
– In *cell textures*, texture is a property of the individual cells. In this case, the special arrangement of the sub-cellular components (e.g. the nuclear chromatin) gives a well-recognisable pattern to the cells (see few examples in Fig. 3).