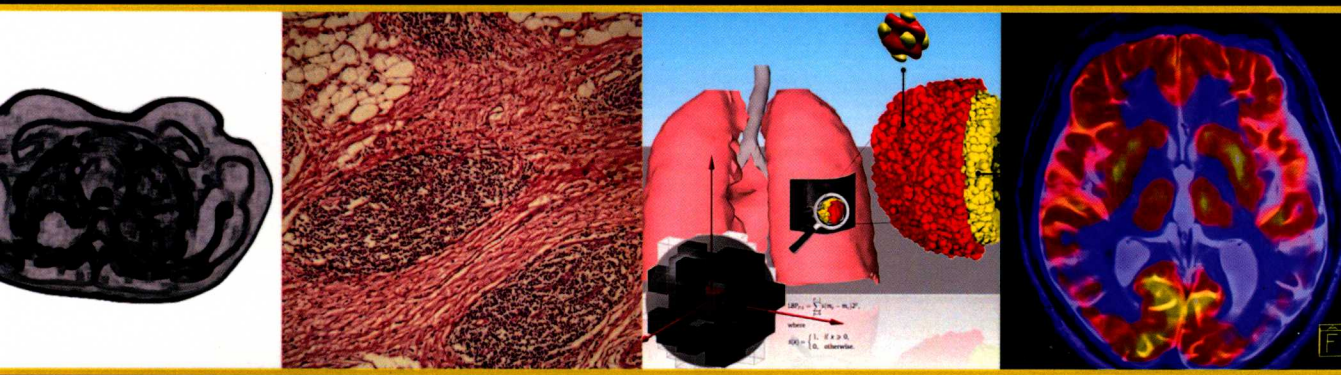
BIOMEDICAL TEXTURE ANALYSIS

FUNDAMENTALS, TOOLS AND CHALLENGES



Edited by
Adrien Depeursinge,
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BIOMEDICAL TEXTURE ANALYSIS

Fundamentals, Tools and Challenges

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PREFACE

Computerized recognition and quantification of texture information has been an active research domain for the past 50 years, with some of the pioneering work still widely used today. Recently, the increasing ubiquity of imaging data has driven the need for powerful image analysis approaches to convert this data into knowledge. One of the most promising application domains is biomedical imaging, which is a key enabling technology for precision medicine (e.g., radiomics and digital histopathology) and biomedical discovery (e.g., microscopy). The colossal research efforts and progress made in the general domain of computer vision have led to extremely powerful data analysis systems. Biomedical imaging relies upon well-defined acquisition protocols to produce images. This is quite different from general photography. Consequently, the analysis of biomedical images requires a paradigm change to account for the quantitative nature of the imaging process. Texture analysis is a broadly applicable, powerful technology for quantitative analysis of biomedical images.

The aims of this book are:

- Define biomedical texture precisely and describe how it is different from general texture information considered in computer vision;
- Define the general problem to translate 2D and 3D texture patterns from biomedical images to visually and biologically relevant measurements;
- Describe with intuitive concepts how the most popular biomedical texture analysis approaches (e.g., gray-level matrices, fractals, wavelets, deep convolutional neural networks) work, what they have in common, and how they are different;
- Identify the strengths, weaknesses, and current challenges of existing methods including both handcrafted and learned representations, as well as deep learning. The goal is to establish foundations for building the next generation of biomedical texture operators;
- Showcase applications where biomedical texture analysis has succeeded and failed;
- Provide details on existing, freely available texture analysis software. This will help experts in medicine or biology develop and test precise research hypothesis.

This book provides a thorough background on texture analysis for graduate students, and biomedical engineers from both industry and academia who have basic image processing knowledge. Medical doctors and biologists with no background in image processing will also find available methods and software tools for analyzing textures in medical images.

By bringing together experts in data science, medicine, and biology, we hope that this book will actively promote the translation of incredibly powerful data analysis

methods into several breakthroughs in biomedical discovery and noninvasive precision medicine.

Adrien Depeursinge, Omar S. Al-Kadi, J. Ross Mitchell

CONTENTS

CHAPTER 1

Fundamentals of Texture Processing for Biomedical Image Analysis

A General Definition and Problem Formulation

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Abstract

This chapter aims to provide an overview of the foundations of texture processing for biomedical image analysis. Its purpose is to define precisely what biomedical texture is, how is it different from general texture information considered in computer vision, and what is the general problem formulation to translate 2D and 3D textured patterns from biomedical images to visually and biologically relevant measurements. First, a formal definition of biomedical texture information is proposed from both perceptual and mathematical point of views. Second, a general problem formulation for biomedical texture analysis is introduced, considering that any approach can be characterized as a set of local texture operators and regional aggregation functions. The operators allow locally isolating desired texture information in terms of spatial scales and directions of a texture image. The type of desirable operator invariances are discussed, and are found to be different from photographic image analysis. Scalar-valued texture measurements are obtained by aggregating operator's response maps over regions of interest.

Keywords

Quantitative image analysis, Spatial stochastic process, Texton, Heterogeneity, Texture analysis

1.1 INTRODUCTION

Everybody agrees that nobody agrees on the definition of *texture* information. According to the Oxford Dictionaries[1] texture is defined as "the feel, appearance, or consistency of a surface or a substance." The context in which the word *texture* is used is fundamental to attach unambiguous semantics to its meaning. It has been widely used in extremely diverse domains to qualify the properties of images, food, materials, and even music. In the context of food and sometimes material sciences, characterizing texture information often involves measuring the response of the matter subject to forces such as shearing, cutting, compressing, and chewing [1,2]. Starting from the early

[1] https://en.oxforddictionaries.com/definition/texture, as of October 10, 2016.

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developmental months of newborn babies, tactile perception of textured surfaces is an important stage of the human brain development [3]. It is an essential step to be successfully acquainted with the physical properties of the surrounding environment [4]. To some extent, estimating the properties and diversity of the latter without having to touch every surface can be efficiently carried out through vision. Human vision learns to recognize texture patterns through extensive experimentation confronting visual and tactile perception of textured surfaces [5]. This provides hints on why human visual texture recognition performs much beyond the use of low level descriptive terms such as *coarse*, *edgy*, *directional*, *repetitive*, and *random*.

In the context of biomedical imaging, texture information relates to the micro- and macro-structural properties of biomedical tissue. Radiologists, pathologists, and biologists are trained to establish links between visual image patterns and underlying cellular and molecular content of tissue samples [6]. Unfortunately, very large variations of this complex mapping occur, resulting in image interpretation errors with potentially undesirable consequences [7–9]. These variations are partly due to the diversity of human biology and anatomy as well as image acquisition protocols and reconstruction, compounded by observer training. Important efforts were initiated by medical imaging associations to construct unified terminologies and grading scores in the context of radiology and histopathology, aiming to limit variations in image interpretation and reporting [10–13]. However, in the particular context of biomedical texture information, the terms used (*e.g.*, *heterogeneous enhancement*, *hypervascular* [12]) are often as inadequate as low level descriptive terms of general textures (*e.g.*, *coarse*, *edgy*) while the perception of human observers is much richer (see Sections 9.4.1 and 9.4.2 of Chapter 9). When considering three-dimensional architectures of biomedical tissue, human observers have limited intuition of these 3D solid textures, because they cannot be fully visualized [14]. Only virtual navigation in Multi-Planar Rendering (MPR) and semitransparent visualizations are made available by computer graphics and allow observing 2D projections.

Computer-based quantitative image texture analysis has a tremendous potential to reduce image interpretation errors and can make better use of the image content by yielding exhaustive, comprehensive, and reproducible analysis of imaging features in two and three dimensions [15–17]. Nevertheless, besides the lack of a clear definition of biomedical texture information, several challenges remain, such as: the lack of an appropriate framework for multiscale, multispectral analysis in 2D and 3D; validation; and, translation to routine clinical applications. The goal of this book is to illustrate the importance of these aspects and to propose concrete solutions for optimal biomedical texture analysis. This chapter will first propose a definition of texture in the particular context of biomedical imaging (Section 1.2). Second, a general theoretic framework for Biomedical Texture Analysis (BTA) will be proposed in Section 1.3. The latter is designed to best leverage the specific properties of biomedical textures. Differences with the classical texture analysis paradigm in computer vision will be highlighted.

Important aspects of texture operator and aggregation function design will be further discussed and illustrated through several concrete examples in Chapter 2. It will also recapitulate key aspects of biomedical texture processes and analysis, with an aim of raising awareness of limitations of popular texture operators used in the biomedical literature while providing directions to design the next generation of BTA approaches. Chapter 3 will use the comparison axes established in Chapters 1 and 2 to compare most popular modern biomedical texture analysis approaches. With the purpose of guiding neophyte or experienced users, a simple checklist is proposed to assess the relevance of the BTA approach in a particular medical or biological applicative context.

1.2 BIOMEDICAL TEXTURE PROCESSES

This section proposes an extensive definition of biomedical texture information under biological, medical, physical, statistical, and mathematical viewpoints.

1.2.1 Image intensity versus image texture

Low-level quantitative image analysis (*i.e.*, pixel-level[2]) can be separated into two main categories: intensity and texture. Image intensity relates to the statistical distribution of the pixel values inside a defined Region Of Interest (ROI). The pixel values can be either normalized across images (*e.g.*, Hounsfield Units (HU) in X-ray Computed Tomography (CT), Standardized Uptake Values (SUV) in Positron Emission Tomography (PET)), or unnormalized (*e.g.*, Hematoxylin and Eosin (H&E) stains in histopathology, Magnetic Resonance Imaging (MRI)). Classic quantitative measures of image intensity are the four statistical moments of the pixel values' distribution (mean, variance, skewness, and kurtosis). Other measures are specific to the considered imaging modality (*e.g.*, SUV max or Total Lesion Glycolysis (TLG) in PET) [18]. The latter are extremely useful to characterize the image content, but cannot measure the spatial relationships between pixel values (see Fig. 1.1). A qualitative keyword such as *tumor heterogeneity* is ambiguous because it is unclear if the heterogeneity concerns pixel values (intensity) or their spatial organization (texture). It is though commonly used to describe the visual aspect of tumors in radiological images with ambivalent meaning [19–21].

The spatial relationships (*i.e.*, the transitions) between pixel values are precisely what texture information is encoding. Haidekker defined texture as "a systematic local variation of image values" [22]. Petrou stated that "the most important characteristic of texture is that it is scale dependent" and that "different types of texture are visible at different scales" [23]. This highlights the importance of the variation *speed* or *slope* or *oscillation* between pixel values, which will be different in *smooth* versus *rough* textures (see Fig. 1.1 left and right). This first notion of the texture scale relates to the spatial

[2] The word *pixel* is used to design both 2D and 3D (*voxels*) image samples.

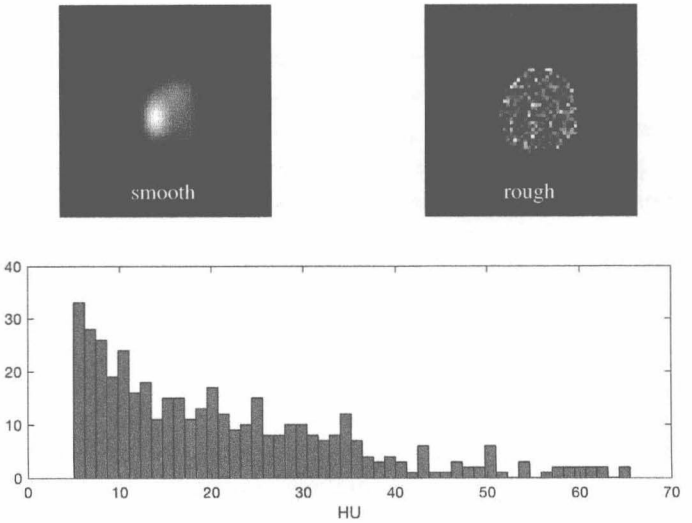

Figure 1.1 The two simulated tumors have identical distribution of the pixel's values and cannot be differentiated using intensity image measures only. They differ in the spatial relationships between the pixels, which is specifically captured by image texture analysis.

frequencies in the image. The higher the spatial frequency, the finer the scale of the transition between proximate pixel values. A second important notion is the direction of the transition. These two notions of spatial scale and direction are fundamental for visual texture discrimination (see Fig. 1.2) [24].

Blakemore et al. provided initial evidence that the human visual system possesses neurons that are selectively sensitive to directional spatial frequencies [25], which has been widely confirmed later on [26]. Most approaches proposed for computerized texture analysis are leveraging these two properties either explicitly (*e.g.*, Gray-Level Cooccurrence Matrices (GLCM) [27], Gray-Level Run Length Matrices (GLRLM) [28], Gray-Level Size Zone Matrices (GLSZM) [29], directional filterbanks and wavelets [30], Histogram of Oriented Gradients (HOG) [31], Local Binary Patterns (LBP) [32], Scattering Transforms (ST) [33,34]) or implicitly (*e.g.*, Convolutional Neural Networks (CNN) [35,36], Dictionary Learning (DL) [37–39]).

A natural mathematical tool to study directional spatial frequency components in D-dimensional signals and images is the Fourier transform and is defined in Eq. (1.1). It is straightforward to see that the Fourier transform for $\boldsymbol{\omega} = \mathbf{0}$ computes the mean of the function, which is not considered as texture information since it relates the mean intensity of the pixels in the image. For $||\boldsymbol{\omega}|| > 0$ the modulus of the Fourier transform quantifies the magnitude of the transitions, where $||\boldsymbol{\omega}||$ is inversely proportional to the scale and the orientation of the vector $\boldsymbol{\omega}$ defines the direction of the spatial frequencies.