Image Analysis

Image analysis is a process by which meaningful information or measurements can be extracted from digital images, typically by computer algorithms.

From: Retina (Fifth Edition), 2013

Related terms:
Neoplasm, Magnetic resonance imaging, Microscopy, Chromosome, Probe, Lesion, Vessel, Melanoma, Segmentation

Learn more about Image Analysis

MICROSCOPY | Image Analys

A. Flook, in Encyclopedia of Food Scie
2003

Introduction
Image analysis is a computer-based p
information from images. The proces
and ends with the output of numerica
it from image processing where both

Image Processing

Michael Abràmoff, Christine N. Kay, in Retina (Fifth Edition), 2013

Retinal image analysis
Image analysis is a process by which meaningful information or measurements can be extracted from digital images, typically by

an image.

Image processing is the means by wh
one or more mathematical algorithms
enhanced in some way. For example,
reduced. Image processing is often us
analysis.

Image analysis requires specialized co
imaging device, such as a television ca
macroviewer.

The first commercial image-analyzing
early 1960s for grading steel by measu
value of using an automated method
of images was soon recognized for ma
materials sciences. Image analyzers w
developed but initially the application
high cost of the instrumentation. How
hardware has steadily decreased over
manufacturers offer relatively inexpen
computer as the host processor. With
equipment, applications have prolifer
including food science and technolog

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computer algorithms. In ophthalmology, image analysis is primarily used to extract clinically relevant measurements from images of the eye, but also to estimate retinal biomarkers, most commonly from fundus color images and from OCT images. The purpose of this section is to familiarize the reader with the main concepts used in the ophthalmic image analysis literature. Image analysis is best understood as a process consisting of a combination of steps. Not all steps are performed in all image analysis algorithms, and some steps may be explicit as multiple steps in one algorithm and form a combined step in another, different algorithm, but the steps described below are typical.

Common image-processing steps

- Preprocessing: remove variability without losing essential information
- Detection: locate specific

Gastrointestinal System

In Nuclear Medicine (Fourth Edition), 2014

Analysis and Quantification

Image analysis of sequential images in conjunction with cinematic display is often adequate for diagnosis of severe motility abnormalities (Figs. 13-2 and 13-3). Quantification can be helpful for diagnosis of less severe abnormalities and for comparison of serial studies over time to determine therapeutic effectiveness. TACs can be derived for the entire esophagus or selected regions (Figs. 13-3, *C*, and 13-4).

Esophageal transit can be quantified by calculating a transit time or the percent residual activity in the esophagus. *Transit time* is defined as the time from the initial entry of the bolus into the esophagus until all but 10% of peak activity clears (abnormal >15 seconds). *Percent residual esophageal activity* is calculated using the formula $([E_{max} - E_t]/E_{max}) \times 100$, where E_{max} is maximum esophageal counts and E_t is the counts after dry swallow number t (abnormal, >20%). For a semisolid meal, abnormal retention at 20 minutes is greater than 5%.

pigmentation of th... cornea/lens/vitreous opacities are all examples of variation between images taken for the same

Molecular Pathology

Lekan Oyejide*, ... Igor Mikaelian**, in A Comprehensive Guide to Toxicology in Preclinical Drug Development, 2013

Computer-Aided Diagnosis (CAD)

Image analysis can be used for detection of 'abnormalities' in histology sections of a tissue or organ, including for the diagnosis of cancer lesions. CAD allows biopsy specimen analysis by creating a quantitative image composed of metrics against tissue patterns that can be compared, reducing diagnostic time and enabling the pathologist to analyze data with

more detail. This system performs a multi-hierarchical multi-scale analysis that uses a large set of texture features to describe each pixel in the image. Based on these features a classifier is trained to distinguish between non-neoplastic and cancerous patterns. Images can be scanned at 40× magnification to high resolution whole slides which are decomposed into constituent scales. Each scale has a number of image features extracted. Each feature in the set assessed for its performance and subsequently used to discriminate between 'cancer' and 'non-cancer' [238].

This same principle can be applied to the detection of other (or any) pathological lesions or even certain histological features. The validation of the features in the set is time- and resource-intensive, and requires constant QA by an experienced pathologist.

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Detection
The purpose of detection is to locate, typically in a preprocessed image, the specific structures of interest, or features, without yet determining their exact

Molecular Pathology

L. Oyejide, ... I. Mikaelian, in A Comprehensive Guide to Toxicology in Nonclinical Drug Development (Second Edition), 2017

Computer-Aided Diagnosis
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pathologist to analyze data with more detail. This system performs a multihierarchical multiscale analysis that uses a large set of texture features to describe each pixel in the image. Based on these features a classifier is trained to distinguish between nonneoplastic and cancerous patterns. Images can be scanned at 40× magnification to high-resolution whole slides, which are decomposed into constituent scales. Each scale has a number of image features extracted. Each feature in the set is assessed for its performance and subsequently used to discriminate between "cancer" and "noncancer" [238].

This same principle can be applied to the detection of other (or any) pathological lesions or even certain histological features. The validation of the features in the set is time- and resource-intensive and requires constant QA by an experienced pathologist.

The output of the matching process indicates if and where the features were detected in the image. In some image analysis systems, this output is interpreted directly, while in others, a

Correlations and Convolutions

Michael F. Moody, in Structural Biology Using Electrons and X-rays, 2011

Publisher Summary

Image analysis uses either Fourier transforms (FTs) or cross-correlations (CCs) and FTs are based on CCs, which are usually calculated with FTs. This chapter introduces the concept of correlation function, referring to situations in molecular biology. Correlation is used in sequence comparisons. Cross-correlation function can be considered from two different viewpoints. Although they give identical answers, they differ in

their intuitive significance, and one viewpoint may be more appropriate than another for certain applications. Convolution is discussed as a process of replacing every element of one function by an entire copy of the other function. Correlation of a function with itself gives its auto-correlation function (ACF). The ACF is always an even function, because the later stages of overlap exactly mirror the early stages, except that the top and bottom curves are exchanged. In electron microscopy, this should apply to two exact copies of a particle in the same orientation. In X-ray crystallography the ACF is called the Patterson function, which can be calculated directly from the experimental intensity data, without the arduous and uncertain search for the phases of the diffraction pattern. Consequently, much effort has gone into finding its uses.

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mathematically best-fitting boundary, given the specific detection output(s). The output of the segmentation step can be used directly for assessment, for example when showing the

Lipid Droplets

Huajin Wang*, ... Richard Lehner‡, in Methods in Cell Biology, 2013

7.2.3.4
Image processing and analysis
Image analysis can be performed by a variety of software, including open architecture software, such as Image J and CellProfiler, commercial imaging software, such as MetaMorph and Volocity, or a high-level language for data analysis and visualization, such as MATLAB. Each of the abovementioned software has its own strength and weakness, but in all cases, object segregation is the most challenging task in order to identify

objects as well as possible. This is especially valid when CLDs are vastly different in their sizes, because it might be difficult, if possible at all, to precisely identify all objects. Paramete different samples are compared, it is for the object of interest in all sample should be obtained for quantification.

For our processing and analysis, imag microscopy are processed with Voloci contrast, density, and blackness are ac photobleaching is corrected for quant calculate the transfer of newly synthes preformed LDs (BODIPY 558/568 C_{12} areas containing red fluorescent signa a defined density threshold in the Cy3 the region of interest (ROI), and objec setting object size and shape referenc and objects selected under these crite area. Data from all time points are co Fluorescence intensity within preform quantified for both GFP and Cy3 chan percentage of initial fluorescent inten exported to Microsoft Excel for plottin incorporation can be reflected clearly: relatively stable, suggesting of low tur channel increase gradually with time, incorporation of the newly synthesized reesterification of new LDs, or by fusic preformed LDs. When hepatocytes fr were compared, differences in fatty ac preformed CLDs can be clearly observ

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High-Resolution Analysis of Genetic Events in Cancer Cells Using Bacterial Artificial Chromosome Arrays and Comparative Genome Hybridization

John K. Cowell[1], Norma J. Nowak[1,2], in Advances in Cancer Research, 2003

B

Analysis of CGHa Arrays

Image analysis is the first step in analyzing CGH arrays and is performed identically to cDNA expression arrays. Imagene (BioDiscovery, Marina Del Rey, CA) software is used to identify the spots and to measure the fluorescent intensity at each element on the array. Optimal cDNA expression array analysis requires that the experiments are designed to incorporate a dye flip, addressing the possibility of dye bias and providing a replicate experiment. CGH arrays are far more robust as a result of significantly higher signal-to-noise

ratios and are, thus, more reproducible than cDNA-expression arrays, allowing a single slide hybridization to accurately measure genomic copy number changes. The issue of dye bias in CGH arrays, however, should be addressed either by performing a dye-flip experiment or by applying an intensity dependent

Volume I

Andrew J. Burghardt, ... Sharmila Majumdar, in Vitamin D (Third Edition), 2011

Image Analysis

Image analysis techniques to segment both the inner and outer cortical boundary from their surroundings are commonly semiautomatic. An algorithm previously presented [252] featured a deformable contour (snake) to conform to the strongest gradient edges in the neighborhood of the manually placed ROI. The accuracy of the method was tested by comparing MR images ($0.16 \times 0.16 \times 2$ mm^3) at 1.5 Tesla to high-resolution CT images (spatial resolution $0.07 \times 0.07 \times 0.8$ mm^3) of ex vivo porcine femora specimens. The in vivo feasibility was tested in the distal radius of a cohort of human subjects. The cortical area was calculated as the area enclosed by the concentric contours. The mean thickness was calculated as area divided by mean contour length. Using this method, very good in vivo reproducibility for cortical volume (CV = 2.19%) and for cortical thickness (CV = 1.96%) was found. Another method used is the distance transform method [50]. The measurements of cortical thickness are further improved by fitting a sphere into the segmented cortical shell. Comparing thickness measurements from MR data with HR-pQCT significant correlations were found but also higher values for the MRI data

[35]. One limitation of MRI is the segmentation close to the endplate, where the cortex becomes thin and flares from the narrow diaphysis to the wider epiphysis. This geometry limits axial MR images and therefore render difficult. Another semiautomatic segn presented for the proximal femur [25 the cortical contour, radial profiles pe normalized to the marrow signal and operators before computing the cross similar CV of around 2% was found f technique.


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Magnetic Resonance Imaging of Cancer Therapy

Feng Chen*†, Yicheng Ni*, in
Cancer Theranostics, 2014

Data Analysis

The image analysis for DCE-MRI needs to be done offline. For instance, in a rat liver tumor model, DCE-MRI data was quantified on a Linux workstation using dedicated software (Novartis' Biomap). In the first step, pixel-wise, relative contrast agent concentration (C^{rel}) maps were generated by a first-order approximation of the signal changes:

$$Crel(t)=S(t)–SbSb \quad (7.4)$$

where $S(t)$ is the measured signal at time point t, and S_b is the average SI of the images before contrast administration. On the original DCE-MR images, three ROIs were contoured: the entire tumor, the normal liver, and the abdominal aorta, with the last one used to determine the arterial input function (AIF, or $C_p(t)$). The

ROIs were copied to the relative contrast agent concentration maps and the curves for these three tissues were generated. Next, the measured values were fit with the

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subsets of this infinite set can be considered optimal for classifying the image according to some reference standard. Hundreds of features for a pixel can be calculated in the training stage to cast as wide a net as possible, with algorithmic feature selection steps used to determine the most distinguishing set of features. Extensions of this approach include different approaches to classifying groups of neighboring pixels subsequently by utilizing group properties in some manner, for example cluster feature

classification, where the size, shape, and average intensity of the cluster may be used.

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