Cancer Cell Image Analysis and Visualization

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ABSTRACT

We review computerized cancer cell image analysis and visualization research over the past 30 years. Image acquisition, feature extraction, classification, and visualization from two-dimensional to three-dimensional image algorithms are introduced with case studies of bladder, prostate, breast, and renal carcinomas.

Keywords: 3D-Image Algorithms, Cancer Cell Image Analysis, Classification, Feature Extraction, Image Acquisition, Visualization

INTRODUCTION

Microscopy has long been used as the standard for histological cancer cell image analysis, but the visual interpretation is subjective. Computer-based microscopy image acquisition, processing, and analysis started in the 1960s (Bergkvist, 1665), and at that time, personal computers lacked the capacity to process medical images; only workstations were powerful enough. Despite the controversy over whether decisions made by a machine could prevail over intelligent human visual cognition, the biggest issues in computing were accurate classification and reproducibility.

First, Stenkvist (1978) and Bengtsson (1976) applied computing to examining cervix cancer cell tissue sections in Sweden. They developed a prescreening program for cervix cancer that simply classified normal and abnormal cells, i.e., benign and malignant cells.

Mathematical parameters can be used to extract two types of microscopic features: morphological and textural. In the Netherlands, Baak (1990) used morphological features to classify breast carcinomas. Pressman (1976) was the first to make use of textural features, and Haralick (1973) subsequently developed more defining characteristics. Over time, the image resolution increased from 1 bit black-and-white to 8-bit gray scale to 16- and 42-bit red–green–blue (RGB) colors with high resolution. In addition, images have progressed from two-dimensional (2-D) to three- (3-D) and even four-dimensional (Choi, 2005).

Consequently, developments in both computer software and hardware have contributed

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greatly to the diagnosis and prognosis of patients with cancer.

**MATERIALS AND METHODS**

**Image Acquisition**

Early microscopic image acquisition involved attaching an analog charge-coupled device (CCD) camera to a microscope (Choi, 1994). Then, the analog signals were converted into digital signals using a frame grabber. Recently, digital CCD cameras have been attached directly to microscopes.

**Histological Cell Feature Extraction**

Once cells are stained with a biochemical reagent, the most important process is to identify the cell nucleus, which involves subtracting the region of interest (ROI) from the background. Then, we quantify the features of the cell nucleus, including the size, perimeter, major and minor axes, and cell numbers. Textural features include entropy, contrast, moment, and intensity variation. We can calculate more than 1,000 features. Then, we select significant features using statistical analyses (Cox, 1972).

Finally, we determine the cell densitometry of an area (Choi, 2007; Kayser, 1992). Generally, the most important objects in a ROI are the cell nuclei, for which we have calculated the cell features. Figure 1 shows the (a) morphology, (b) texture, (c) intensity, and (d) special staining for molecules in sample cells.

**Data Classification**

Normally, two methods are used for numerical data classification: statistical classification (i.e., the conventional method) and neural network methods. Statistical analyses include multivariate, factor, regression, principal components, and independent component analyses (John, 1992). Neural networks methods include back propagation networks, Hopfield networks, and

![Figure 1. Examples of various cell characteristics](image)
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