



A Java application for tissue section image analysis

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Received 5 November 2003; received in revised form 21 April 2004; accepted 21 April 2004

KEYWORDS

Java;
Object-oriented;
Platform-independent;
Quantitative
histopathology;
Quantitative cytology;
Image cytometry

Summary The medical industry has taken advantage of Java and Java technologies over the past few years, in large part due to the language's platform-independence and object-oriented structure. As such, Java provides powerful and effective tools for developing tissue section analysis software. The background and execution of this development are discussed in this publication. Object-oriented structure allows for the creation of "Slide", "Unit", and "Cell" objects to simulate the corresponding real-world objects. Different functions may then be created to perform various tasks on these objects, thus facilitating the development of the software package as a whole. At the current time, substantial parts of the initially planned functionality have been implemented. Getafics 1.0[®] is fully operational and currently supports a variety of research projects; however, there are certain features of the software that currently introduce unnecessary complexity and inefficiency. In the future, we hope to include features that obviate these problems.

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1. Introduction

Many industries have taken significant advantages of Java and Java technologies during the last few years, and medicine is no exception [1]. Since Java is designed to be an object-oriented language from the ground up, writing software applications in Java means that one can benefit from object-oriented concepts [2]. Apart from this important aspect, there are other specific reasons

why Java is our programming language of choice. Java is platform-independent, has a complete collection of GUI elements and supports Java Native Interface (JNI), web-services, multithreading, and connection with databases.

2. Background

There are two main reasons why Java is an ideal language with which to construct a tissue section analysis software package. First, Java is platform-independent. A platform simply refers to an underlying computer system on which various

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applications are run. Examples include UNIX, Mac OS X, Windows, and Linux. Platform-independence, then, indicates that a program developed on one platform may be executed on any other computer regardless of platform. From this, we see that Java proves powerful, because many different users (on several different platforms) may use the tissue section analysis software without the need for software modifications [3–5].

Secondly, Java is an object-oriented language. In essence, this means that the language simulates real-world objects. Rather than having raw code that is not easily decipherable in terms of functionality and semantics, object-oriented structures and syntax allow for facilitated understanding and manageable design. A simple example is the creation of a “Cell” object in the code of the software (to simulate a real-world cell). Rather than using complex code, object-oriented programming allows for the declaration of an object called “Cell”, and consequently lets a user code in such a way that he or she may easily implement all the real-world functions and structures indicative of a cell. Like platform-independence, this proves extremely powerful, as we are coding for software that deals with tangible, real-world objects, not abstract concepts [3–5].

Much of screening in medicine involves obtaining cytologic (cell) samples. These samples are obtained by scraping cell surfaces of organ sites, such as the cervix, the mouth, or even the lungs. These samples are fixed in solutions, placed on slides, stained with chemicals, and viewed under the microscope by technologists and physicians with special training called cytopathologists. A great deal of expertise is required to distinguish the range of possible diagnoses, which include cells from normal to those with cancer. The chemical stains that are used by cytopathologists by convention for training have no mathematical logic. A Feulgen-thionin stain is a type of stain that is stoichiometrically related to the amount of DNA in the cell nucleus and therefore makes an ideal stain for a mathematical interpretation of a slide. Fig. 1 shows a Papanicolaou smear from the cervix stained with both the conventional and the Feulgen-thionin stains [6–8].

Computer-assisted image cytometry or computer reading of cells, attempts to sample the objects on the slide and subject them to mathematical analysis. In this case, the Cytosavant® measures 144 features (Table 1) on a cell-by-cell basis. Fig. 2 is a photograph of the Cytosavant®, which was used as a prototype for Getafics 1.0® the system discussed in this paper. The microscope is programmed to randomly sample 2000 cells on each slide. Statistical analyses can be used to derive algorithms (de-

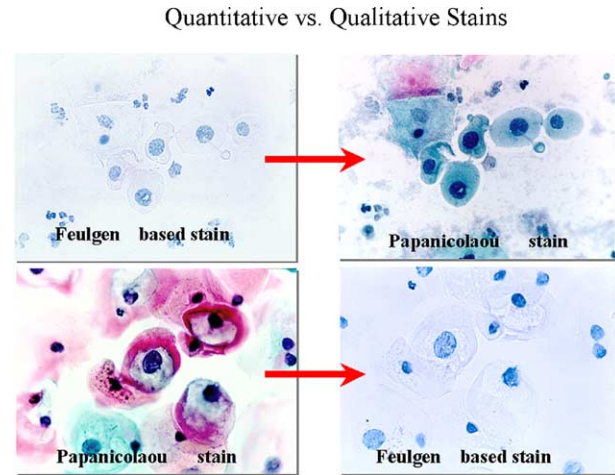


Fig. 1 Quantitative vs. qualitative stains. This figure demonstrates a cytologic sample of cells from the cervix. The top left panel shows that cells from the cervix can be stained with the Feulgen stain, and then, on the right panel, counterstained with the Papanicolaou stain. On the bottom left panel, the cells from the cervix are stained first with the Papanicolaou stain and then counterstained with the Feulgen stain. The Feulgen stain is a quantitative stain, while the Papanicolaou stain is a qualitative stain. The Papanicolaou stain is used by physicians to judge the amount of abnormality of the Pap smear, while the Feulgen stain is used by computer-assisted image cytometry for quantitative measurement.

scribed elsewhere) that classify the cells. These algorithms, once validated, can classify the cells objectively without much human intervention. Figure shows a cell sample with Feulgen and Papanicolaou staining. Table 1 outlines the cytometry features that are mentioned [6–8].

Histopathology or tissue sections are obtained from biopsies (small pieces of tissue). These



Fig. 2 Cytosavant® is a computer-assisted image analysis system for the quantitative measurement of cytopathology and histopathology. The system consists of an autofocusing microscope, two computers, and an automatic slide loader.

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