

perform diagnostic review functions including visiting an image 422, accept/reject of cells 424, nucleated cell counting 426, accept/reject of cell counts 428, and saving of pages at 430. The report level 418 allows an operator to generate patient reports 432.

In the configuration level 406, the operator can select to configure preferences at 434, input operator information 437 at 436, create a system log at 438, and toggle a menu panel at 440. The configuration preferences include scan area selection functions at 442, 452; montage specifications at 444, bar code handling at 446, default cell counting at 448, stain selection at 450, and scan objective selection at 454.

Computer Implementation

Aspects of the invention may be implemented in hardware or software, or a combination of both. However, preferably, the algorithms and processes of the invention are implemented in one or more computer programs executing on programmable computers each comprising at least one processor, at least one data storage system (including volatile and non-volatile memory and/or storage elements), at least one input device, and at least one output device. Program code is applied to input data to perform the functions described herein and generate output information. The output information is applied to one or more output devices, in known fashion.

Each program may be implemented in any desired computer language (including machine, assembly, high level procedural, or object oriented programming languages) to communicate with a computer system. In any case, the language may be a compiled or interpreted language.

Each such computer program is preferably stored on a storage media or device (e.g., ROM, CD-ROM, tape, or magnetic diskette) readable by a general or special purpose programmable computer, for configuring and operating the computer when the storage media or device is read by the computer to perform the procedures described herein. The inventive system may also be considered to be implemented as a computer-readable storage medium, configured with a computer program, where the storage medium so configured causes a computer to operate in a specific and predefined manner to perform the functions described herein.

A number of embodiments of the present invention have been described. Nevertheless, various modifications may be made without departing from the spirit and scope of the invention. Accordingly, the invention is not to be limited by the specific illustrated embodiment, but only by the scope of the appended claims.

We claim:

1. An automated method for the measurement of residual protein in a cellular specimen, comprising:

- (a) providing a plurality of stained subsamples from a cellular specimen;
- (b) automatically selecting a Z position in each subsample for imaging a candidate object of interest;
- (c) automatically obtaining a low magnification image of the candidate objects of interest comprising obtaining a plurality of pixels in each subsample;
- (d) automatically filtering the candidate object of interest pixels in each subsample with a low pass filter;
- (e) automatically morphologically processing the candidate object of interest pixels in each subsample to identify artifact pixels;
- (f) automatically identifying the candidate object of interest in each subsample by eliminating pixels identified as artifact pixels;
- (g) adjusting the apparatus to a higher magnification;
- (h) automatically acquiring a higher magnification image of the subsample, at the location coordinates corre-

sponding to the low magnification image, for each candidate object of interest identified in (f);

- (i) automatically transforming pixels of the higher magnification image in a first color space to a second color space to differentiate higher magnification candidate object of interest pixels from background pixels;
- (j) automatically identifying, at high magnification, an object of interest from the candidate object of interest pixels in the second color space; and
- (k) determining a protein level in the subsamples, wherein the protein level is indicative of the residual component of a cellular protein.

2. The method of claim 1, wherein the first color space comprises red, green, and blue components for each pixel and the transforming step includes converting the red, blue and green components for each pixel in the first color space to pixel values in a hue, saturation, and intensity space.

3. The method of claim 2, wherein the hue, saturation, and intensity pixel values are compared to a threshold to identify pixels having a component value equal to or greater than said threshold as candidate object of interests pixels.

4. The method of claim 1, wherein the cellular protein is an enzyme.

5. The method of claim 4, wherein the enzyme is alkaline phosphatase (AP).

6. The method of claim 4, wherein the enzyme is acid phosphatase (AcP).

7. The method of claim 4, wherein the enzyme is  $\alpha$ -naphthyl butyrate esterase.

8. The method of claim 1, wherein the cellular protein is assayed immunologically.

9. The method of claim 1, wherein the image is a color image.

10. The method of claim 1, wherein the image is a digital image.

11. A computer program, residing on a computer-readable medium, for obtaining images of subsamples of a cellular specimen, the computer program comprising instructions for causing a computer to:

- (a) select a Z position for imaging a candidate object of interest in a subsample;
- (b) obtain a low magnification image of the candidate object of interest comprising obtaining a plurality of pixels;
- (c) filter the candidate object of interest pixels in each subsample with a low pass filter;
- (d) morphologically process the candidate object of interest pixels in each subsample to identify artifact pixels;
- (e) identify the candidate object of interest by eliminating pixels identified as artifact pixels;
- (f) adjust the apparatus to a higher magnification;
- (g) acquire a higher magnification image of the subsample, at the location coordinates corresponding to the low magnification image, for each candidate object of interest identified in (e);
- (h) transform pixels of the higher magnification image in a first color space to a second color space to differentiate higher magnification candidate object of interest pixels from background pixels;
- (i) identify, at higher magnification, an object of interest from the candidate object of interest pixels in the second color space; and
- (j) score a protein level in the subsample.