A Topological Approach to Cell Counting

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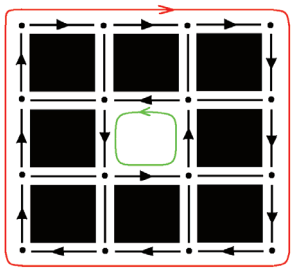
Cell counting and identification is a common task in biology and pathology. To automate this task one has to approach it as an image segmentation problem. Many researchers have solved this problem following various strategies. However, these methods may have drawbacks. For example, some methods partially discard information contained in the image. Ours is lossless.

Method.



The approach we propose relies on topology, which is the science of continuity and connectedness that studies spatial relations within the image. An image pixel is defined to have 4 vertices (corners), 4 edges, and one face. Algebraic topology uses algebraic operations with these objects to capture and count the number of completed cycles - circular sequences of edges. The completion of a cycle indicates the presence of a cell.

In binary images, this approach allows us to find cells as black objects with white background or white objects with black background. In the case of gray scale, our strategy is to count dark objects with light background and light objects with dark background. The types of images our algorithm is most suitable for are those that represent something 2-dimensional (rather than 2D images of 3D objects) such as images of cellular tissue or blood cells under a microscope.

The topological nature of the algorithm makes it especially suitable for cell counting:

- The count of cells is independent of their locations.
- The measurements of cells are independent of their orientations with respect to the image grid.
- The cells and other features are captured with no deformation, smoothing, blurring or approximation.

Software.

We have developed a software suite called *cellAnalyst*. For each image, it is intended to produce the following output data:

- the image with cells' contours displayed, and
- a spreadsheet with cells' locations and characteristics such as area, perimeter, intensity, contrast, and many others.

The processing starts with an *automatic analysis* of the image that produces a graph that contains complete data about the image. An initial segmentation of the image is also provided. Next, in the *semi-automatic mode* the user can interactively visualize multiple segmentations. By moving sliders corresponding to cells' characteristics the user instantly changes cells' boundaries and can choose the most appropriate segmentation. The output data is then updated in real time. In the *manual mode* the user can also exclude noise and irrelevant details from the analysis by simply clicking on them.

The software also has all the necessary image management and image manipulation capabilities.

For every image in the user's collection, the compete set of image analysis data is saved as an entry in a *database*. This allows the user to search the whole collection for images with desired content. For example, the user is able to find all images that contain a given number of cells with given size and shape.

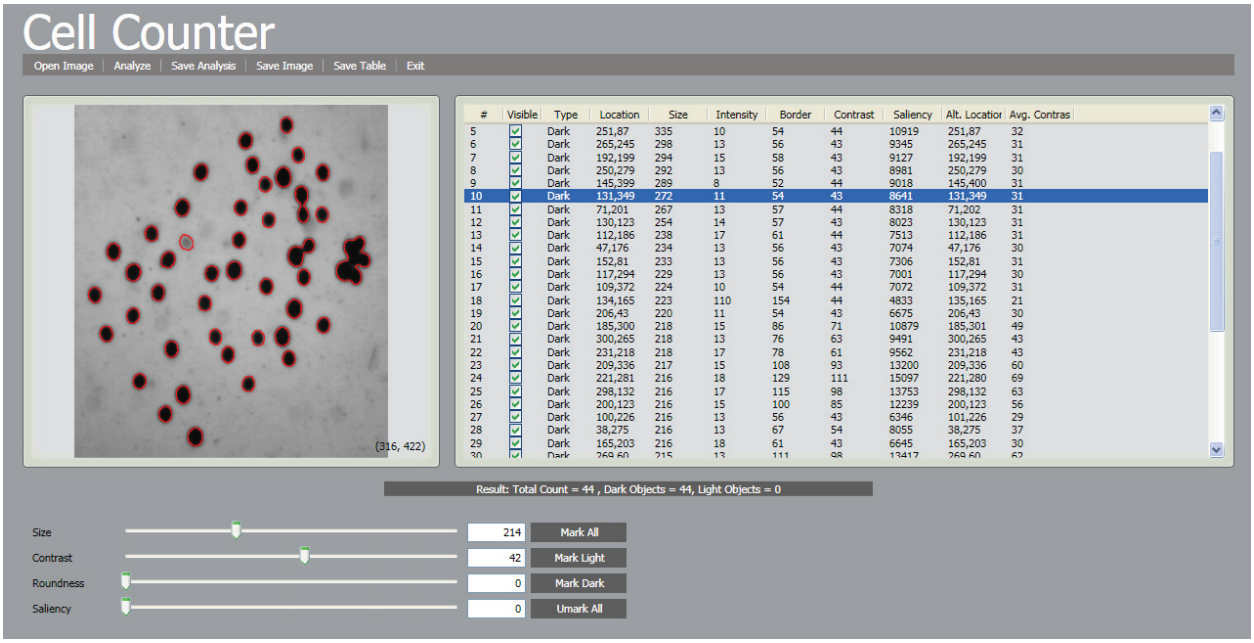


Figure 1. The cell counter part of the user interface of cellAnalyst.

Examples.

The analysis data has been verified using pathology and retinal images. The images are analyzed by manually counting, identifying, and measuring cells and the results are compared with the output of cellAnalyst. The matches have been reliable and repeatable.

The examples below show a good match between the counts produced manually and those obtained with cellAnalyst.

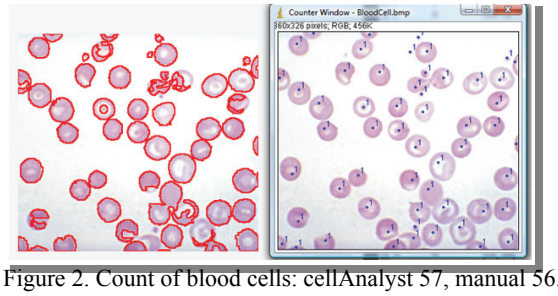


Figure 2. Count of blood cells: cellAnalyst 57, manual 56.

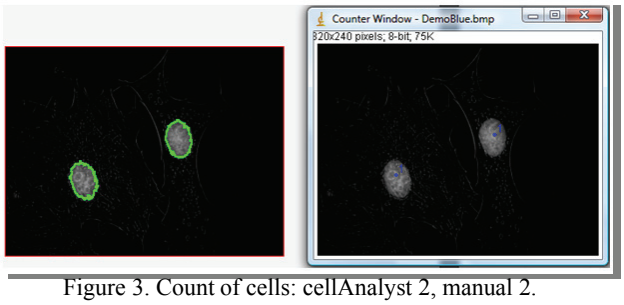


Figure 3. Count of cells: cellAnalyst 2, manual 2.

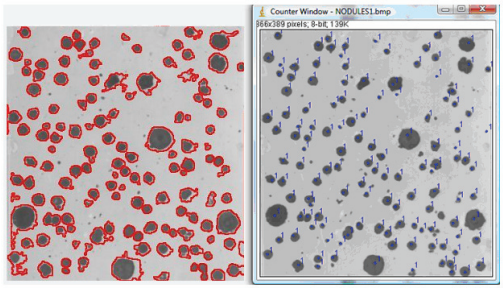


Figure 4. Count of nodules: cellAnalyst 129, manual 128.

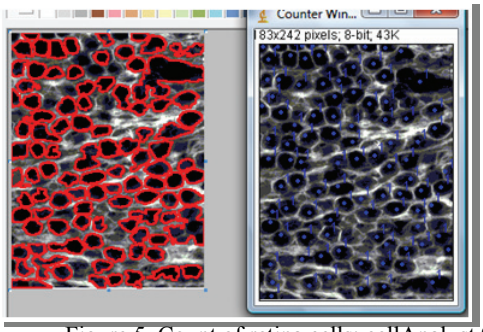


Figure 5. Count of retina cells: cellAnalyst 91, manual 91.