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. 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 count the number of completed cycles - circular sequences of edges. The completion of a cycle indicates the presence of a cell. In the case of gray scale, our strategy for counting cells 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. First, the count of cells is independent of their locations. Second, the measurements of cells are independent of their orientations with respect to the image grid. Third, the algorithm captures cells and other features regardless of their sizes, shapes, and locations with no deformation, smoothing, blurring or approximation.

We developed a software suite called cellAnalyst with the following output: the image with cells' contours captured and a spreadsheet with cells' locations and characteristics such as area, perimeter, intensity, and contrast. The processing starts with an automatic analysis of the image that produces a graph that contains complete data about the image. The user proceeds in a semi-automatic mode to interactively visualize various segmentations. By moving sliders corresponding to cells' characteristics the user instantly changes the cells' boundaries and can choose the most appropriate segmentation. The output data is then updated in real time. The user can also exclude noise and irrelevant details from the analysis by simply clicking on them.

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.

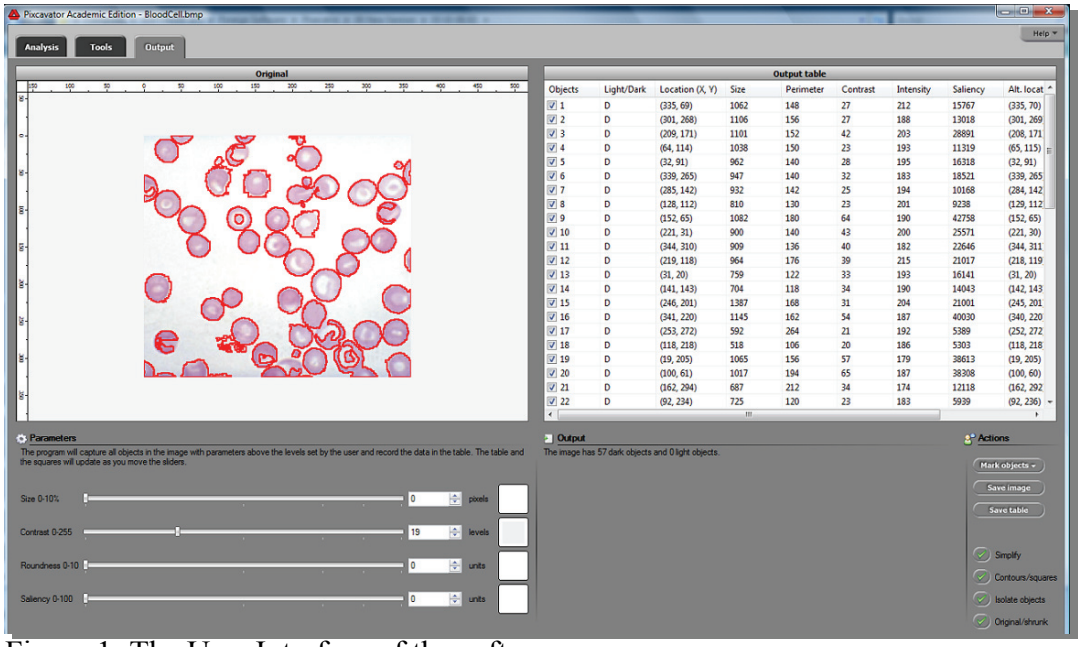

Figure 1: The User Interface of the software

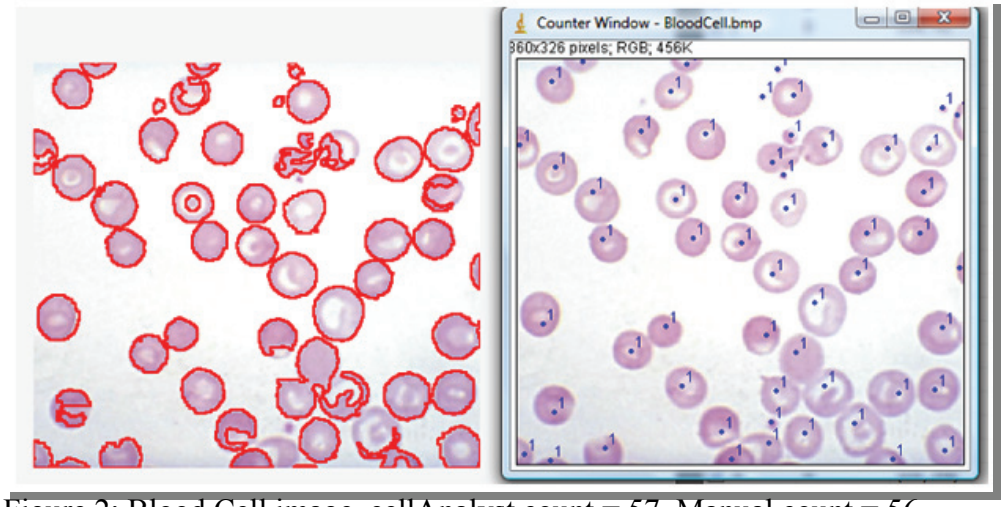

Figure 2: Blood Cell image. cellAnalyst count = 57, Manual count = 56

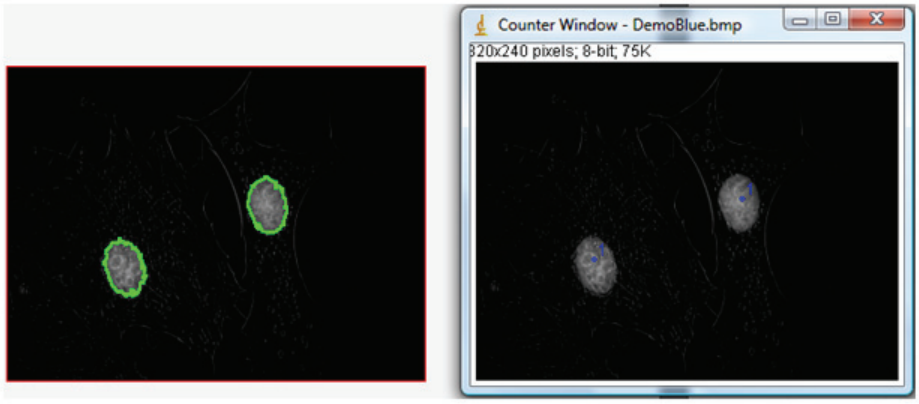

Figure 3: Cell image. cellAnalyst count = 2, Manual count = 2

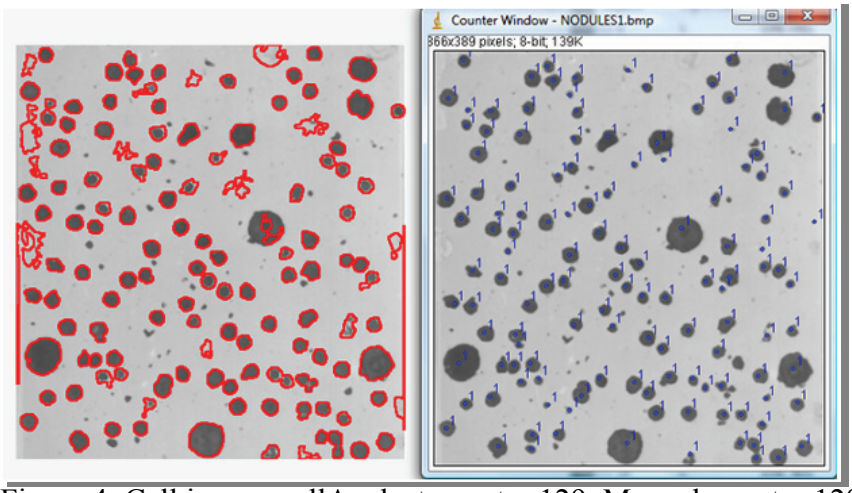

Figure 4: Cell image. cellAnalyst count = 129, Manual count = 128

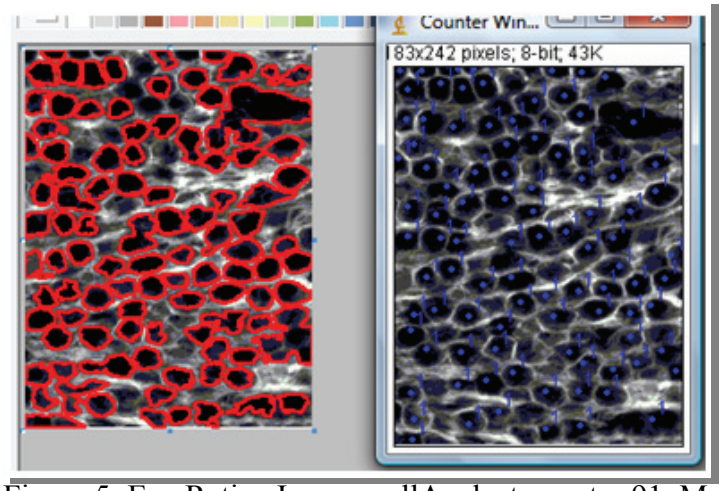

Figure 5: Eye Retina Image. cellAnalyst count = 91, Manual count = 91

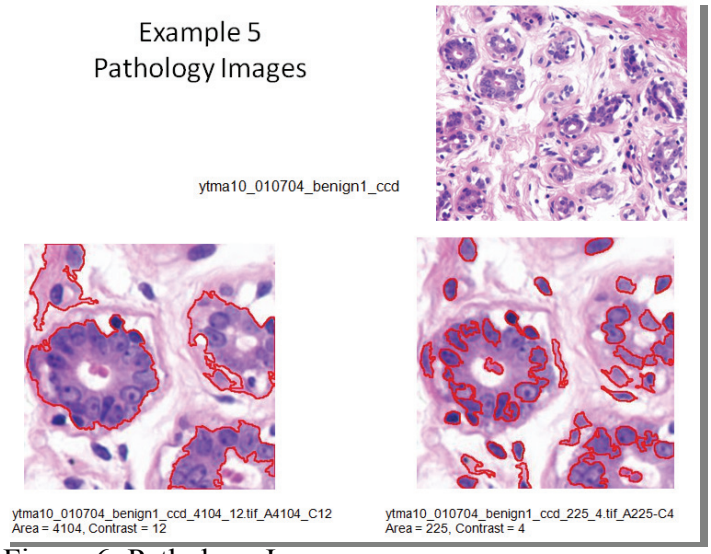

Figure 6: Pathology Images