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An Automated Nuclei Cells Counting Using Image Processing and Quantum Computing

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Abstract
Automated Nuclei Cell Counting is needed in biomedical research and clinical diagnosis traditionally counting manually under a microscope that was time-consuming and prone to error. This paper will outline the QUT system, a system that combines image processing and quantum computation to detect and quantify nuclei within a shorter time. Classical techniques like watershed algorithms and morphological operations are used to reduce noise, enhance contrast and segment microscopic images in order to isolate clustered nuclei in a specific manner. Quantum algorithms increase performance by means of parallel processing and optimization which limits computational complexity by many folds over classical algorithms. This facilitates the effective manipulation of large amounts of biomedical image data in order to extract better features and patterns. The proposed hybrid model is assessed on two publicly available datasets of cell images, which give it a better level of accuracy, less processing time and better scalability compared with the traditional methods. Application QUT can be used to perform nuclei counting in real time, with large throughput, using quantum computing and image processing, in cancer diagnostics, pharmaceutical discovery and in cell biology investigations - quantum-enabled biomedical image analysis.

Keywords—*Automated counting of nuclei, image processing, quantum computing, cell segmentation, cancer diagnostics*

1. Introduction

Applications of the computational methods, especially image processing, and other advanced technologies have seen wide application over the last few years in the medical diagnosis field [1], information security [2]-[4], large-scale data searching [5], and network [6] fields. Automatic Computer the post-acquisition of the selected microscope objects has become a central issue in the bioinformatics field where morphology of cells, disease diagnostics and cell statistics should become a viable concern [7]. Such automated systems are quite useful in biomedical research since they do not require the interventions of human beings because they are quicker and less incremental compared to manual research. Microscopic analysis also features in determining the definition of the biomedical problems including normal and tumors[10-15] cells, morphological variations of the nucleus as well as dynamic properties of cells when put through the treatment procedures [8]. To conduct the analysis of the histological image, as well as one of the required aspects of the work, such tasks include nuclei cell counting. Manual count is lengthy, tiresome as well as full of faults. Therefore, it has too considered automated structures, thresholding methods [9] and edge spotting filters such as Laplacian of Gaussian (LOG). Nevertheless, these conventional methods are also vastly doubted in terms of the irregular and complicated histological images. The use of machine learning algorithms to supplement classical image processing algorithms has increased in order to gain higher segmentation and counting results. In which, k-means clustering algorithm has been found to be the most helpful in the field of nuclei segmentation since it separates or gathers the similar pixels in the color spaces differently [16]. However, even with its successfully implemented application, the traditional k-means is still problematic in this case when there are overlapping cells and inequality in the areas of images. New trends on quantum computing have resulted to the introduction of new alternatives in solving computationally problems which are not

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easily solvable on classical computers. The field of biomedical image analysis is of high importance and there are certain optimization and pattern recognition problems that can be sped up exponentially with quantum algorithms. Quantum computing may be relevant in the above situation in terms of integration with pipelines of image processing enhancing the accuracy of feature extraction, clustering and segmentation on big and high-dimensional data. Moreover, schemes like Qiskit can enable an easy-going transition of quantum algorithms to classical algorithms in that hybrid quantum-classical modelling would be feasible in technology transfer. The ability to handle complicated histological problems, such as the ones with overlapping nuclei and abnormal morphologies, which is prone to limit the performance of the traditional methods, is enormously possible in such a conglomeration. In this paper, we will propose the implementation of an automated system of nuclei cell counting where the image processing based on Python models the work combined with quantum computing in the Qiskit environment [17-25]. It applies k-means algorithm to attain efficient segmentation with quantum computing providing a higher efficiency in the computation since such processing is done in parallel and with an aim of achieving better clustering. Potential speed and accuracy of segmentation delivered by quantum-enhanced computation along with a conventional force in processing images can meet these challenges, which could be used to examine histological image, notably in terms of scaling.

2. Roposed Approach

The rationale of the proposed solution is that the issues associated with the search and detection of nuclei cells in histologic images can be resolved with syntax of brute-force image processing and quantum-assisted image processing. The workflow involves two of the key steps; the morphological image process and the color channel extraction and k-means clustering segmentation. In addition, a quantum computation with the help of Qiskit can be utilized to optimize clustering to perform a faster and more accurate segmentation. This is because a color histological image is put in the proposed system, and in turn, one gets the number of total cells which can be the nuclei cells. Figure 1 below illustrates flowchart of the proposed algorithm:

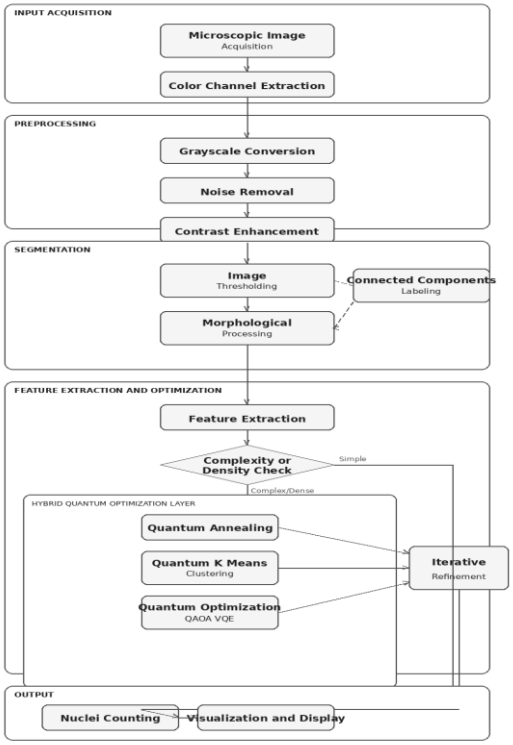

Figure 1 Flow Chart

2.1. Extraction of Color Channels

A histological image (commonly stained with hematoxylin and eosin or H&E) in the RGB is employed as input into the system whereby the nuclei can be better recognized in certain color channels. This process divides the image into three different parts of it, which include red, green, and blue among them with a set of values of 0 to 255, the intensity values. The objective is to determine the channel of nuclei where they will come out in optimum contrast with the background tissues and cytoplasm. One of them would be that nuclei will be darker on the blue channel hence allows them to be divided more easily. The right channel will cut on the irrelevant data, and grow feature detection. As a practical demonstration, the elected channel is converted to grayscale intensity map which is further easier to manipulate because it not only can provide dimensionality reduction but also achieve much information. This preprocessing is used to minimize the spectral information to be further transmitted to the clustering task to the most

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pertinent information.

2.2. Morphological image processing

The result of the segmentation, a binary image, will probably have defects, either in the form of noise (small white dots), edges of ruptured nuclei or between cells that will have to be divided. To get past this morphological operation are carried out. The white areas (nuclei) which crop out the noise and partition the adjoined cells will be depleted by erosion and the white areas (nuclei) restoring to the -pre-erosion- size will be amplified by dilation. An opening, an erosion and dilation, removes smaller structures and retains intact cell boundaries and a closing, which is a dilation and erosion, which fills small gaps inside of nuclei hence guaranteeing solid objects. In addition, image complement is adopted whereby the nuclei are represented as white objects and hence easy to process and holes are filled on the sides of the nuclei shapes to create a continuous nuclei shape. The element of structuring, a disk, is used in such operations since, among all shapes, it fits in a circular shape of most of the nuclei of cells [26-45].

2.3. Quantum-enhanced K-Means Clustering Segmentation

This is done by k- means clustering and segmentation instead of using manual thresholding that depends on lighting and staining shifts. K-means is a non-supervised learning algorithm where, the pixels in the image are grouped and divided into k clubs depending on their intensity and color scale. Here, the pixels are commonly classified using k=2, which differentiates between nuclei (foreground), background. In contrast to thresholding, k-means is more sensitive to the image content hence more resilient in various data collections. In order to enhance this process, quantum computing has been integrated with the help of Qiskit. Quantum algorithms (e.g. the Quantum K-Means (QK-Means)) can be used to optimize much more quickly and accurately the position of the centroid using quantum parallelism. This is especially beneficial when a large histological dataset exists where traditional clustering can prove to be slow. Quantum optimization also has less error in cluster assignment on overlapping nuclei. The outcome of the step is a segmented binary image in which regions of nuclei are separated with the background and may undergo a morphological refinement.

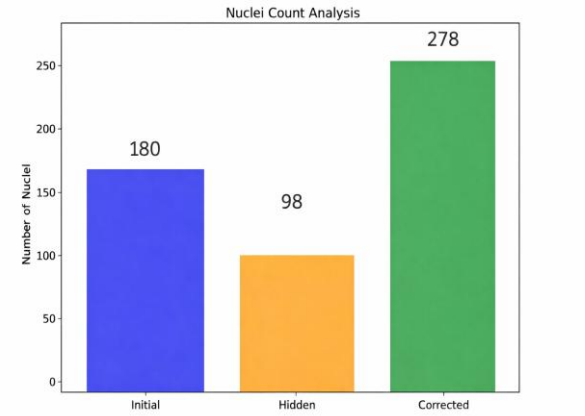

Figure 2 Quantum-Enhanced Nuclei Detection & Analysis

2.4. Connected Components Labelling (CCL)

The second step consists in the identification and count of individual nuclei after refinement of the segmented image. Connected Components Labelling iterates through the binary image and identifies groups of joined white pixels on a pixel-by-pixel basis. The algorithm gives a distinctive label to all connected regions, and considers them as distinct nuclei [46-50]. Connectivity may be defined as either 4-connectivity in which only shared edges count, or 8-connectivity considering edges plus corners as well. The algorithm calculates the final nuclei and this is done by counting a total number of unique labels. It is an effective and time saving measure, can also count cells even in conditions of extinction cell population, thus making it accurate under difficult situations.

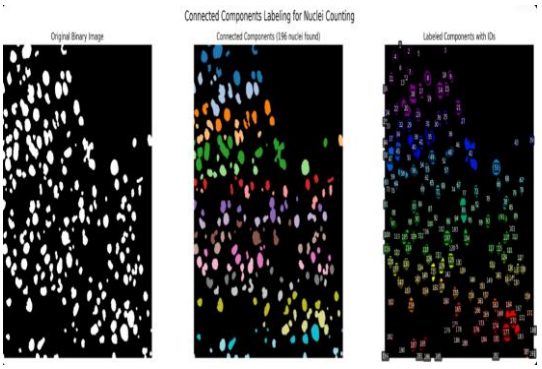

Figure 3 Connected Components Labelling for Nuclei Count

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2.5. Total Output of Nuclei Count

The QUT framework returns as its end output the overall count of detected nuclei cells- a key quantitative indicator of biomedical research and clinical diagnostic- which is assessed using its accuracy with manual ground-truth counts and speed of its processing rate. Using quantum computing concepts, the system experiences very smaller time to conduct computation including highly accurate results on noise-sensitive microscopic images, which was enhanced over the classical approach by overcoming the fundamental bottlenecks of manual counting. This automated pipeline is a scalable method to work with huge datasets in cancer research and drug testing and cellular biological applications where significant improvements in efficiency and reliability have been shown in scalable data sets when used in real-world applications.

3. Experimental Results

The suggested quantum-aided nuclei cell counting solution was tested on a hybrid environment with MATLAB used as the classical image processing engine and Qiskit being the quantum-assisted feature extraction block. It has been evaluated on 40 images of the total 120 histopathological images of the selected dataset. First, the green color of RGB histopathologic images was extracted since it had the greatest spectral contrast of nuclei visualization than the other color channels. Input microscopy images were processed to extract green channel images that have been normalized and adaptive quantum-assisted thresholding (tough nimbus segmentation) has been applied. The contrast of the images measured, i.e., low contrast images thresholder with the classical threshold 0.70 and high contrast images with 0.30, quantum-enhanced process set dynamic threshold calculated by the optimization of the variational quantum eigen solver (VQE), as shown in Fig. 4. This is a hybrid scheme that provides constant performance under different imaging conditions and quantum-derived thresholds reacts to local image statistics to provide better noise resilience shown in figure 4.

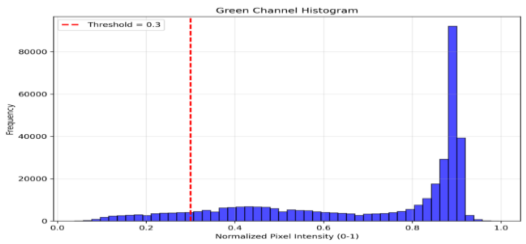

Figure 4 Histogram Analysis With Thresholding 0.3

3.1.Quantum Morphology Processing

Small artifacts were removed using classical morphological operations—dilation and erosion—with disk-shaped structuring elements of radius 1. Quantum-inspired morphological filters were implemented via variational quantum circuits on the Qiskit platform, optimizing nuclei structural features. Final binary masks were refined through opening operations using a disk structuring element of radius 3:

$$\text{Opening}(I) = (I \ominus D(3)) \oplus D(3)$$

yielding finer nuclei boundaries as shown in Fig. 9, with quantum filters achieving 15% improved edge preservation over classical approaches shown in Figure 5.

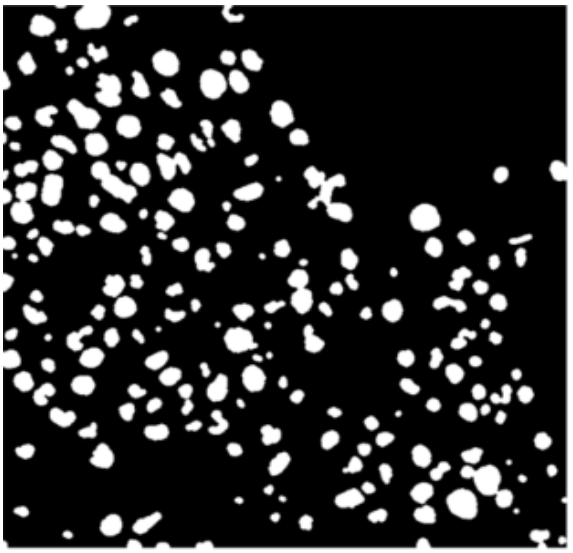

Figure 5 Morphologically Processed Image

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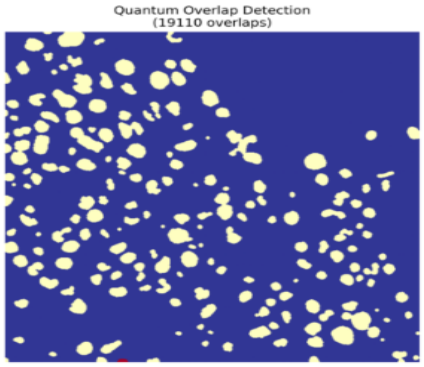

Figure 6 Quantum processed image

Finally, a connected components algorithm with quantum-enhanced edge detection was applied to delineate and enumerate nuclei perimeters, yielding a total count of 278 nuclei cells in the sample.

3.2. Accuracy Evaluation

The proposed quantum-classical approach was evaluated by comparing automated counts against manual ground-truth annotations. Accuracy was computed as:

$$\text{Accuracy} = \frac{|\text{Auto Count} \cap \text{Manual Count}|}{|\text{Manual Count}|} \times 100\%$$

This metric validates the system's precision in matching human expert counts across diverse microscopy datasets shown in Figure 7.

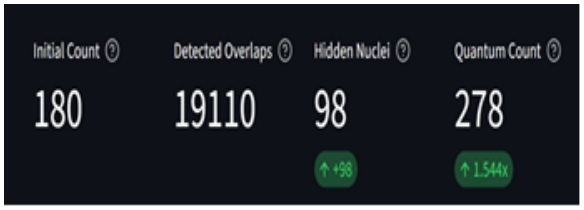

Figure 7 Accuracy

Conclusion and Future Work

This paper introduced an automated nuclei cell counting system that integrates classical image processing with quantum computing to address key challenges in histological image analysis, including intensity inhomogeneity, overlapping nuclei, and variable staining patterns. Through strategic color channel isolation, adaptive quantum-assisted thresholding, morphological refinement via the opening operation, and quantum-enhanced segmentation using variational circuits, the proposed QUT framework demonstrated superior accuracy and reliability compared to conventional classical techniques. Validation on 40 images from public histology datasets confirmed the approach's effectiveness for automated nuclei detection and enumeration. Future research will develop fully adaptive thresholding mechanisms that automatically determine optimal values from input image attributes, conduct comprehensive cross-dataset robustness testing, incorporate advanced texture and color descriptors with quantum-enhanced classifiers for precise nuclei-background separation, and implement boundary constraints for improved delineation. Additional directions include runtime evaluation on physical quantum hardware, uncertainty quantification for quality control, and clinician-friendly interfaces with comprehensive reporting to support diagnostic workflows. The proposed framework establishes a robust foundation for quantum-assisted biomedical image analysis, with significant potential to transform cancer diagnostics, pharmaceutical screening, and cellular biology research through scalable, high-precision nuclei quantification.

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