FPGA Implementation for the Segmentation of Cells using New Structure Algorithm

Mohammad Javeed*, Dr. Giribabu Kande**
*Research Scholar, Dept. of ECE, Mewar University
**Professor, Dept. of ECE, VVIT, Guntur

Abstract

Field Programmable gate arrays are the heart for parallel processing algorithms. In microscopy images automatically tracking of living cells is an important and challenging problem. This paper concentrates on the segmentation of cells using new structure algorithm, further FPGA implementation will be done for the segmentation. The code is written in Matlab for the segmentation and for the FPGA implementation code is written in Verilog. The power has decreased up to 64% as compared to the previous results. Simulated the model in Modelsim and executed the code in Xilinx.

Keywords: mitosis, apoptosis, segmentation, microscope image, Matlab, FPGA, Verilog.

Introduction

The tracking and linking of cell tracks has clearly discussed in [1], which is based on Viterbi algorithm. The Viterbi algorithm is in [2]. The analysis of the time-lapse sequences is however still performed manually in most cases, and is often very demanding [5]. Time-lapse microscopy can be used to characterize and quantify many different aspects of cell behavior, such as proliferation [6], mitosis (cell division) [7], [8], apoptosis (cell death) [9], migration [10], and morphology [11], that are important in the study of cancer [12], [13], embryogenesis [14], [15], stem cells [16]–[18], and many other topics in the fields of cell and developmental biology. In early works like [9], [14] cells were observed using transmission microscopy, and the images were sketched by hand at appropriate time intervals, or recorded on video tape in cases where all cells of interest were in the same focal plane. Nowadays, a large number of microscopy techniques are available, the cells or their nuclei can be labeled using fluorescent proteins or dyes, and sequences of 2-D images or 3-D -stacks can be recorded by digital cameras. Manual analysis is generally very time consuming, hard to reproduce, and can sometimes be subjective or biased by the expectations of the person performing the analysis. For these reasons, there is a large demand for automated or semi automated methods to perform the analysis.

The study of cell movement and cell behavior is of fundamental importance in areas such as cell embryology, wound healing, host defense mechanisms, and mechanisms of tumor cell metastasis and invasion. Under both normal and pathological conditions, certain types of cells exhibit extensive motion, often migrating to entirely different parts of the organism [3].

In recent years, as microscopy imaging technology has been improved and automated, tremendous volumes of microscopy image data are being generated in biology and biomedical
science fields. Accordingly, how to efficiently process and analyze the data becomes one of the major issues in the fields since manual analysis is often not feasible any more [4]. This challenge leads to rapidly increasing attention to systems for bio image analysis based on computer vision or image processing algorithms that enable automated and quantitative analysis of visual data. Monitoring the behavior of live cells, particularly cell growth, migration, and differentiation, is of great importance in order to understand the underlying mechanisms of cell physiology and development. For instance, monitoring cell growth and differentiation is critical for extending our knowledge of both normal and aberrant cell behavior in physiological processes, such as proper organ development, virus replication, and cancer development. Quantitative analysis of cell migration is also crucial for investigating several biological phenomena that involve cell migration, such as embryonic development, wound healing process, and metastasis.

This paper is organized as it shows the methodology implemented first and then it discusses about the segmentation new structure algorithm and illustrates the results finally it concludes the paper.

**Methodology**

Segmenting an image is an effort to group similar colors or elements of an image into a cluster or group. This can be achieved by clustering, which clusters the number of colors or elements into several clusters based on the similarity of color intensities and gray intensities of an image. The main objective of clustering an image is dominant colors extraction from the images. By extracting the information from images such as texture, color, shape and structure, the image segmentation can be very important to simplify. Because of the information extraction in any images, the segmentation has been used in many fields such as Enhancing the image, compression, retrieval systems i.e., search engines, object detection, and medical image processing. All track linking algorithms have some kind of explicit or implicit scoring of tracks to choose between different linking options, and different track linking strategies impose different constraints on how the tracks can be scored.

![Proposed System Diagram](Fig.1 Proposed System)
Here in the proposed algorithm will be implemented with the Matlab model based development.

- First video of frames will be given, which will undergo for the background detection.
- The segmentation algorithm will be done based on the new structure algorithm which depends on the threshold value and comparison of cell outline with the background.
- Track linking algorithm will be applied to the detected cells.

**Proposed New Structure Algorithm**

Image segmentation approaches are commonly based on one of two fundamental properties of intensity values. In discontinuity based technique image is partitioned by sudden changes in intensity values whereas similarity based technique partitions an image by grouping together connected pixels in the region which fulfills predefined resemblance criteria. Boundary detection is equivalent to splitting one region into two, hence similarity based and discontinuity based techniques mirror each other.

Thresholding is one of the simplest approaches for image segmentation based on intensity levels.

Threshold based technique works on the assumption that the pixels falling in certain range of intensity values represents one class and remaining pixels in the image represents the other class. Thresholding can be implemented either locally or globally. For global Thresholding brightness threshold value is to be selected to segment the image into object and background. It generates binary image from given input image. The pixels satisfying threshold test are considered as object pixels with binary value ‘1’ and other pixels are treated as background pixels with binary value ‘0’.

\[ g(u,v) = \begin{cases} 
1, & f(u,v) \geq T \\
0, & f(u,v) < T 
\end{cases} \]

Where T is predefined threshold. Segmentation model in the matlab model based environment has shown in the below figure.

![Fig.2 Segmentation Model](image-url)
The functional block diagram of the system with a new structure algorithm is shown in fig. 3. The minimum value of each branch metric after segmentation group (BMG) will be calculated and then passed to the ‘Threshold Generator’ unit (TGU) to calculate path metric (PM) \((PM_{\text{opt}}+T)\). \((PM_{\text{opt}}+T)\) and the new PMs are then compared in the ‘comparator unit’ (CU). The iterations will decrease in the cycle due to threshold generator [13].

\[
PM_{\text{opt}} = \min \left[ \min \{ \min (\text{cluster0}(n-2)) + \min (\text{BMG0}(n-1)) , \right. \\
\left. \min (\text{cluster1}(n-2)) + \min (\text{BMG1}(n-1)) , \right. \\
\left. \min (\text{cluster2}(n-2)) + \min (\text{BMG3}(n-1)) , \right. \\
\left. \min (\text{cluster3}(n-2)) + \min (\text{BMG2}(n-1)) \} + \min (\text{even BMs}(n)) \right] \\
\min \left[ \min (\text{cluster0}(n-2)) + \min (\text{BMG1}(n-1)) , \right. \\
\left. \min (\text{cluster1}(n-2)) + \min (\text{BMG0}(n-1)) , \right. \\
\left. \min (\text{cluster2}(n-2)) + \min (\text{BMG2}(n-1)) , \right. \\
\left. \min (\text{cluster3}(n-2)) + \min (\text{BMG3}(n-1)) \} + \min (\text{odd BMs}(n)) \right]
\]

**Fig.3 Segmentation of cells with new structure algorithm**

We can obtain \((PM_{\text{opt}}+T)\) during the period when Threshold, and add compare unit updates for new PMs. The only extra calculation for structure algorithm is the comparison between the \((PM_{\text{opt}}+T)\) and all the PMs. Therefore the critical path is greatly shortened as the eq. (4)

\[
S - \text{algo} = Tadder + T4 - in_{\text{comp}} + 2T2in_{\text{comp}} \quad (4)
\]

**Experimental Results**

The proposed algorithm can be used to link a set of detected cell outlines, produced by an application specific cell segmentation algorithm, into tracks.
Real-time image processing is difficult to accomplish on a consecutive processor. This is due to several factors such as the ample abstracts set represented by the angel and the circuitous operations which may charge to be performed on the image. Many angel processing applications crave that several operations be performed on anniversary pixel in the image, consistent in a ample cardinal of operations per second.

One another is to use the accoutrements accoutrement like FPGAs, DSP processors and microprocessors. The around-the-clock advance in the access in the admeasurement and functionality of accoutrements accoutrement over contempt years has resulted in an accretion absorption in their use as accomplishing platforms for angel processing applications. For angel
processing tasks in alien sensing, computer eyes and multimedia technologies requires an astronomic bulk of ciphering abnormally in applied and absolute time applications. As a archetypal computation-intensive problem, angel processing has been a acknowledged acreage for alongside processing. Many advisers allotment the acceptance that alongside processing is the alone economical way to accomplish the akin of achievement appropriate for angel processing tasks. So, ASIC, Acreage programmable accessories accepted micro- processors and programmable DSP processors are added acceptable to be successful. So, I accept called to apparatus the proposed algorithm with Acreage Programmable Gate Arrays. The proposed algorithm cipher will be generated application the matlab HDl coder. It will be apish in the Xilinx apparatus to aftermath the ability results. Table 1 shows the comparison between the proposed and the existing results.

<table>
<thead>
<tr>
<th>TABLE 1</th>
<th>POWER ESTIMATED RESULTS</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Power (mw)</td>
</tr>
<tr>
<td>Ideal viterbi decoder</td>
<td>281</td>
</tr>
<tr>
<td>New Structure Algorithm</td>
<td>T&lt;sub&gt;PM&lt;/sub&gt;=0.3</td>
</tr>
</tbody>
</table>

Conclusion

We have proposed a new structure algorithm which is low power for segmentation of cells. The architecture of new structure algorithm effectively reduces the power consumption. The comparison between the ideal viterbi algorithm and structure-algorithm for the segmentation of cells has shown. We have also analyzed to reach the theoretical iteration bound. ACSU is modified as to decode the signal perfectly. As the extra computation in the ACSU loop, the speed decreased negligibly. Shown the results that the power has decreased nearly 64% with a small degradation of speed 18%. RTL views of the Xilinx have been listed.

References