

# A Survey on Linking of Cell Tracks Using Segmentation

<sup>1</sup>Mohammad Javeed and <sup>2</sup>Dr. Giribabu Kande

*Research Scholar, Department of Electronics and Communication Engineering, Mewar University, India.  
Professor, Department of Electronics and Communication Engineering, VVIT, Guntur, India.*

## Abstract

In maximum of image process algorithms Segmentation is a key technique. It splits a digital image into several regions so as to examine them. Once segmentation is done, linking of frames is additionally a very important task. It is additionally accustomed distinguish completely different objects within the image. Several image segmentation techniques are developed by the researchers so as to form pictures swish and simple to judge. It is troublesome to process parallel algorithms in serial processors. This paper presents a literature review of basic image segmentation techniques, linking algorithms and want to process in hardware tools.

**Keywords:** Segmentation, Matlab, Verilog, linking, computer vision.

## INTRODUCTION

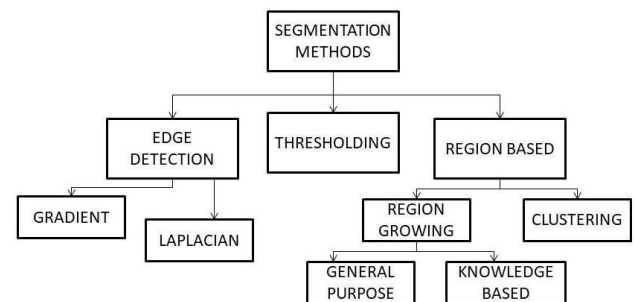
Medical image process is an ever increasing and dynamic space with applications reaching out into our daily life like medication, area exploration, surveillance, authentication, machine-driven business review and plenty of areas. Applications like these involve completely different processes like image enhancement and object detection. Implementing such applications on a general purpose pc are often easier, however not terribly time efficient because of further constraints on memory and different peripheral devices.

Application specific hardware implementation offers abundant larger speed than a software system implementation. As the VLSI (Very large Scale Integrated) technology hardware implementation has become a beautiful various system, executing advanced computation tasks on hardware and implementing parallelism and pipelining algorithms makes maximum fall in execution times.

There are 2 sorts of technologies accessible for hardware design. Full custom hardware design conjointly stated as Application Specific Integrated Circuits (ASIC), that are programmable devices like Digital signal processors (DSPs) and Field Programmable Gate Arrays (FPGA's). Full custom ASIC design offers highest performance, nevertheless the complexness and likewise the price related to the development is extremely high. The ASIC design can't be modified and also the design time is additionally terribly high. ASIC designs are employed in high volume industrial applications.

Throughout the design fabrication the occurrence of even one error makes the chip useless. DSPs are a sort of hardware devices that exists everywhere between an ASIC and a PC in terms of the performance and also the design excellence. DSPs are dedicated microprocessors, generally programmed

in C, or with assembly code for improved performance. It is similar temperament to very complicated scientific discipline intensive tasks like image processing. Information of hardware design remains needed, however the learning curve is way less than alternative design selections.



**Figure 1:** Segmentation methods

Hardware design techniques like parallelism and pipelining techniques are often technologically advanced on a FPGA, that is not potential in dedicated DSP designs. Executing image processing algorithms on reconfigurable hardware diminishes the time-to-market value, allows fast prototyping of complicated algorithms and make simpler debugging and verification. Therefore, FPGAs are a substitute for execution of real time image processing systems.

The review of segmentation algorithms are clearly mentioned in [1], that are discussing within the further sections. The tracking and linking of cell tracks has clearly mentioned in [2], that is based on Viterbi algorithmic program. The Viterbi algorithmic program is in [3].

## BASIC ALGORITHMS

The algorithms used in automated cell tracking are generally classified as one of the following four categories: Sequential tracking approach, Particle filtering based approaches, Model-based evolution approaches, Segmentation & Association based approach and Detection-based association approaches [4], [5], [6], [7], [8].

Several object tracking at a time can be done by the Particle filtering method. In multiple models like measurement models and dynamic models must be known before approximating the posterior distributions of an object's recent positions. Model based evolution approach first generates the object to be tracked and progressively informs the deviations in its appearance. Active contour methods are different from the particle filtering methods. This active contour method works

fine even for dissimilar shaped objects. Detection based association approach contain intensity thresholding, watershed algorithms, morphological operations and gradient (edge) detection. Yet, due to intensity dissimilarities, image noise and artifacts from the optical system, intensity thresholding are not operative. In this method the thing is to segment and locate the cells and next link those objects. Edge detection displays improved performance than thresholding. Yet, on little contrast images edge detection is mistake disposed to. The drawback of watershed algorithm is that it is disposed to noise and frequently over segments the image. As Smal et al. [9] and Li et al. [10] discussed particle filtering with spatiotemporal information is based on the sequential tracking approach. Zhou et al. [11] discussed in their research on tracking of sperm cells which is based on an orientation adaptive mean shift optimization into particle filter framework. Ray et al. [12] engaged sequential Bayesian framework to establish cell correspondences. Ryo and Aggarwal et al. [13] proposed a computationally well-organized algorithm for tracking lower than unadorned occlusion. Various sequential tracking methods explained above are computationally intensive and later suffer from the difficulty of scalability. Segmentation-based frame-by-frame association approach is also operative for automated cell tracking. Al-Kofahi et al. [14] use adaptive thresholding method, Liu et al. [15] introduced the Hidden Conditional Random Field Model. However, these approaches do not indicate the time of completion of cell division and they are computationally intensive. Active Contour model [10], Watershed method [16], Adopting Motion Model [10] has been widely used for cell tracking [17].

## COMPUTER VISION BASED ALGORITHMS

We will discuss, the modern algorithms and cell tracking techniques in this section, which have been modified to develop an automated cell tracking system, with a focus on the application. A tracking system in frame to frame based on track compilation and track linking and link the track trajectories so discovered to develop the entire lineage tree discussed by Kanade et al. [18]. Multiple Model Filters (IMM) in tracking biological events the Communicating are also shown in this method which are improved performance than Kalman Filter.

By evolving a machine learning method which calculates an energy term in the level-set based cell tracker and improves the tracking performance has discussed by Li et al. [10] have well tracked stem cells. To reduce an edge based approach and noise level Bilateral filtering was used effectively in cell detector is active to capture dissimilar stages in mitosis. In segmentation graph cut method from Yang et al. [19] proposed. The have discussed on tracking brain cells, as this method assurances to obtain universally best solution. Huh et al. [20] tells that tracking based method, tracking-free method are two types in automated mitosis detection algorithms. Tracking by nearest-neighbor approach, Park et al. [21] investigated on single mRNA tracking in live cells and adopted particle automated tracking of mRNA in cells Multiple Hypothesis Tracking (MHT) algorithms and Kalman

Filtering. Kanade et al. [4] pursued their work further and presented an image restoration and segmentation method which uses a quadratic optimization function to restore the original image eliminating the artifacts like shadows, shading and halos. Thresholding gives excellent performance while segmenting the restored image. Additionally, a three step approach is also presented for detection of cell division (mitosis), which includes creating patch sequence, extracting features and finally detecting whether the patch contains a mitosis occurrence and the specific location of incidence.

Scherf et al. [22] presented an algorithm to automatically compute characteristics of single cells in a highly dense population and construct its entire lineage history. This algorithm also employed levelset segmentation for object detection and watershed algorithm was applied to alleviate the problem of cell occlusion. Padfield et al. [8] introduced the graph theoretic minimum cost flow framework to resolve the data association which was accurate in cell tracking. However, this method failed for overlapping cells. As a solution to this problem Bise et al. [7] proposed the contour tracking method based on partial contour matching which could detect multiple overlapping cells. This technique uses contour shapes of cells and clusters and successfully incorporates it to track overlapping cells of Human Central Nervous System stem cells during migration and proliferation [7].

Kang et al. [23] proposed a novel method for tracking nuclei of *C.elegans* during embryogenesis. The algorithm consists of two aspects: tracking of nuclei by using a simple spherical mask, and detection of cell division by tracking multiple objects locally and detects the new born sister cells at a later point of time when its existence becomes more clear in order to avoid false detection. This algorithm shows accurate and robust tracking result even in low Signal-to-Noise Ratio (SNR) images. Yuan et al. [24] have mentioned that Mean-shift algorithm is a fast and powerful object tracking method and has been successfully applied to surveillance and segmentation system. To eliminate the problem of combining, splitting objects and disappearing Jaqaman et al. [25] intended an algorithm, the linear assignment problem (LAP). Based on the Kalman filter Yang et al. [26] projected an algorithm for consistent tracking of large scale dense antiparallel particle signal. These algorithms are not suitable for low Signal-to-Noise Ratio. Subsequently, Smal et al. [9] presented a powerful algorithm using particle filtering which was capable of tracking objects in noisy image sequences. Though, this technique uses generic particle filtering (GPF), which is executable expensive. Sargin et al. [27], Koulgi et al. [28] defined dissimilar methods to track the shortening, elongation, gliding hidden Markov model and a graphical model-based algorithm, respectively. The limitation of this approach was that it only works well for small displacements. The latest development in the field of object tracking is the use of kymographs. Kymograph signifies the motion information in a single graph which is an important method. Yet, in this once the object moves quickly, discontinuous routes are created and the method fails to provide the desired concert. Yuan et al. [24], in his work on tracking axons, he used particle filtering approach. The idea of him was to vigorously bound the spatial

space to the shape of the axon. The path of the axon motion is developed with a piecewise polynomial function expressed using cubic spline interpolation. Huang et al. [29] developed a 3-D online system for monitoring and tracking of cells in a suspension.

Without explicit target detection in a sequence of image a novel method of visual tracking of multiple targets presented by Hoseinnezhad et al. This algorithm is based on multi-Bernoulli filter. This technique stretches finest results when practical to many targets with parallel visual pattern. Likewise, it accounts for targets coming in and going out of the scene. In microscopic images an algorithm for multiple targets tracking for tracking cells have proposed by Magnusson et al. [30]. Viterbi algorithm is used in this method which was applied to the image sequence and global data association is attained due to here data from the whole image is used to make local decisions about building of the cell tracks.

To evaluate the algorithm experiments were performed on 115 image sequences of Muscle Stem Cells (MuSCs) and the precision and recall rate (called mitosis branching correctness) computed by the algorithm was observed to be to 0.78 and 0.75 for mitosis (cell division event) 0.74 and 0.62 for apoptosis (cell death event), as compared to Huh et al. [20] the recall rate was 0.65. Based on a temporal probabilistic model an automated mitosis detection algorithm proposed by Huh et al. [31] for validation of mitosis event detection. The algorithm was achieved god results as 97.4% precision and 96.6% recall proceeding 14 cell populations of Hematopoietic Stem cells (HSC) and it was observed that 97.4% precision. Chatterjee et al. [6] proposed an automated system of tracking human monocyte cells in a video sequence in which first the image is preprocessed to eliminate any background noise and the position of centroids of the cells is obtained. Then the Maximum Cardinality Minimum Weight Bipartite Matching is applied to create the cell trajectory. Mkrtychyan et al. [32] developed an efficient technique for fully automated registration of image and applied it to images of shoot apical meristem (SAM) of Arabidopsis to evaluate its performance and observed that this algorithm improves cell lineage and data statistics. The process of transforming different sets of data is Image registration into one coordinate system.

From these different measurements in order to be able to compare or integrate the data obtained registration is required. They adopted Iterative Closest Point algorithm with slight modification. Features of the local neighborhood area to mark the corresponding landmark pairs used in this case IPC uses for image registration. Cell tracking and identifies the correct cell path eliminating occlusion events accurately proposed by Baker et al. [33]. This algorithm incorporates four modules: correlation analysis, cell tracking, occlusion detection and correction and cell and sibling identification. Here contour based segmentation is used. Konda et al. [34] worked to report the tests of tracking a population of cells which exhibit variations in behavior, dynamics and density. They projected an Event Indicator Function classifier (EIF) for identifying cell tracking faults and phenotypes. The EIF is designed to specifically perform to perform the many image processing techniques. Hagwood et al. [35] evaluated performance of

four general segmentation algorithms: Otsu, K-means, Canny, and Watershed based on their misclassification error. Experiments were done as sequence of images of A10 rat smooth muscle cells and NIH-3T3 cells and decided that Canny and Watershed were strong and actual for a variability of samples.

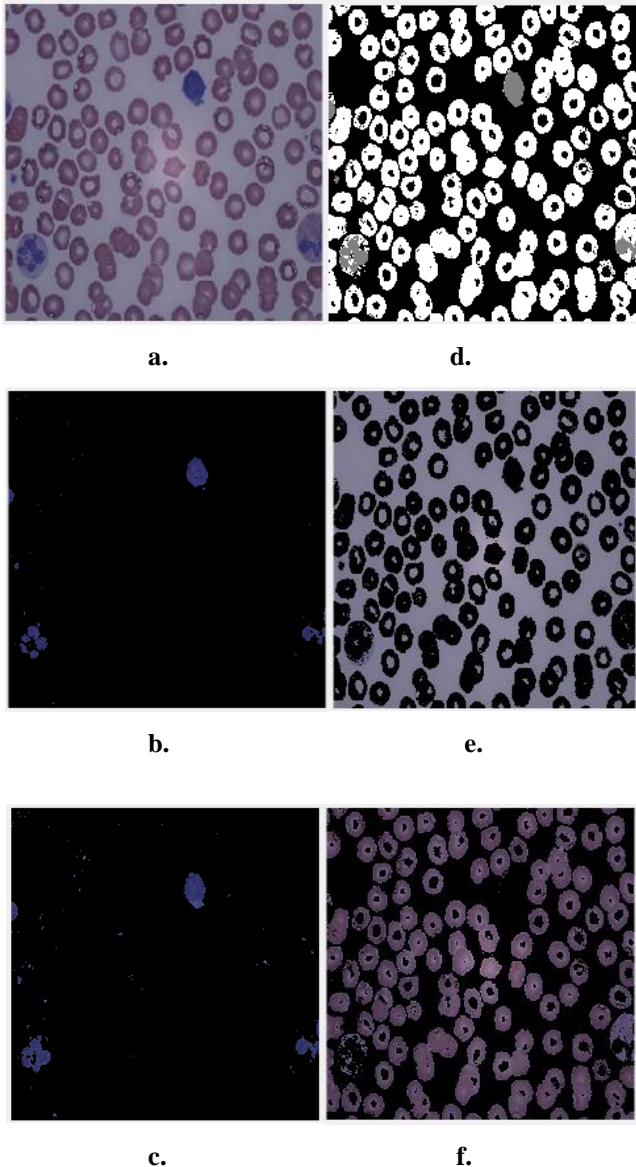
## AUTOMATIC CELL TRACKING

Kanade et al. [18] familiarized An Automated Cell Tracking System for concurrently tracking thousands of cells using phase-contrast time-lapse microscopy. In this method five modules were integrated: dynamic filter, cell tracker, cell detector, track linker and track compiler to attain spatiotemporal linking of cell paths. The system performance was assessed and achieved exactness in the range of 85.9 % and 92.5 %, which is 9 % more in contrast to the preceding system. Li et al. [10] developed a computer vision based cell tracking system that is capable of tracking the performance of a large population of cells as well as cell movement, death, quiescence, division and differentiation. In this method the experiments he overcome the many aspects like discriminating between overlapping cells, increasing cell densities during population expansion and cell entering/leaving the field of.

A system for cell tracking is designed which is based on contour-based cell tracking in Bise et al. [17]. The system was used for thorough analysis of Human Nervous System stem cells and achieved 97% accuracy. In this system each image sequence undergoes three steps: cell-blob correspondence, preconditioning and segmentation and separation of overlapping cells. Yang et al. [19] discussed Tracking and Segmentation Framework to overcome boundary uncertainty problem and used it to abstract 2D contour boundaries from Serial Block Face Scanning Electron Microscopy image stacks. In this methodology graph cut system was used to get the worldwide best solution of an energy function which comprises of the flux of the gradient vector fields, the distance function and the image gray-scale intensity. This energy function can solve the boundary ambiguity problem occurring in densely packed EM images. A Real-time Cell Tracking System was technologically advanced which was able to measure cell migration routes underneath cell culture situations. The consequences are single cell path (x, y) during migration, migration speed, migration distance, cell size, real-time pictures and plenty. This system is appropriate to all kinds of researches related to cell migration such as cell angiogenesis, chemo taxis, and furthermore cancer metastasis [36]. An automated system proficient of counting cell proliferation metrics in vitro in real time was developed by Kandade et al. [4] which was reinforced online natural experiments.

Three cell image examination algorithms: image restoration, mitosis detection and error-tolerant data association was initiated into a public website. Researchers all across the world can upload their cell images for processing. The system's performance was tested to be very efficient. Magnusson et al. [30] describes the above system as arguably the most advanced system at this point in time. Bise et al.

[7] proposed an automated method to obtain cell trajectories and lineages which was proven to be more efficient than the previous method that used level-set technique. Experimental results on a challenging data set show that the proposed method significantly improves the tracking performance including target effectiveness, track purity; mitosis branching correctness by globally associating tracklets.



**Figure 2:** example of segmentation of a cell a. original image, b. Segmented image, d. Intermediate image, (c)(e)(f) objects in clusters.

The utilization of convolutional codes with probabilistic deciphering might essentially move forward the lapse execution of a correspondence framework[37]. Trellis coded modulation schemes are utilized within numerous data transfer capacity proficient frameworks. Regularly a TCM framework utilizes a helter skelter rate convolutional code, which prompts secondary intricacy from claiming viterbi

decoder for those TCM decoder, At those demand length for Convolutional code is Additionally typical. For case the rate  $\frac{3}{4}$  convolutional code utilized within trellis coded regulation framework for whatever requisition need a demand period from claiming 7 will be in the unpredictability of the comparing viterbi decoder for An rate  $\frac{1}{2}$  convolutional code with demand period from claiming 9 [38] because of those vast number of moves in the trellis. So, As far as force consumption, those viterbi decoder may be overwhelming module On a TCM decoder.

Set up should diminishing the individuals computational many-sided nature What's more also control consumption, low drive schemes ought should make abused of the vd Previously, an TCM decoder. All results to low energy viterbi decoder outline will be muller over to our usage fill in. Force diminishment over VDs Might make attained by decreasing the number about states, (for instance diminished state succession deciphering [37], M-algorithm [39] and T-algorithm [37],[40],) alternately by again scaling those supply voltage[41]. Again scaling of the supply voltage will be Hosting an issue that it needs with take entire framework under thought including with vd at which we would not centering from claiming our Look into. For useful provision RSSD will be additional regularly utilized over M-Algorithm which will be by and large not Likewise effective Likewise M-algorithm [39] and T-Algorithm. Essentially M-Algorithm obliges An foray methodology for a sentiment circle while T-calculation main searches to the ideal way metric that is those most extreme quality alternately the base esteem of Ps.

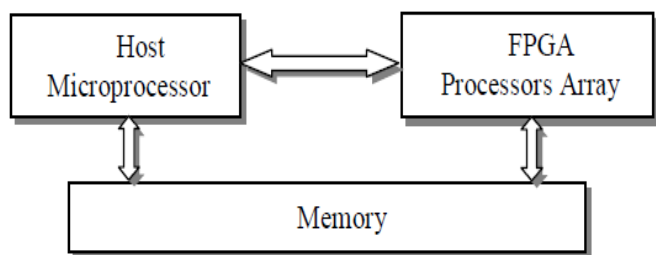
T-Algorithm Need been demonstrated will precise productive in decreasing the control utilization [42], [43]. However, seeking for those ideal way metric in the sentiment circle still lessens those deciphering velocity. Will beat this drawback, T-Algorithm need suggested over two variations, the loose versatile vd [44], Which infers utilizing a evaluated ideal way metric, As opposed to finding those genuine person every cycle and the limited-search parallel state vd In view of rare state move [SST][45].

At connected will secondary rate convolutional codes, the loose versatile vd suffers An extreme debasement of Bit-Error-Rate(BER) execution because of those intrinsic floating slip the middle of the evaluated ideal way metric and the exact one[46]. On the great holders kept all those SST based plan obliges pre deciphering Furthermore re encoding transform What's more may be not suitability for TCM decoders. For TCM, the encoded information would continuously connected with an intricate multilevel regulation plan such as 8-ary stage shift keying (8PSK) or 16/64-ary quadrature abundance tweak (16/64QAM) through An heavenly body purpose mapper. At the receiver, a delicate enter vd if a chance to be utilized with assurance a great coding addition. So, those computational through leader and deciphering inactivity because of pre deciphering What's more re encoding of the TCM indicator turned into secondary. An add-compare select unit (ACSU) building design In view of pre calculation for VDs incorporating T-Algorithm [46], which proficiently enhances the clock pace of a vd for T-Algorithm for An rate  $\frac{3}{4}$  code. Now, we further dissect those pre calculation calculation. A precise path with determine those ideal pre calculation steps

will be shown, the place the least amount of steps for incredulous way on accomplish the hypothetical cycle bound may be ascertained and the computational multifaceted nature overhead because of pre calculation will be assessed. Later, The complete low-power VD design for the rate  $\frac{3}{4}$  convolutional code discussed in [37], [47].

On a serial processor implementation of image processing algorithms is much difficult. This is due to several factors such as the large data set represented by the image and the complex operations which may need to be performed on the image. Several image processing applications need that several operations be executed on each pixel in the image, causing in a huge number of processes per second.

One alternative is to use the hardware tools like FPGAs, DSP processors and microprocessors. The frequent growth in the rise in the area and functionality of hardware tools from the modern years has caused in an increase in interest in their use as application platforms for image processing applications. For image processing tasks in remote sensing, computer vision and multimedia technologies requires a huge amount of computation especially in practical and real time applications. As a typical computation-intensive problem, image processing has been a successful field for parallel processing. Several researchers share the confidence that parallel processing is the individual economical way to attain the level of performance compulsory for image processing tasks. So, ASIC, Field programmable devices standard micro- processors and programmable DSP processors are more likely to be successful.



**Figure 3:** Image processing techniques based on FPGAs

## CONCLUSION

In this we have clearly discussed the segmentation methods and the advantages and disadvantages of the different techniques. Segmentation and linking based on the Viterbi algorithm is taking interest because linking after segmentation is also having the most importance in medical image processing to segment the blood cells. Viterbi algorithm for convolution codes decoding having a vital role in the encoding and decoding processes. Linking of the cells with Viterbi algorithm after segmentation is having more advantages as it has decreased the linking time and power when we execute this algorithm in hardware tools.

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