www.ijecs.in
International Journal Of Engineering And Computer Science
Volume 14 Issue 11 November 2025, Page No. 27929-27944
ISSN: 2319-7242 DOI: 10.18535/ijecs/v14i11.5322

State-of-the-Art Algorithms for Cell Image Processing, Segmentation, and Tracking in Time-Lapse Microscopy

Mohammed Babiker Ali Mohammed*, Fahmi Alsadig*, Abuzer Hussein Ibrahim*

Dean, Faculty of Computer Science and Information Technology Department of Computer Science University of Albutana
Faculty of Computer Science and Information Technology Department of Computer Science University of Albutana
Department of Computer Science Faculty of Computer Sciences and Information Technology University of Al-Butana, Sudan

Abstract
In cell bioscience, microscopy has always been an essential tool to study cell conduct in reply to various cultural terms and handling. Propagation and cell demise are often examine using microscopy, however, more knotty statistics like movement pattern and morphology could be analyzed. The cell tracking method poses sensible challenge to the computer vision and pattern recognition. This study conducted a comprehensive review on cell tracking and segmentation studies. This study analyses the current segmentation. It also discusses the cell tracking algorithms. Moreover, it presents the cell tracking and segmentation CNN architectures, and provides description of design cell tracking approach. Finally, it identifies the gaps in cell tracking and segmentation for future research. This review forms a basis for future cell tracking research.

Keywords Image nosie Image filter Image segmentation Time lapse Cell Events Cell tracking

Abbreviations

MR	Magnetic resonance
SAR	Synthetic-aperture Radar
SPECT	A Single Photon Emission Computed Tomography BF Band Pass Filter
ACM	Active Contour Model
CTC	Cell Tracking Challenge
MRI	Magnetic Resonance Imaging WBC White Blood Cells
IMM	Interacting Multiple Models FCN Fully Conventional Network
AOGM	Acyclic Oriented Graphs Matching BASC Bovine Aortic Endothelial Cells DIC Differential Interference Contrast

1 Introduction

In cell bioscience, microscopy has always been an essential tool to study cell conduct in reply to various cultural terms and handling. Propagation and cell demise are often examine using microscopy, however, more knotty statistics like movement pattern and morphology could be analysed (Magnusson and Jalde´n, 2012). It is especially difficult to dissect essential undifferentiated organism populaces, as these are heterogeneous and one thusly needs to fol- low an enormous number of cells to have the option to make inferences about the populaces. It isn't until as of late that progresses in magnifying instrument equipment, programming, and information capacity have made it basic and plausible to obtain informational indexes

enormous enough to dissect these parameters in an orderly manner . Presently, the primary bottleneck is rather dissecting the images once they have been gained. As a rule, image successions of cells have been broken down effectively utilizing manual methodologies, regularly supported by computer program to information and store data. This kind of manual investigation is anyway very tedious, the number of parameters that can be broke down is restricted, and the examination strategies are difficult to replicate precisely (Magnusson and Jalde´n, 2012).

It is hence important to do all of the investigations in a completely mechanized man- ner utilizing computer programming. This requires naturally finding the cells in the images utilizing image segmentation and finding their directions utilizing objective tracking. Robo- tized tracking of cell populaces in vitro in time-lapse by microscopy images empowers high-throughput spatiotemporal estimations of a range of cell behaviours, including the measurement of movement (Mitosis, A poptosis), just as the reconstructing of cell lineages (ancestor and descendant relations) (Li *et al.*, 2008). The term time-lapse implies images are recorded with a much lower outline rate than in conventional video. This makes it achievable to audit forms that are unreasonably delayed for a person's to observe (Magnusson, 2016). Cell tracking and segmentation with high exactness is significant advance in the cell motility inquire about. For example, following the number and speed of moving leukocytes is basic to comprehend and effectively treat inflammatory diseases.Delicate Tracking for moving cells is critical to do numerical demonstrating to cell velocity.The procedure of segmentation relies upon the assurance of the best places of the focuses which speak to the image. The reason for image segmentation is to segment image into important locales dependent on estimations taken from the image and may be dim level, shading, surface, profundity or movement (Aly *et al.*, 2014).

Best in class cell tracking methodologies can be extensively arranged into two classi- fications : tracking by detection and tracking by model evolution.The Previous model by and large includes two stages. firstly, cell nucleus segmentation algorithm recognizes all target questions in the whole time-lapse by arrangement independently for each edge. Second, the distinguished objects are related between progressive casings, commonly by streamlining a probabilistic target work. Conversely, the last model fathoms the two stages all the while, typically utilizing either parametric or certain dynamic shape models (Matula *et al.*, 2015). The most straightforward way to deal with taking care of the resulting affiliation issue is to connect each fragmented cell in some random edge to the closest cell in the next edge, where "closest" may allude not exclusively to spatial separation yet in addition to distinction in power, volume, direction, and different highlights. This closest neighbor arrangement functions admirably as long as the cells are very much isolated in at any rate one of the com- ponents of the element space. Basically, this standard additionally applies to alleged online cell following methodologies, which switch back and forth among division and connecting on a for each casing premise. For occasion, layout coordinating, mean-move handling, or deform-able model fitting is applied to one casing, and the discovered positions or shapes are utilized (Meijering *et al.*, 2012).

1.1 Previous Study

(Emami *et al.*, 2021) provide comprehensive review on cell tracking stages and computational methods and techniques used to locate and monitor cells and its behavior in sequential images (time lapse video sequences) .This paper discuss cell tracking Methods and Tools is that cell scientists can use these computational techniques to find another method to get additional information for their question of interest.
In our paper we presents segmentation algorithms that used to allocate cells inside every image in time lapse video sequence and how to detect behavior by discuss recent tracking algorithms in more mathematical and computational details and how monitoring cell events like mitosis , apoptosis and migration and how show the results in easy manner to visualize these behaviors for biologists and help researcher to select proper way for design methodology to solve cell tracking challenges .

1.2 Paper Structure

This review paper will be very helpful for future researchers and practitioners in cell tracking and image

segmentation. The rest of this review is structured in the following manner: Section 2 describes background of image processing, types of noise, and image filtering
techniques, Section 3 describes the current segmentation methods, Section 4 discusses cell tracking algorithms. Section 5 presents cell tracking and segmentation CNN architectures, and Section 6 provides description of design cell tracking approach, Section 7 presents the conclusions of the study and future directions.

2 Background

In the Digital Image process field, improvement and removing the noise from the image is that the crucial issue. Gaussian noise , Salt and Pepper noise and Speckle noise are the kinds of noises that are typically found in images, and additionally denoising them with the assistance of some economical technique is of main concern. Noise once get additional to image destroy the small print of it. therefore so as to preserve the real image, noise ought to get aloof from it(Mahakale and Thakur, 2007).

2.1 Kinds of Noise

1. **Gaussian Noise:** in image process. Even a high resolution icon is bound to have some noise in it. For a high-resolution photo an easy box blur could also be spare, because even a small options like eyelashes or artefact texture will be depicted by an outsized cluster of pixels. Unfortunately, this is often not the case with video wherever real-time noise reduction continues to be a theme of the many researches(Tania and Rowaida, 2016).

$$F(g) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-(g-m)^2/2\sigma^2} \qquad (1)$$

2. **Salt and Pepper Noise:** Salt and pepper noise could be a sort of noise usually seen on images. It represents itself as at random occurring white and black pixels. a good noise reduction technique for this kind of noise involves the usage of a median filter or a contra mean value filter. Salt and pepper noise creeps into pictures in situations wherever a fast transient, akin to faulty switching, takes place (Mahakale and Thakur, 2007; Tania and Rowaida, 2016).

$$F(g) = \begin{cases} P_a & g = a, \\ P_b & g = b, \\ 0 & otherwise \end{cases}$$

3. **Speckle Noise:** The speckle noise is usually found within the ultrasound medical pictures. it's a granular noise that inherently exists in and degrades the standard of the Active measuring device and artificial Aperture measuring device (SAR) images. Speckle noise in typical measuring device results from random fluctuations within the come back signal from associate object that's no larger than one image process part. It will increase the mean gray level of an area area.Speckle noise in SAR is usually more serious, inflicting difficulties for image interpretation. it's caused by coherent process of back scattered signals from multiple distributed targets. In SAR earth science, as an instance, speckle

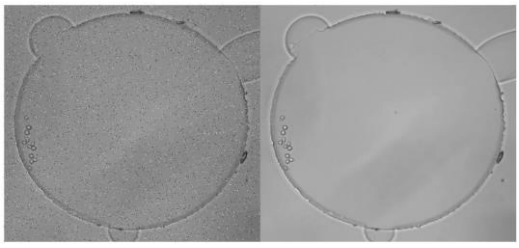

Fig. 1: Sample of salt noise and remove by mean filter

noise is caused by signals from elementary scatterers, the gravity-capillary ripples, and manifests as a pedestal image, at a lower place the image of the ocean waves (Tania and Rowaida, 2016; Sheikh *et al.*, 2017).

$$F(g) = \frac{g^{\alpha-1}e^{-g/a}}{(\alpha-1)!\,a^{\alpha}} \quad (2)$$

2.2 Image Filtering Techniques

Image filtering is beneficial for several applications, including smoothing, sharpening, re- moving noise, and edge detection. A filter is outlined by a kernel, that may be a little array applied to each pixel and its neighbours at intervals a picture . Filters are normally classified into two types: Linear Filter and nonlinear filter (Afrose, 2012).

2.2.1 Mean Filter

A mean filter acts on image by smoothing it. it reduces the intensity variation between adjacent pixels.The mean filter could be a easy window spacial filter that replaces the middle price within the window with the average of all the neighboring component values as well as itself. it's enforced on the premise of digital convolution using linear filters, that provides a result that's a weighted total of the values of a component and its neighbors. It is also referred to as as a linear filter.The mask or kernel could be a square. If the total of the coefficients of the mask is one, then the common brightness of the image isn't altered. If the total of coefficients is zero, then the common brightness is lost, and it returns a picture that is dark. the common or mean filter works on the principle of shift-multiply-sum (Afrose, 2012; Gupta and Negi, 2013);See Fig.1 .

2.2.2 Bandpass Filter

The filter could be a band pass filter that gets obviate noise by removing high spacial frequencies and non-uniform background illumination by removing low spatial frequencies. The filtered image I_{BF} is given by

$$I_F = I_b * G_1 - \alpha I * G_2 \quad (3)$$

where I_b is that basic image, G_1 and G_2 are two Gaussian kernels, and α is a tuning parame- ter**?**.The bandpass filter can typically work well once α is ready to one, however it's generally possible to realize a good higher result by employing a slightly smaller α . If α is ready to zero, the algorithmic program is like Gaussian smoothing followed by thresholding. That is a terribly easy and sometimes fairly effective algorithmic program, however the bandpass filtering has a couple of vital blessings. By subtracting the low spatial frequencies, the al- gorithm removes some non-uniform illumination, and makes it easier to phase objects with completely different brightness. once Gaussian smoothing is applied to an image with objects of various brightness, it'll not be doable to seek out a threshold that accurately segments all objects. If the brink is ready so the dim objects are segmented accurately, the outlines of the brilliant objects are large because of the spreading impact of the Gaussian kernel. If the brink is instead set so the bright objects are segmental accurately, the outlines of the dim objects can shrink or maybe disappear (Magnusson, 2016; Szeliski, 2010) ; See Fig.2.

Fig. 2: Image filtered by band Pass Filtering after background removing

3 Segmentation Methods

Image segmentation is that the task of finding teams of pixels that "go together". In statistics, this problem is understood as cluster analysis and may be a wide studied space with many totally different algorithms.In computer vision, image segmentation is one among the oldest and most generally studied issues. Early techniques tend to use region ripping or merging that correspond to factious and a gglomerative algorithms within the cluster literature.newer algorithms usually optimize some international criterion, equivalent to intra-region consistency and inter-region boundary lengths or difference (Szeliski, 2010). Segmentation is that the method of separation of needed data from an information for additional processing. Image segmentation is outlined because the segregation of pixels of interest for effective process. the most aim of image phaseation is to segment the meaning regions of interest for process. Region of interest possesses a bunch of pixels outlined with a boundary and these might contribute to totally different forms admire circle, ellipse, polygon or irregular shapes. the method of segmentation doesn't offer data regarding the whole image rather associates component knowledge of solely the region of interest (Hemalatha *et al.*, 2018).

3.1 Active contour

Active contour may be a form of segmentation technique which might be outlined as use of energy forces and constraints for segregation of the pixels of interest from the image for more processing and analysis. Active contour delineated as active model for the method of segmentation. Contours are boundaries designed for the realm of interest needed in image. Contour may be a assortment of points that undergoes interpolation method. The interpolation method will be linear, splines and polynomial that describes the curve within the image . completely different models of active contours are applied for the segmentation technique in image process. The main application of active contours in image process is to outline swish form within the image and forms closed contour for the region. Active contour models involve snake model, gradient vector flow snake model, balloon model and geometric or geodesic contours(Szeliski, 2010; Hemalatha *et al.*, 2018).ACM models treat segmentation as associate energy reduction drawback wherever the energy of an energetic spline/contour is decreased by PDEs-based strategies toward the objects' boundaries. In classic ACMs, sleuthing objects' boundaries is by image gradients. However, this has one main limitation that it'll be stuck at a neighborhood minimum. Therefore, it cannot get satisfactory segmentation results. within the past 20 years, variety of ACMs are planned, appreciate active contour while not edge (ACWE) model and quick global minimization- based active contour model (Chen *et al.*, 2019).

$$\min_{\omega,c_1,c_2}\{\omega,c_1,c_2,\lambda\} = \int_0^{\text{length(c)}} ds + \lambda\int_{\omega}(c_1 - f(x))^2 dx + \lambda\int_{\omega/\omega_c}(c_2 - f(x))^2 dx \quad (4)$$

3.2 Split and Merge Technique

The simplest doable technique for segmenting a gray scale image is to pick out a threshold so calculate connected elements. sadly, one threshold is never sufficient for the entire image attributable to lighting and intra-object applied mathematics variations(Szeliski, 2010).we describe variety of algorithms that proceed either by recursively ripping the total image into items supported region statistics or, conversely, merging pixels and regions along in a very stratified fashion. it's additionally attainable to mix each ripping and merging by beginning with a medium-grain segmentation then permitting both merging and splitting operations.

3.2.1 Watershed Method

The watershed rework applied to the image doesn't produce contours of the options. On the contrary, it

partitions the image into the associated areas by the intensity gradient and considers the gradient image as a topographic relief, wherever the intensity of a component denotes the altitude of that component. every component during this digital image is assigned a label throughout the transformation of the catchments basin of a regional minimum. once finished, the ensuing network of dams defines the watershed of the image.The disadvantage is that for textural pictures the watershed transformation doesn't use of texture data and produces excessive over-segmentation. the explanation is that the image contains tons of texture data that herald too much seeds(Wang *et al.*, 2007).

To understand the watershed, one will assume of an image as a surface wherever the brilliant pixels represent mountaintops and also the dark pixels valleys. The surface is punctured in a number of the valleys, then slowly submerged into a water tub. The water can pour in every puncture and start to fill the valleys. However, the water from completely different punctures isn't allowed to combine, and thus the dams would like to be designed at the points of initial contact. These dams are the boundaries of the water basins, and conjointly the boundaries of image objects(Rogowska, 2000).

3.2.2 Region merging

Region merging techniques additionally go back to the beginnings of computer vision. The concept is to use a twin grid for representing boundaries between pixels and merge regions supported their relative boundary lengths and therefore the strength of the visible edges at these boundaries. Automatic image segmentation will be phrased as associate abstract thought drawback . as an example, we'd observe the colours in a picture, that are caused by some unknown principles. within the context of image segmentation, the observation of a picture is given however the partition is unknown. during this respect, it's potential to formulate the abstract thought drawback as finding some illustration of the pixels of a picture, akin to the label that every component is appointed. With these labels, a picture is partitioned off into a purposeful assortment of regions and objects (Szeliski, 2010; Peng *et al.*, 2011).

In this approach we have a tendency to begin with a collection of "seed" pixels and from these grows regions by appending to every seed picture element those neighboring pixels that have similar properties, reminiscent of gray level, texture, or colour. the method starts by dis- tribution the primary picture element of the image into consideration because the initial seed picture element.This seed picture element would be compared to its 8-connected neighbours: eight neighbours of the seed pixel(Ikonomatakis *et al.*, 1997). Any of the neighboring pixels that satisfy a homogeneity perform would be allotted to the primary region and its pixel worth would modification to the seed picture element value. This neighbour comparison step would be continual for each new picture element allotted to the primary region till the region is totally finite by the sting of the image or by pixels that don't satisfy the homogeneity per- form. The next seed picture element for the second region would be determined by selecting the primary unassigned (to the antecedently adult region) pixel whereas moving through the image in a very right-to-left and bottom-to-top fashion. The higher than mentioned steps for growing a vicinity would once more be applied till the second region becomes complete. This method would be continual till each pixel i n the image would belong to a vicinity. once gray scale pictures are thought of the homogeneity perform wont to incorporate a given picture element into a vicinity is that the absolute distinction between the grey level of that pixel and also the grey level of the seed pixel. specially, i f the distinction between the gray level of a given picture element and also the seed pixel is a smaller amount than a threshold T then the pixel is enclosed into the region specific by the seed pixel (Ikonomatakis *et al.*, 1997). this will be written as :

$$|G - G_s| <= T \qquad (5)$$

where $G$is that the gray level of the picture element being tested and G_s, is that the gray level of the seed picture element. The optimum value o f T is downside dependent and would vary among images.

3.2.3 Graph-based segmentation

The graph G will be divided into 2 connected components A and B specified A B = V and A B = by omitting the sides linking these 2 elements. The degree of association between A and B will be inferred from the full weight of the discarded edges, that is solely known as as a graph cut.An optimum bi-partition minimizes this graph cut price By appropriately and repeatedly partitioning the graph created from a picture

victimization the graph cut, completely different homogeneous regions may well be obtained. In differently, every vertex may well be thought-about as a district. By utilizing graph cut values, that may be a live to point out what proportion 2 neighboring regions are homogeneous, regions may well be united repeatedly to create image partitions (Camilus and Govindan, 2012).

$$Cut(A, B) = \sum_{u \in A, v \in B} W(u, v) \qquad (6)$$

This approach has some advantages and downsides additionally. The advantage of this approach is to bridges the massive gaps exploitation global context and also the disadvan- tage is, it needs computation time a lot of bigger than the straightforward pre-processing techniques.development of diagnosis techniques like ultrasound, antilepton emission pic- torial representation (PET), Single gauge boson Emission computerized axial tomography (SPECT), Magnetic resonance (MR) it's turning into troublesome to trace the boundary of the item. These graph primarily based techniques are accustomed extract the boundary of the actual object in medical pictures (Singhal and Verma, 2016).

3.3 Mixtures of Gaussian Model

This is soft clump algorithmic program. every cluster is taken into account as a generative model with mean and variance.Mixture models are to estimate the parameters of chance distribution like mean and variance (Baid and Talbar, 2016).Gaussian mixture model is variable distribution. it's a mix of one or a lot of variable normal distribution part. Gaussian part is outlined by a vector of blending proportions in Gaussian mixture model for every variable distribution (Shukla, 2017).

$$d(\emptyset) = \sum_{k=1}^{i} C_k N(u_i, \sum k) \qquad (7)$$

Where k vector part is characterized by traditional distributions with weights C_k, suggests that N and variance matrices k. alphabetic character specifies the variance of every part. statistical distribution can have a mean and variance for parts.

$$\delta(x) = \sum_{n=1}^{N} \delta(x|s_n, \emptyset_n)\nabla_n \qquad (8)$$

$with \quad parameter(u_n, \sum_n)$

3.4 Deep Learning Cell Segmentation

Image segmentation may be developed as a classification downside of pixels with linguistics labels (semantic segmentation) or partitioning of individual objects (instance segmentation). linguistics segmentation performs pixel-level labeling with a collection of object classes (e.g., cell ,bone,leaves) for all image pixels, therefore it's typically a tougher endeavor than image classification, that predicts one label for the complete image. Instance segmentation extends linguistics segmentation scope more by sleuthing and delineating every object of interest within the image (Minaee *et al.*, 2020). Segmentation by CNNs is a crucial downside in computer vision and important progress has been remodeled the past few years . cell segmentation exploitation CNNs has been self-addressed a minimum of once before within the literature. Van Valen, et al. developed DeepCell, that treats the segmentation task as clas- sification downside on a pixel-by-pixel basis. whereas successful at classifying completely different cell sorts in pictures, DeepCell produces fairly low-resolution segmentation masks and doesn't aim to count cells(Herna´ndez *et al.*, 2018).As example see Fig.3

4 Cell Tracking Algorithms

Biological experiments of these days tend to get vast amounts of dynamic image informa- tion showing many objects at identical time. The image sequences can so not be analyzed manually with spare speed and accuracy. Instead automatic processed ways are needed and over the past decades a number of image

analysis techniques for cell chase are developed. However, a majority of those techniques have a restricted performance. As a consequence chase remains performed by hand in several laboratories , limiting and deceleration down any analytical work (Lindmark, 2014).

Accurate cell following may be a necessary task for microbiologists and biologists inquis- itive about dominant and finding out the behavior of micro-organisms. it's a troublesome

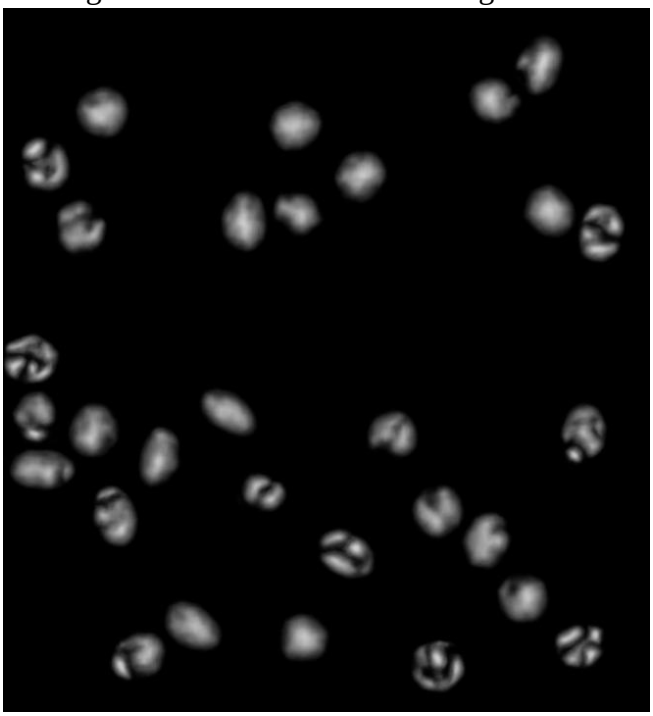

Fig. 3: Example for deep cell segmentation

drawback due to massive variations in experimental conditions each between trials and in several laboratory settings. to Illustrate, mud or different unwanted particles will contaminate the sphere of read, external stimuli resembling light-weight will modification the looks of research pictures and therefore the cells, themselves, will close up one another. moreover, there are several types of research and cell culturing techniques, every with distinct char- acteristics, resembling scale, resolution and color. Two common approaches to performing arts cell following, within which totally different implementations handle a number of these challenges higher than others, are Tracking by model evolution and tracking by detection (Hernandez *et al.*, 2018)

1. **Tracking by model evolution** : Tracking by model evolution approaches perform seg- mentation associated chase at the same time exploitation an evolving mathematical illustration of cell contours over time. These approaches can result in additional correct contours and individual cell tracks in some applications, however are computationally in- efficient for multi-cell chase and need initial seeding of cell contours. Examples embody constant quantity strategies, admire a full of life contour "snake" model in 2-D and a deformable model exploitation active meshes in 3D , and implicit strategies,which natu- rally handle splits, merges, and new appearances of cells (Magnusson, 2016; Hernandez *et al.*, 2018)
2. **Tracking by detection** : Tracking by observeion approaches initial detect cells victimi- sation image segmentation, and so perform chase to determine correspondence between cells in numerous frames. The segmentation part may be performed via gradient options , intensity options, wave decomposition and regionbased or edge-based options . Recently, convolutional neural networks have shown nice success in segmenting cells (Hernandez *et al.*, 2018).

4.1 Cell Events

1. **Mitosis Event** is the process whereby the genetic material of a organism cell is equally distributed between its descendants through nuclear division, leading to the birth of girl cells, as illustrated in Figure a pair of.1. Detection of cellular division is vital as a result of ways for assessing the proliferative

activity of stem cells have traditionally relied on detective work mitosis . In different words,mitosis detection may be a crucial tool for observance the health and rate of growth of a cell population.Presently, several cell proliferation assays that are compatible with machine-controlled sample handling and high-throughput screening are developed to live cell proliferation. However, the bulk of those procedures utilize fluorescent, light or quantitative chemical analysis assays which can need harmful ways of cell manipulation, similar to cell lysis and in vitro staining, and don't give continuous observance of cells in culture (Huh, 2013).

2. **A poptosis Event** is programmed necrobiosis, that happens in associate degree orderly, step-wise manner beginning with a series of organic chemistry events that result in char- acteristic changes within the cell before its death. The process of cell death includes cell shrinking, membrane blebbing, deoxyribonucleic acid degradation, and the formation of apoptotic bodies that serve to attenuate spillage of the interior contents of a dying cell to its surroundings (Huh, 2013; Bise *et al.*, 2011).
3. **Migration Event** is a vital process that's concerned within the major biological process stages of all advanced organisms and ends up in the arrangement of cells into an explicit design, the organization of the systema nervosum, and therefore the generation of spe- cialised organs and tissues. as an example, cell migration within the adult permits the immune cells to traffic through tissues and to gain wounds to facilitate the healing pro- cess (Keely, 2013).Cell migration could be a elementary process, from straightforward, uni-cellular organisms cherish rhizopod, to advanced multi-cellular organisms cherish mammals. Whereas its main functions comprise sexual practice and therefore the seek for food in straightforward organisms, quality brings a demand for specialization, that ne- cessitates cell migration-mediated tissue organization, organogenesis and physiological condition (Vicente-Manzanares *et al.*, 2005).

4.2 Track Cells Using Viterbi Algorithm

Given a sequence of I microscope pictures indexed by i, each image with a collection of N_i detections doubtless containing zero, one, or multiple cells, the goal of the planned cell chase rule is to link these detections temporally and to make a cell linage tree that's per the detections. A detection is here merely a collection of pixels obtained by the segmentation

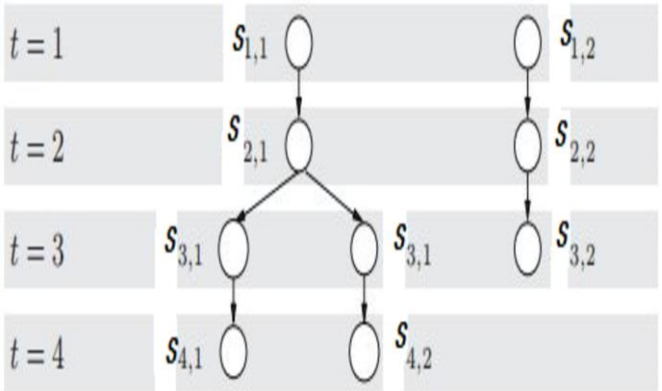

Fig. 4: Example graph F for cells in image sequence of length T = 4 . Two cells are gift in image t = 1 , and that they occupy detections $\mathcal{S}_{1,1}$ and $\mathcal{S}_{1,2}$ severally. The cell in $\mathcal{S}_{1,1}$ occupies $\mathcal{S}_{2,1}$ in image t = 2 and divides between image t = 2 and t = 3, where the two girl cells are divided in concert in $\mathcal{S}_{3,1}$ and so occupy separate detections, $\mathcal{S}_{4,1}$ and $\mathcal{S}_{4,2}$, in image t = 4. The cell beginning in $\mathcal{S}_{1,2}$ dies in image t = 3

We refer to the set of detections in image $i$as

$$S_i = \{S_{i,1}, S_{i,2}, \dots, S_{i,N_i}\},$$

and to the collection of all detections across the sequence as S(Magnusson and Jaldén, 2012; Magnusson, 2016). Ideally, each detection $S_{i,j}$would contain pixels belonging to exactly one cell. However, due to segmentation difficulties, this is rarely achievable in practice. In many cases, multiple cells merge into a single detection, while debris or background artifacts may generate false detections. Several of these errors can be corrected in the subsequent tracking step, where information from multiple images in the sequence is

jointly considered. Therefore, it is important not to make hard decisions during segmentation about how many cells each detection contains (Magnusson and Jaldén, 2012).

A set of cell tracks over an image sequence can be represented as a directed, layered graph F with labeled nodes. Each node in F corresponds to one cell in one of the images, and the node label specifies the detection to which that cell is associated in that image. Nodes belonging to the same cell across consecutive images are connected by directed edges. If a cell divides, its final node is connected by two directed edges to the first nodes of the two daughter cells. This construction yields an acyclic graph with one or more connected components, commonly referred to as a forest (Magnusson and Jaldén, 2012; Magnusson, 2016). See Fig. 4 for an example.

4.3 Cell Detection Using Deep Convolutional Neural Network(CNN)

This approach consists of three major components: (1) cell location encoding part mistreatment random projection, (2) a CNN primarily based regression model to capture the relationship between a cell research image and also the encoded signal $\mathcal{y}$, and (3) decryption phase for recovery and detection. During coaching, the bottom truth location of cells is indicated by

a pixel-wise binary annotation map B. detect two cell location cryptography schemes, that convert cell location from the component area illustration B to a compressed signal repre- sentation y. Then, coaching pairs, every consisting of a cell image and also the compressed signal y, train a CNN to figure as a multi-label regression model. we tend to use the geome- trician loss function throughout coaching, as a result of it's typically additional appropriate for a regression task. Image rotations is also performed on the coaching sets for the aim of information augmentation as well as creating the system additional sturdy to rotations. During testing, the trained network is accountable for outputting associate calculable signal
$\hat{y}$ for each take a look at image. After that, a decryption theme is meant to estimate the bottom truth cell location by playacting L_1 minimisation recovery on the calculable signal $\hat{y}$, with the known sensing matrix (Xue and Ray, 2017).

4.4 Cell Tracking Using Bipartite Graph Matching

A bipartite graph G = (V_1, V_2, E) is constructed where cell centers in two frames form the disjoint vertex sets V_1 and V_2.
The geometric distance between a cell center i ∈ V_1 (with coordinates (x_i, y_i)) and a cell center j ∈ V_2 (with coordinates (x_j, y_j)) is given by:

$$d_E(i,j) = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2} \qquad (9)$$

Since cell movements have a characteristic rate equal to displacement over time (separation between the frames), we modify the weight matrix elements by adding a mean displacement term.
Let dx and dy be the average x-displacement and y-displacement of the cells.
They can be estimated using the following equations (Chowdhury et al., 2010):

$$d_x = \frac{\sum_{j=1}^{|V_2|} x_j}{|V_2} - \frac{\sum_{i=1}^{|V_1|} x_i}{|V_1} \qquad (10)$$

$$d_y = \frac{\sum_{j=1}^{|V_2|} y_j}{|V_2} - \frac{\sum_{i=1}^{|V_1|} y_i}{|V_1} \qquad (11)$$

From equations (10)–(11), **dx** and **dy** represent the x- and y-displacements of the center-of-mass of the first frame.
The modified weight $\mathbf{z_{ij}}$ between a cell center **i ∈ V_1** and a cell center **j ∈ V_2** is given by:

$$z_{ij} = \sqrt{(x_j - (x_i + d_x))^2 - (y_j - (y_i + d_y))^2} \qquad (12)$$

5 Cell Tracking and Segmentation CNN Architectures

The expansion of deep learning in recent years has greatly advanced the progress in computer vision. as an instance, the performance of ResNet exceeded the performance of humans on the ImageNet take a look at set. Cell tracking has evolved from contour evolution, filtering templates, to tracking-by-detection strategies . Researchers still improve the strength of algorithms (Zhou *et al.*, 2019).

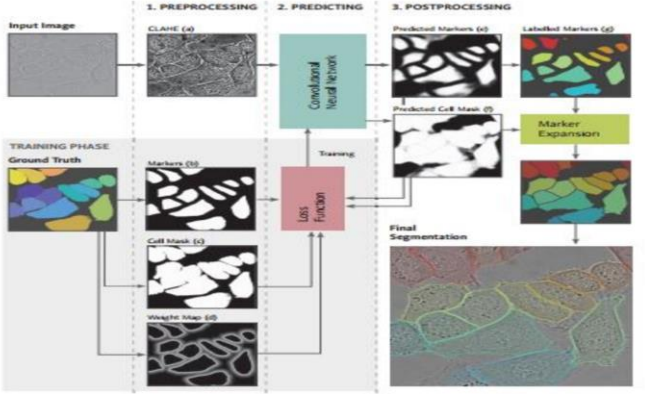

Fig. 5: Schema of the segmentation method. the the strategy consists of 3 steps: one. informa- tion Preprocessing, wherever AN input image is normalized in contrast restricted adjustive bar chart leveling: (a) within the training procedure, we tend to extract 3 pictures from the given ground-truth image: Markers (b), the Cell Mask (c), and therefore the Weight Map (d).

2. Predicting using a convolutional neural network. The network produces expected Markers (e) and therefore the expected Cell Mask (f). These pictures are utilized in the computation of the loss perform throughout the network coaching part. three Image Post processing. the expected markers (e) are filtered, tagged (g) and dilated by the watershed rework to the ultimate Segmentation (Lux and Matula, 2019)

5.1 DIC Image Segmentation of Dense Cell Populations BY Combing Deep Learning And Watershed

(Lux and Matula, 2019),proposed a unique approach based mostly on a mix of deep learning and also the watershed rework to phase differential interference contrast (DIC) pictures with high accuracy. the most plan of our approach is to train a convolutional neural network to notice each cellular markers and cellular areas and, supported these predictions, to split the individual cells using the watershed rework. The approach was developed supported the photographs of dense HeLa cell populations enclosed within the Cell chase Challenge info.See Fig.5

5.2 Tracking-Assisted Segmentation of Biological Cells

(Gupta *et al.*, 2019) ,we augmented U-Net with Siamese matching-based pursuit and planned to track individual nuclei over time. By modelling the activity pattern of the cells, we have a tendency to deliver the goods improved segmentation and following performances through a re-segmentation procedure. Our preliminary investigations on the Fluo-N2DHSIM+ and Fluo-N2DH-GOWT1 datasets demonstrate that absolute enhancements of up to 3.8 % and

3.4 % can be obtained in segmentation and tracking accuracy, respectively.

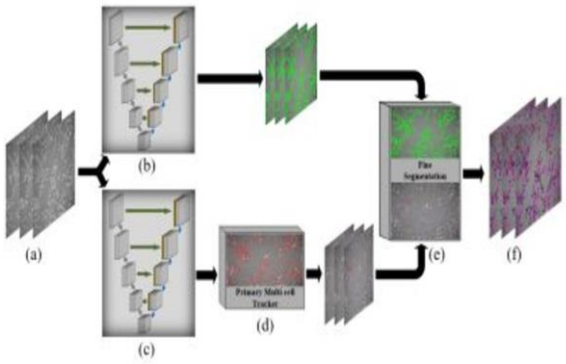

Fig. 6: An overview of planned tracking framework. (a) Input. (b) UNet for primary cell segmentation. (c) UNet for cell centroid detection with multi-frame images. (d) Primary multi-cell tracker. (e) Fine segmentation. (f) Final tracking results(Zhou *et al.*, 2019).

5.3 Joint Multi-frame Detection and Segmentation for Multi-cell Tracking

In (Zhou *et al.*, 2019) , UNet is employed to extract inter-frame and intra-frame spatio- temporal info of cells. Detection performance of cells in mitotic section is improved by multi-frame input. sensible detection results facilitate multi-cell trailing. A cell division detection rule is planned to detect cell mitosis and also the cell lineage is made up. Another UNet is employed to amass primary segmentation. together victimization detection and first segmentation, cells are often fine divided in extremely dense cell population. Experiments are conducted to judge the effectiveness of our methodology, and results show its state-of-the-art performance .See Fig.6

5.4 Cell Tracking via Proposal Generation and Selection

(Akram *et al.*, 2017) proposed 1) a deep learning primarily based cell proposal methodology, which proposes candidates for cells along side their scores, and 2) a cell tracking method- ology, that links proposals in adjacent frames in a graphical model using edges representing completely different cellular events and poses

joint cell detection and pursuit because the choice of a set of cell and edge proposals. Our methodology is totally automated and given enough training knowledge are often applied to a good form of research sequences. we tend to judge our method on multiple visible light and section distinction research sequences containing cells of varied shapes and appearances from ISBI cell pursuit challenge, and show that our methodology outperforms existing cell tracking strategies.See Fig.7

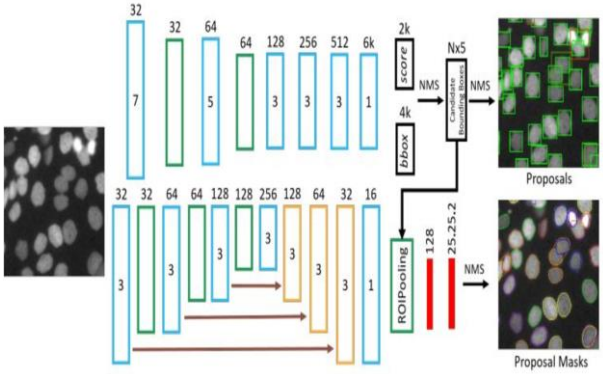

Fig. 7: Cell Network : top half shows the primary network, that proposes N bounding boxes and their scores. Bottom half shows the second network that generate segmentation masks for the N proposals. Convolutional (blue) (filter size within the box), max-pooling (green), absolutely connected (red), and deconvolutional (orange) layers, with the quantity of feature maps on prime of every layer, are shown. ! indicates that feature maps are combined by summation. projected bounding boxes and segmentation masks when non-maxima suppres- sion are shown for a particular space from Fluo-N2DL-HeLa dataset. Box color indicates proposal score, with bright green representing high score and bright red representing low score (Akram *et al.*, 2017).

5.5 Cell Tracking using Convolutional Neural Networks

(Jackson-Smith), proposed a system for tracking fluorescent cell nuclei in research informa- tion, using hierarchical visual chase on convolutional neural networks. we tend to instrument AN existing cell-segmentation CNN to produce feature information for cell tracking, addi- tionally to training our own network, Recog-Net, to produce higher-quality options on-line. The tracker reaches 60%.

6 Description of Design Cell Tracking Approach

6.1 Segmenting Cells

Cell tracking ways typically accommodates two main image process steps: (1) cell segmen- tation (the spacial facet of tracking), and (2) cell association (the temporal aspect). Seg- mentation is that the process of dividing a picture into (biologically) pregnant components (segments), leading to a brand new image containing for every element a label indicating to that phase it belongs (such as "foreground" versus "background"). One approach to seg- mentation is to check the worth of every image element to a planned threshold value and to label pixels with values on top of (below) the brink as foreground (background) . because of its simplicity, thresholding is one in every of the most commonly used segmentation ways, however it's additionally one in every of the most fallible . it'll achieve success providing cells are well separated and their intensities dissent sufficiently and systematically from the background—a condition seldom met in live-cell imaging because of severe noise, motorcar visible light and exposure bleaching (in the case of visible light microscopy), or powerfully varied intensities and halos (in the case of phase- or differential interference distinction microscopy) (Meijering *et al.*, 2009).

6.2 Linking Cell Over Time

After segmentation, the second step in achieving cell Tracking is cell association. This refers to the method of distinguishing and linking divided cells from frame to border within the image sequence to get cell trajectories. the only approach to accomplish this can be to associate every cell in any frame to the spatially nearest cell in the next frame with during a predefined vary. However, once addressing several cells or fast cell movements, this might simply result in mismatches. so as to permit for higher discrimination of

potential matches, the definition of "nearest" could also be extended to incorporate similarity in (average) intensity, space or volume, perimeter or extent, orientation of major and minor axes, boundary curvature, calculable displacement, and alternative options. Increasing the quantity of options used for comparison reduces the danger of ambiguity. an identical argument applies once mistreatment questionable mean-shift processes to iteratively calculate cell positions (Lindmark, 2014; Meijering *et al.*, 2009)

Table 1 : Summery of cell segmentation and tracking studies

Publications	Study Type	Dataset	Algorithm /measurement	Tracking Accuracy/performance
(Magnusson and Jalde´n, 2012)	Tracking cells	115 image sequences	Viterbi Algorithm	0.81- 0.88 %
(Li *et al.*, 2008)	Tracking cells	40,000 frames	(IMM)	86.9–92.5 %
(Magnusson, 2016)	Tracking Cells	CTC-14 and CTC-15	Track-linking	90 %
(Aly *et al.*, 2014) (Matula *et al.*, 2015) (Meijering *et al.*, 2012) (Lindmark, 2014)	Tracking cells Tracking Cells Tracking cells Tracking cells	WBC fluorescence datasets fluorescence sequences 30 frames	Novel algorithm AOG Measure Multiple tracking algorithms Rao-Blackwellized	RMSE <= 8 % 80 %
(Hernandez *et al.*, 2018) (Mahakale and Thakur, 2007) (Tania and Rowaida, 2016)	Deep tracking model filtering algorithms filtering algorithms	Escherichia coli	FCN and Viterbi Image Quality Metrics Image Quality Metrics	94.2 %
(Hemalatha *et al.*, 2018) (Wang *et al.*, 2007) (Camilus and Govindan, 2012)	Segmentation algorithm Segmentation algorithm Segmentation algorithm	MRI images	Active contour Watershed algorithm Graph cut technique	
(Huh, 2013)	Cell Behavior analysis	BASC	Mitosis apoptosis technique	
(Bise *et al.*, 2011) (Xue and Ray, 2017)	Tracking Cells Cell detection	Vitro Dataset 7 benchmark Datasets	Spatio-temporal measurement CNN	0.634 %
(Chowdhury *et al.*, 2010) (Meijering *et al.*, 2009) (Lux and Matula, 2019)	Tracking Cells Tracking Cells survey Segmentation approach	10 datasets DIC-C2DH-HeLa	Bipartite graph matching Multiple methods CNN and Watershed	95.65 % 0.8511
(Gupta *et al.*, 2019)	Tracking cells	Fluo-N2DH-GOWT1	U-net	3.8 % and 3.4 %
(Zhou *et al.*, 2019)	Tracking cells	PhC-PSC and Fluo-HeLa	U-net	87.7 %

7 Conclusion and Future Directions

In the summary, the main issue of this paper is how to track the cells and algorithms needed to do this.In the

beginning we addressed the algorithms of processing images of distortions and nosies to improve the image quality to be able to implement the next step which is to segment cells from within images using the algorithms of segmentation and we concluded whenever the segmentation of cells from within the images well led to improved tracking result through a sequences of images. In addition, we have addressed the tracking algorithms by taking some of them and the expected events of the tracking and the steps required to build normal or CNN tracking cells models .

The main difficulties for the designed algorithmic rule seem once there are segmentation mistakes in cell dense areas. betting on the scale of the information set, it can be an inspiration to travel through the detentions that in how take issue from the others then correct them by hand. By adjusting some mistakes, there is a higher chance that the algorithmic rule will handle the remainder.For some applications it would be an honest plan to incorporate the form or intensity of the cell within the model. this could be weighed against the requirement for additional particles within the filter once the model is of a better dimension. an enormous challenge in automatic cell pursuit is that there's a large variability within the knowledge sets. A segmentation that works well with one combination of cells and research techniques, could be virtually useless with another, a minimum of before the parameters are set for this specific combination. an equivalent is true for the tracking algorithms and a unique motion model would possibly even be required once used for a unique application. If utterly automatic strategies with easy-to trim parameters or semi-automatic methods wherever the user as an example points out correct and incorrect things then re-runs the algorithmic rule can work best remains to be seen, however in how it ought to be easier to use the developed strategies with quite one specific knowledge set.

There are variety of promising future directions for cell tracking. the subsequent are a number of the longer term research directions that will see improvement in cell tracking performance:

- Focus on more rising pursuit accuracy for automatic cell lineage construction, and applying the system to tackle difficult biological issues.
- Most of the time was spent on image stabilization, segmentation, and have computation.
- A manual separation of cells clustered within the initial frame is needed to trace every of them properly over time.This complicates the employment of the projected pursuit theme in experiments with high density of tightly corpuscle.
- Cell tracking by exploitation form descriptions and different options and think about other issues with image segmentation comparable to pictures with high noises.

Authors' contributions

All authors had equal contribution towards this work. All authors scan and approved the ultimate manuscript.

Competing interests

The authors declare that they have no competing interests.

Author details

[1]University of Albutana ,Faculty of Mathmatics and Computer Science

References

1. K. E. Magnusson and J. Jalde´n, 2012 9th IEEE International Symposium on Biomedical Imaging (ISBI), 2012, pp. 382–385.
2. K. Li, E. D. Miller, M. Chen, T. Kanade, L. E. Weiss and P. G. Campbell, *Medical image analysis*, 2008, **12**, 546–566.
3. K. E. Magnusson, *Ph.D. thesis*, KTH Royal Institute of Technology, 2016.A. Aly, S. B. Deris and N. Zaki, *International Journal of Computer Science & Information Technology*, 2014, **6**, 21.
4. P. Matula, M. Masˇka, D. V. Sorokin, P. Matula, C. Ortiz-de Solo´rzano and M. Kozubek, *PloS one*, 2015, **10**, e0144959.
5. E. Meijering, O. Dzyubachyk and I. Smal, in *Methods in enzymology*, Elsevier, 2012, vol. 504, pp. 183–200.
6. N. Emami, Z. Sedaei and R. Ferdousi, *Visual Informatics*, 2021, **5**, 1–13.

7. S. R. Mahakale and N. V. Thakur, *image*, 2007, **17**, year.
8. S. Tania and R. Rowaida, *International Journal of Signal Processing, Image Processing and Pattern Recognition*, 2016, **9**, 113–124.
9. S. Sheikh, B. Suthar, M. Uddin *et al.*, 2017 International Conference on Innovations in Control, Communication and Information Systems (ICICCI), 2017, pp. 1–6.
10. Z. Afrose, *International Journal of Computer Applications*, 2012, **47**, year.
11. B. Gupta and S. S. Negi, *International Journal of Computer Science Issues (IJCSI)*, 2013,**10**, 149.
12. R. Szeliski, *Computer vision: algorithms and applications*, Springer Science & Business Media, 2010.
13. R. Hemalatha, T. Thamizhvani, A. J. A. Dhivya, J. E. Joseph, B. Babu and R. Chandrasekaran,
14. *Med Biol. Image Anal*, 2018, **17**, year.
15. X. Chen, B. M. Williams, S. R. Vallabhaneni, G. Czanner, R. Williams and Y. Zheng, Proceedings of the IEEE conference on computer vision and pattern recognition, 2019,
16. pp. 11632–11640.
17. S. Wang, X. Ma, X. Zhang and L. Jiao, 2007 International Symposium on Intelligent Signal Processing and Communication Systems, 2007, pp. 312–315.
18. J. Rogowska, *Handbook of medical imaging, processing and analysis*, 2000, 69–85.
19. B. Peng, L. Zhang and D. Zhang, *IEEE Transactions on image processing*, 2011, **20**, 3592– 3605.
20. N. Ikonomatakis, K. Plataniotis, M. Zervakis and A. Venetsanopoulos, Proceedings of 13th International Conference on Digital Signal Processing, 1997, pp. 299–302.
21. K. S. Camilus and V. Govindan, *International Journal of Image, Graphics & Signal Pro- cessing*, 2012, **4**, year.
22. P. Singhal and A. Verma, 2016 10th International Conference on Intelligent Systems and Control (ISCO), 2016, pp. 1–6.
23. U. Baid and S. Talbar, International Conference on Communication and Signal Processing 2016 (ICCASP 2016), 2016.
24. M. Shukla, 2017.
25. S. Minaee, Y. Boykov, F. Porikli, A. Plaza, N. Kehtarnavaz and D. Terzopoulos, *arXiv preprint arXiv:2001.05566*, 2020.
26. C. X. Herna´ndez, M. M. Sultan and V. S. Pande, *arXiv preprint arXiv:1802.10548*, 2018.
27. S. Lindmark, *Cell Tracking in Microscopy Images Using a Rao-Blackwellized Particle Filter*, 2014.
28. D. E. Hernandez, S. W. Chen, E. E. Hunter, E. B. Steager and V. Kumar, 2018 International Conference on Manipulation, Automation and Robotics at Small Scales (MARSS), 2018,
29. pp. 1–6.
30. S. Huh, *Ph.D. thesis*, Carnegie Mellon University, 2013.
31. R. Bise, T. Kanade, Z. Yin and S.-i. Huh, 2011 Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2011, pp. 6174–6179.
32. P. Keely, 2013.
33. M. Vicente-Manzanares, D. J. Webb and A. R. Horwitz, *Journal of cell science*, 2005, **118**, 4917–4919.
34. Y. Xue and N. Ray, *arXiv preprint arXiv:1708.03307*, 2017. S. Chowdhury, R. Chatterjee, M. Ghosh and N. Ray, 2010 20th International Conference on Pattern Recognition, 2010, pp. 2456–2459.
35. Z. Zhou, F. Wang, W. Xi, H. Chen, P. Gao and C. He, International Conference on Image and Graphics, 2019, pp. 435–446.
36. F. Lux and P. Matula, 2019 IEEE 16th International Symposium on Biomedical Imaging (ISBI 2019), 2019, pp. 236–239.
37. D. K. Gupta, N. de Bruijn, A. Panteli and E. Gavves, *arXiv preprint arXiv:1910.08735*, 2019.
38. S. U. Akram, J. Kannala, L. Eklund and J. Heikkila¨, *arXiv preprint arXiv:1705.03386*, 2017.
39. E. Meijering, O. Dzyubachyk, I. Smal and W. A. van Cappellen, Seminars in cell & devel- opmental biology, 2009, pp. 894–902.