Object Localization and Spatial Analysis Using Computer Vision

Erkan Bostanci and Betul Bostanci

Abstract—**This paper presents a new localization method which uses two classical algorithms from computer science and computer vision. Described method was successfully applied to the problem of cell localization and the results show that it can be used as a part of a whole autonomous segmentation process. Furthermore, methods from spatial statistics were employed to model the spatial distribution of the localized objects. In-depth discussion of these methods including density plots and the Ripley's K function is presented along with the results for test set used in the experiments.**

Index Terms—**Object localization, Spatial Analysis, Segmentation**

I. INTRODUCTION

In many computer vision applications, finding the position of an object is an important part of the process. Especially for object recognition, the objects in the image must be first isolated from the remaining objects or clutter in the scene. Then it is straight-forward to match these objects with the ones stored in an image database [1]. Literature presents several methods for this purpose. Clustering algorithms as in [2], [3] and segmentation methods similar to [4], [5], [6] are well-known techniques in this regard.

However, there are some issues which prevent current algorithms from being tools for an autonomous system. For instance, clustering algorithms require the number of clusters which will be generated as the output of the system [2]. Similarly, the segmentation methods generally require a seed point for the algorithm [5]. This need for human supervision obviously reduces the autonomy of the system if the intended systems are autonomous systems like robots.

Furthermore, finding and modelling a relationship between these detected objects is also an important issue in many cases. Spatial Data Analysis concerns drawing such relationships between objects based on their spatial properties i.e. positions, area coverage, density [7]. These types of applications are generally used in biological analysis of populations for different ecosystems at larger scales [8] or other GIS related studies [9].

A new approach for automated object localization which is based on Minimum Spanning Trees and the convex-hull is described in this paper. To our best knowledge, the closest

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approach to the method defined in this paper is presented in [10] where Minimum Spanning Trees are used for image mining. Our approach differs from them both for the purpose of usage and the method itself as our method adds the usage of feature points together with the convex-hull.

In addition, this study also applies techniques from spatial statistics on the objects localized with the proposed method.

The rest of the paper is structured as follows: Section II describes the approach taken for localizing image objects. Later, Section III presents an experiment carried out as a test bed for this approach. Section IV describes the spatial analysis process carried out on the detected objects. Finally, findings of the paper are discussed and future research is presented in Section V.

II. LOCALIZATION METHOD

The localization method proposed here uses Minimum Spanning Trees which are generally used for network routing in order to minimize the number of hops for packages [11]. Application to computer vision is new concept after the recent clustering algorithm for image mining [10]. There are two main algorithms for calculating the Minimum Spanning Tree of a given graph, namely Kruskal [12] and Prim [13].

The graph in our algorithm is constructed using the 2D positions of the point features obtained by the FAST operator [14] which is a state-of-the-art feature extraction method. The graph is in form of an adjacency matrix where the cells with nonzero values denote an edge between the corresponding vertices.

This graph is fully-connected as there will be edges between all vertices. The weights of the edges are the Euclidian distances between the features on the image.

The Minimum Spanning Tree of the graph is constructed using Prim's algorithm (This choice is arbitrary as both methods can be used here since the graph is fully-connected). Prim's algorithm calculates the Minimum Spanning Tree in $O(E*log(V))$ time where E is the number of edges and V is the number of vertices. This minimal graph has the same format as the original graph that is the edges between the vertices still denote the distances.

These distances give clues about the positions of the image objects when we consider a specific region covering features points in the objects. This property is used as the localization approach in the algorithm with the assumption that the feature points of an object must lay within a known distance. When the edges with weights greater than this distance threshold are removed, the remaining edges will define the locations of individual groups along with the vertices.

The convex-hull of the remaining feature group is then calculated to define the outline of the localized object. The

convex-hull itself presents an overestimation as it includes the features at the outer region only and do not consider the features in the inner region. However, the Minimum Spanning Tree approach used here prevents this overestimation and produces a better result.

The method used for localization of image objects can be summarized with the following steps:

1. Extraction of FAST point features.
2. Generation of a graph including these feature points where the vertices will denote the positions of point features and the weights of the edges will represent the distances between the features.
3. Computation of Minimum Spanning Tree.
4. Removal of edges greater than a predefined threshold.
5. Calculation of the convex-hull of the vertex groups based on the remaining graph.

Having defined the localization method, next section will present a sample application showing how this method is successfully applied to the problem of biological cell localization.

III. APPLICATION TO CELL LOCALIZATION

The proposed method was applied to the biological cell localization problem in order to improve the autonomy of the process. Following two subsections will describe the test data used for this purpose and the results of the application.

A. Test Data

The test data for experimentation was obtained from The Cell: An Image Library [15]. The images of fibroblast cells were used for this experiment as shown in Figure 1 in the test culture they were developed.

Figure 1 NIH 3T3 fibroblast cells

The original images included .tif image sequences showing the biological process of localization. A detailed explanation about the whole process is presented along with each data set in the library.

B. Localization of Cells

The experiment carried out on the image datasets aims to identify individual cells as shown in Figure 2 where the cells are placed in a special culture and some chemicals are used to present better imaging results.

FAST operator was applied to the image in order to extract feature points. The operator selects the salient point locations in the image corresponding to the cells. Result is presented in Figure 3.

A graph is created by using the feature points though it is not shown here as it is very complex since it is fully-connected. The Minimum Spanning Tree is calculated as shown in Figure 4.

The edges with a weight which is greater than a predefined threshold (in image pixels while microns are used to define these distances in the actual culture environment) are removed leaving many groups of feature points. These groups identify the positions of the cells in the image as shown in Figure 5. The convex-hull was then used to extract the whole region including the cell.
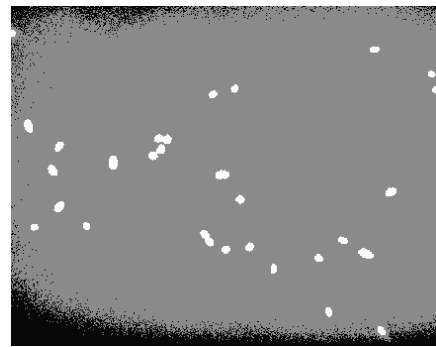

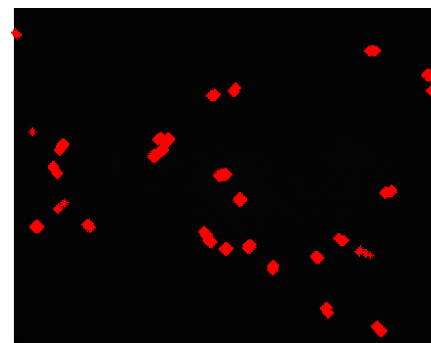Figure 2 Result of biological localization process (7826)
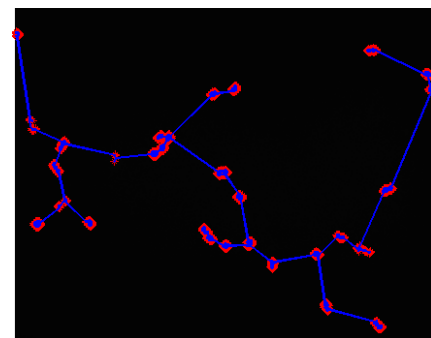

Figure 3 Extracted FAST features

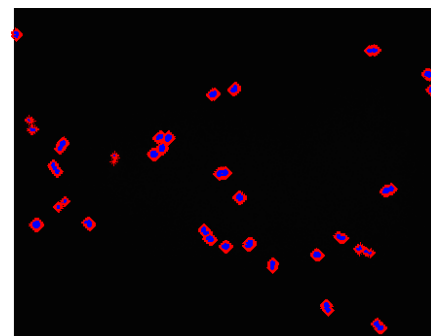Figure 4 Minimum Spanning Tree of the feature points

Figure 5 Localized cells after removing longest edges

The results of application to another test set are presented in Figures 6 and 7 where localized cells are shown with blue marks in the centre.

If the numbers for each tile are close to each other then we can mention about spatial randomness or we can suspect some spatial autocorrelation otherwise. The finer the tile size will mean a smaller number of objects (ideally one object per tile) in a case where random distribution is available.

Figures 8 and 9 show the grid count results for the two test sets respectively. From both figures, some spatial relationship is visible for the test sets.
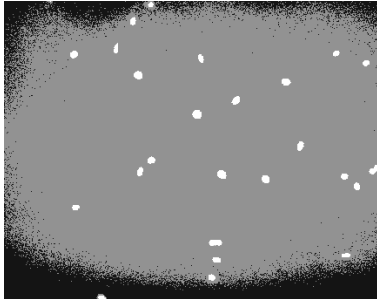

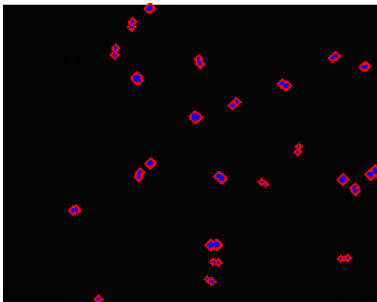Figure 6 A different set for the same cell type (8924)

Figure 7 Result of localization for the cells in Figure 6

IV. SPATIAL ANALYSIS OF DETECTED OBJECTS

Within the context of spatial analysis, a relationship between objects means either spatial autocorrelation or randomness. There are several methods in order to model such relationships [16], [17].

In our application, we used grid counting, density plotting, Ripley's K function and pair correlation function to test spatial randomness between the detected cells using the proposed method in Section II.

A. Grid Counting

The first method used is the grid counting method which is a quadrate-based approach to check for spatial randomness. The method may look simple but it is quite efficient indeed. It works by placing a logical grid on the area where objects lay. This logical grid divides this area into tiles and the number of objects in these tiles is counted.
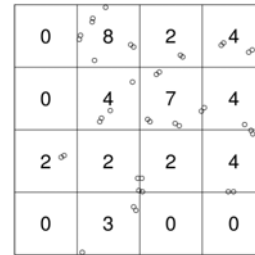

Figure 8 Grid count for test set 7826

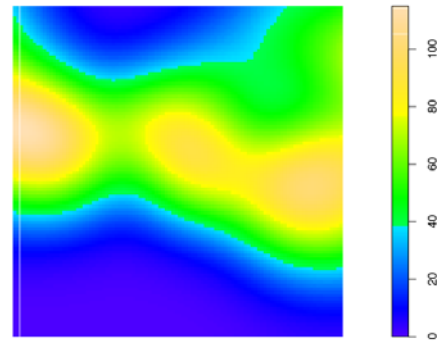Figure 9 Grid count for test set 8924
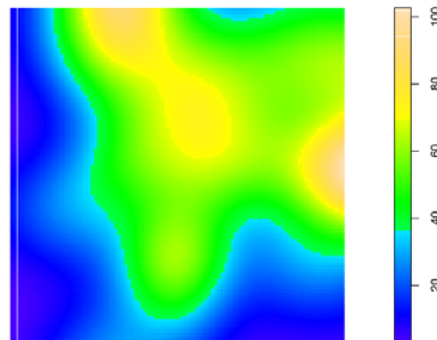

Figure 10 Density plot for test set 7826

Figure 11 Density plot for test set 8924

B. Density Plot

A better visualization of the distribution of the objects can be obtained by using a density plot which shows the change in density within the area.

Figures 10 and 11 show the results for density plots for the datasets. The legends next to the plots show the density measure. Density is visualized by using a colour spectrum ranging from dark blue to bright yellow which indicates increasing density of objects. From both plots, a distribution which can not be interpreted as random is clearly visible.

C. Ripley's K Function

Apart from the two methods above, which are aimed for visual inspection of data, there are also more robust statistical measures in order to analyse the distribution of objects within a specific area.

Methods like mean or variance are referred to as first-order properties and do not include or use any information about the area the objects cover. For this reason second-order properties have been introduced [16] in order to take the area coverage and the change [17] in space into account.

An important measure for the second-order properties for a set of objects is the K function proposed by Ripley [18], [19] which works by using the expected number of objects within a specified distance. This expectation is denoted in Equation (1):

$$\lambda^{-1}E\left[N_o(r)\right] \qquad (1)$$

where λ represents the density of the objects in the area. $N_o(r)$ is the number of objects with parameter r denoting the distance around an arbitrary object [16]. This estimation is calculated as shown in Equation (2) [18]:

$$\hat{K}(r) = \frac{1}{n^2}\left|A\right|\sum_{i \neq j}\sum \frac{I_d(d_{ij})}{w_{ij}} \qquad (2)$$

In the equation, n represents the number of objects within the area $\left|A\right|$. d_{ij} denotes the distances between two objects with indices i and j. $I_d()$ is a function which indicates the points that will be selected as the objects for the given value of r. Finally, w denotes whether edge correction will be applied or not that is some objects that are on the edges on the area may not be accounted for some specific applications [17].

If the objects in the area show complete spatial randomness, then the number of objects within distance r is expected to be:

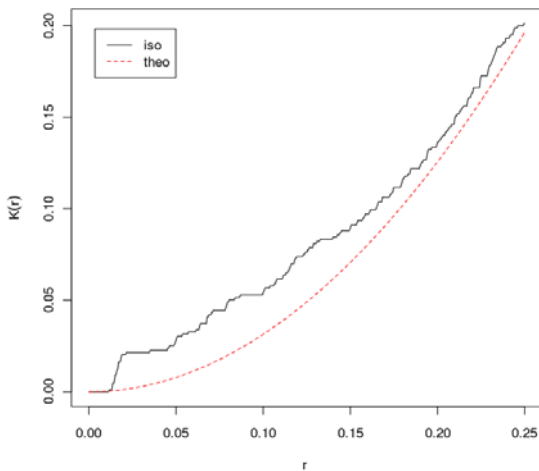$$\hat{K}(r) = \lambda r^2 \qquad (3)$$

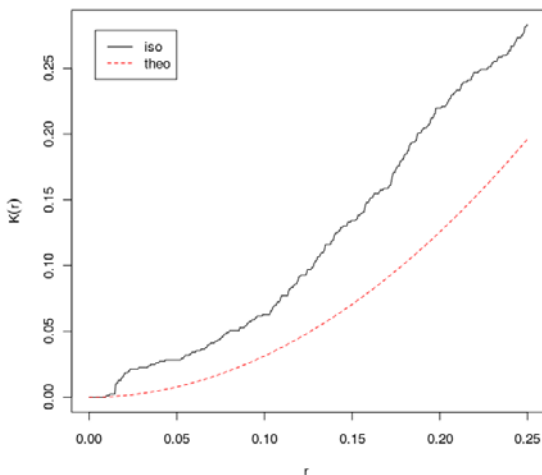Figure 12 Ripley's K function for test set 7826

Figure 13 Ripley's K function for test set 8924

Ripley's K function was applied to the test sets in order to obtain a measure of spatial relation between the cells in the images. Results are presented in Figure 12 and Figure 13 respectively:

The red dashed-line represents the case when complete spatial randomness is existent using within the area for the objects. However, the black lines in both figures denote the actual case where the distribution of the objects deviates from ideal random distribution and display spatial relationship.

This deviation is less visible in the test set 7826 where the black line follows the red line more closely than the result for the test set 8924.

D. Pair Correlation Function

The final test was performed using a different second-order property measure named as the pair correlation function [20]. According to the definition of second-order properties given before, this measure also takes the spatial relationship into account just as the Ripley's K function however this method shows the amount of correlation between pairs of objects within a specified distance.

For sake of simplicity, we used the definition of the pair correlation function based on the Ripley's K function described in [20] as shown in Equation (4).

$$g(r) = \frac{1}{d\kappa_d r^{d-1}}\frac{dK(r)}{dr} \qquad (4)$$

Which is obviously valid for $\forall r > 0$.

In the formula, κ_d is the area for 2-dimensions or volume for 3-dimensions of a unit ball with d-dimensions. The analysis was carried on in 2-dimensional objects (found and localized in images), i.e., $d = 2$, hence $\kappa_2 = \Pi$.
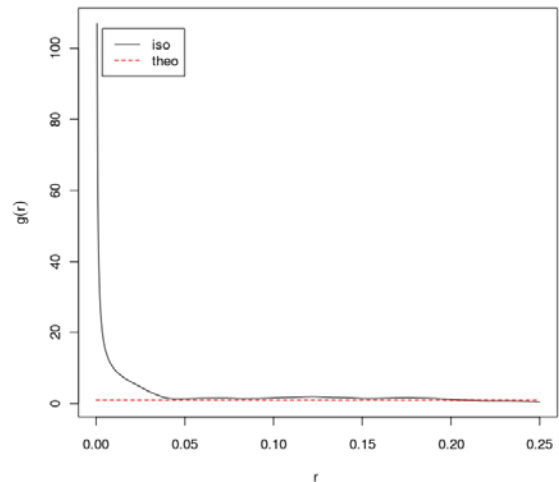

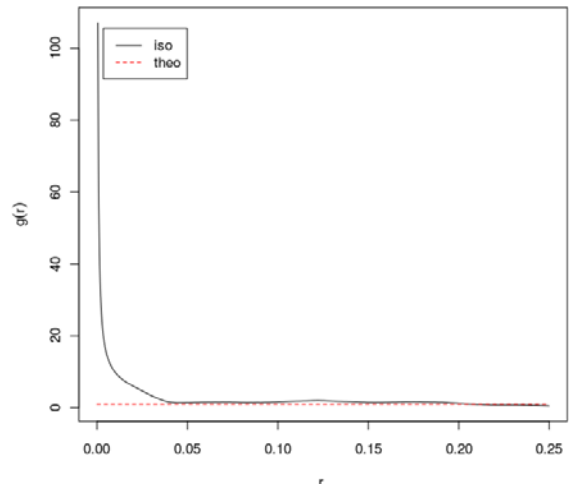Figure 14 Pair Correlation Function for test set 7826

Figure 15 Pair correlation function for test set 8924

The results of the pair correlation function are depicted in Figure 14 and 15. Interestingly, two figures are quite similar though some minor differences are noticeable. From these figures, we can see that the objects with a distance less than 0.05 show stronger correlation measures with respect to greater distances.

V.   CONCLUSION AND FUTURE DIRECTIONS

A novel algorithm for the localization of image objects was proposed in this paper. The method used feature points in order to construct a minimum spanning tree and localize objects using the convex-hull on the individual parts of the generated spanning tree [21].

In addition, a detailed spatial analysis was performed on these localized objects in order to find out spatial relationships.

The methods covered in the paper can be applied to a variety of images including different objects though the experiment was carried out on an image set for fibroblast cells.

This experiment carried out here showed that the method worked very accurately using real world data even in case of severe image noise (which can be seen in Figures 2 and 6) which is inevitable in any real image but generally more significant in a biological process as there will be other substances or cells in the test environment as well.

The method described here cannot be regarded as a complete segmentation method when compared to [5] and [6]; however, it can be used in the localization process in an easy but effective manner. In addition, the assumption that the objects must be well distinguishable should hold otherwise wrong localization results can be obtained.

Future research will focus on extending this method to a complete segmentation method by combining current approach with a region growing algorithm as in [22]. The authors believe that such a combination will result in better segmentation results which are more robust even in cases of high occlusion, more crowded scenes and severe noise.

The spatial analysis carried out here can also be extended to explore more second-order characteristics including the global degree of order [23] which employs the extreme distances in the pair correlation function or following a nearest neighbour approach to model the distribution [20].

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