Segmenting overlapped objects in images. A study to support the diagnosis of sickle cell disease.

Miquel Miró-Nicolau, Biel Moyà-Alcover, Manuel González-Hidalgo and Antoni Jaume-i-Capó

Abstract
Overlapped objects are found on multiple kinds of images, they are a source of problem due its partial information. Multiple types of algorithms are used to address this problem from simple and naive methods to more complex ones. In this work we propose a new method for the segmentation of overlapped object. Finally we compare the results of this algorithm with the state-of-art in two experiments: one with a new dataset, developed specially for this work, and red blood smears from sickle-cell disease patients.

Index Terms—Computer vision, overlapped objects, segmentation, sickle-cell disease.

I. INTRODUCTION
Separate overlapped objects on images is a problem that needs to be solved in multiple fields, from grain analysis [24] to blood cells study [8]. The existence of these overlapped objects reduces the information in some areas of the image, the occlusion zones. This occlusion makes the segmentation of these objects a challenging issue. Multiple approaches have been used to address this problem. In scenarios where the overlapped objects can be detected through differences in colour, Watershed algorithm [13, 16, 20] and level sets [3] are used. These methods are unable to divide overlapped objects with homogeneous colour.

Another type of segmentation methods are the ones based on the detection of concave points. These points are the positions where the contours of the different objects overlap. These methods find the concavities by studying the shape of the objects. Once the concave points are detected, multiple techniques can be used to divide these objects. These methods compared to Watershed and level set has independence to the occlusion zones. This occlusion makes the segmentation of these objects a challenging issue. Multiple approaches have been used to address this problem. In scenarios where the overlapped objects can be detected through differences in colour, Watershed algorithm [13, 16, 20] and level sets [3] are used. These methods are unable to divide overlapped objects with homogeneous colour.

We can find multiple approaches based on concave point detection in literature. Zafari et al. [27] proposed a taxonomy to classify these methods in four groups: skeleton, chord, polygon approximation and curvature.

A. Skeleton
The methods based on skeleton use the information of the boundary and its medial axis to detect concave points. Song and Wang et al. [18] identifies the local minimums of the distance between the boundary of the object and its medial axis as the concave points. Samma et al. [17] find the concave points intersecting the skeleton of the background with the boundary of the object.

These methods are based in different algorithms to find the skeleton. As a result they need a big change in the curvature to be able to detect the concave points. These methods tend to fail in smooth curvatures.

B. Chord
Chord methods use the boundary and the convexity defects to detect concavities. The main idea of these approaches is to identify as concave points the furthest points between the contour and the convexity defect.

Multiple solutions are based on this idea. Yeo et al. [25] and LaTorre et al. [10] methods applied multiple constraints to each area between a chord and the contour to determine its goodness.

Chord methods consider that for every convexity defect exists only one concave point. This assumption is not always true. As a result, the major drawback of this approach is the misclassification of the multiple concave points between a chord and the curvature.

C. Polygon Approximation
Polygon approximation is a set of methods that represents the contours of the objects through a sequence of dominant points. These methods aims to remove noise approximate the contour to a polygon. Bai et al. [1] developed a brand new algorithm to do the approximation. This algorithm analyses the difference between a set of contour points and the straight line that connects their extremes. The points with a big distance to this previously defined line are considered dominant points.

Chavez et al. [4] use the well-known algorithm of Ramer-Douglas-Peucker [6] to approximate the contour. Zhang et al. [28] used a modified version of curvature scale space (CSS) to make a polygon approximation. These polygon approximation algorithm has as a result a set of dominant points. The concave points are detected by evaluating angular change on these dominant points. Most methods use the arc tangent to calculate this angular change. The points with an arc tangent higher than a threshold are considered concave points.

Zafari et al. [26] used, similarly to the previous described approximation, a modified version of curvature scale space method to find interest points. Finally they discriminate them between concave and convex points. Instead of the rest of the other methods they do not calculate the angular change, all
the dominant points of the CSS are considered to be interest points. These methods are highly parametric. The increase in the number of parameters causes those polygon approximation methods are not robust to change of size. Another weakness of these methods is that they deform the original silhouette to simplify it. The amount of approximation is a trade-off between the lack of precision in the position of the concave points and the smooth applied to the contour. This trade-off affects the final results.

D. Curvature

Methods based on curvature identifies the concave points as the local extreme of the curvature. The curvature, $k$, is calculated for every point as.

$$k(i) = \frac{x_i^3 \cdot y_i'' - y_i^3 \cdot x_i''}{(x_i^2 + y_i^2)^{3/2}}$$  

Multiple methods are used to approximate the value of $k$. Wen et al. [22] calculate the derivative by convolving the boundary with Gaussian derivatives. González et al. [8] use the $k$-curvature and the $k$-slope to approximate the value of the curvature.

These methods tend to fail when exists multiple concave points in small areas and with the existence of noise in the contour.

E. Other methods

Besides the taxonomy proposed in [27] there are other techniques to find concave points. The techniques of this category are very different to the others methods analysed.

Fernández et al. [7] defined a sliding window for the contour and calculated the proportion between object and background found in this window. This proportion determined the likelihood of an existing concavity on the evaluated point. He et al. [9] adapted this method to use it on three dimensional contexts. Best results were obtained in scenarios with high concavity. This method accuracy decreased with the existence of noise.

Wang et al. [21] proposed a bottleneck detector. They define a bottleneck as a set of two points that minimise their euclidean distance and maximises the distance over the contour. The pair of points that defines a bottleneck are the concave points. A cluster can contain multiple bottlenecks. This algorithm is unable to discover how many elements form a cluster, the exact number of elements must be indicated to the algorithm. Another limitation is that they do not consider cases with an odd number of concave points in a cluster.

Zhang and Li [29] proposed a method to find the concave points with a two step algorithm. First, they detect a set of candidates points with the well known Harris corner detector. Second, they detect concave points with two different algorithms, one for obvious concave points and another for uncertain concave points. This methods is a highly parametric because of these multiple steps, having a poor ability to generalize for different size objects.

As reader can see, the accuracy of the object separation depends on the accuracy of concave point detection. Motivated by the state-of-art performance on the task of cell segmentation and inspired by its limitations, we adapted the algorithm proposed by [8] modifying the detection of the points of interest and the selection of the concave points, with the aim of improving the results on the challenging task of overlapping objects separation.

As a main contribution we proposed a new method to detect concave points that increase the precision of its position. Using a synthetic dataset to simulate the overlapping cells and providing the position of the concave points as a ground-truth, we compared our proposed method with the state-of-the-art to detect the spatial precision. As a case study, we compared the proposed concave point detector with a well-known application, such as the splitting of overlapped cells, concretely microscopic images of peripheral blood smear samples of red blood cells (RBC) of patients with sickle-cell disease (SCD). The goal of the case study was two check if the spacial precision of the concave points detector method affects the results of a classification algorithm of the morphology of RBC in a real world scenario.

The remainder of this paper is organized as follows. In Section II we describe the proposed method for the efficient detection of concave points. In Section III the experimental environment is specified and the databases used for experimentation are described. In section IV results and discussion are provided after applying the proposed method to synthetic and real images of clusters of objects. Finally, in Section V we give our conclusions.

II. Methodology

In this section, we define a new method to detect concave points. This detection is made analyzing the value of curvature in every contour point. The input of the algorithm is a set of points that define a contour. Its output is a set of concave points. The whole process is summarized in the Figure 1.

The contour of an object is a set of points that defines its shape. The method can be divided into four steps. The first step is the computation of the curvature on every point of the contour of the object. The second step is to select the segments with more curvature, that means the segments with the highest probability to contain an interest point. The third step is to obtain an interest point from each segment calculated in the previous step. Finally, we discriminate the interest points by its type, concave or convex.

A. Curvature

The proposed method approximates the value of the curvature through a well-known technique, the $k$-curvature [15]. This technique considers the curvature of every point as the difference of its slope. The $k$-curvature is separable, allowing to make the calculation independently for each direction. The equations (2) and (3) defines the $k$-slope for the horizontal and vertical axis, while the $k$-curvature in each direction is defined by the equations (4) and (5):

$$k_x = \frac{y \cdot g_2 - x \cdot g_1}{g_0^2}$$  
$$k_y = \frac{z \cdot h_2 - y \cdot h_1}{h_0^2}$$  
$$k = \frac{k_x \cdot k_y}{g_0^2}$$  
$$k_h = \frac{y \cdot g_2 - x \cdot g_1}{g_0^2} + \frac{z \cdot h_2 - y \cdot h_1}{h_0^2}$$  
$$k_v = \frac{z \cdot g_2 - y \cdot g_1}{g_0^2} - \frac{x \cdot h_2 - z \cdot h_1}{h_0^2}$$
Figure 1: Flow chart of the process to obtain concave points.

The next step is a search of more refined regions, we want to obtain regions that contain only one interest point. To accomplish that objective we perform a search process by iteratively splitting each region by increasing its threshold value. This local increase of the threshold is done until the region is smaller than a predefined maximum value, \( l_{\text{max}} \).

The analysis of the curvature levels allows to identify the interest points. There are one interest point for each region. This method considers as this interesting point the weighted median of the curvature of the region.

C. Concave points

Once we have a set of points of interest we need to discriminate between the concave and the convex ones. This part of the algorithm is based on the analysis of the relative position of each point neighbourhood. The classification is done in three steps:

1) **Determine neighbour points:** We determine two points on the contour located on the \( k \) and \(-k\) position relative to the interest point. This parameter \( k \) has the same value of the main parameter of the \( k\)-curvature. The operation described in this parameter can be seen in figure 3a.

2) **Definition of a line between the \( k \) neighbours:** We...
build a straight line between the points selected in the previous step (see figure 3b).

3) Middle point of the line: The value of the middle point of the defined line determine the class of the point analysed. The point is classified as concave if the middle point of the line is outside the object, otherwise is classified as convex, as can be seen in figure 3c.

The algorithm described in this section identifies the position of all concave points inside a contour, it is divided into three main steps: first, the calculation of the curvature for every point. The regions containing points of interest have significant differences in the curvature value from the ones that doesn’t contain points of interest. Second, the extraction of points of interest from each region obtained in the previous step. Finally, we classify these points of interest between concave and convex points.

III. EXPERIMENTAL SETUP

To validate the proposed methods, we present this experimental setup.

On this section we describe the conducted experiments, the datasets and the metrics used to calculate the performance. The first experiment consisted of the detection of concave points in synthetic images, built with overlapped ellipses. The use of this artificial dataset allows us to get analytically the exact position of the concave points. The goal of this experiment is to compare the position of the concavities predicted for each method to the ground truth. In this experiment we only compare the concave-point based methods described in the state-of-art.

The second experiment consisted of the use of multiple algorithms for segmenting highly overlapped objects in a well-known scenario, such as the splitting of cells on blood smears objects. The objective is to check if the differences on the concave detectors are significant for the separation of overlapped objects in a real-world scenario.

We used Python 3.6 for all the experimentation in addition to the next packages: NumPy version 1.15.4 [19], SciPy version 1.3.3 and OpenCV version 3.4.3.11 [2].

A. Datasets

As we stated in the previous section we use two types of images to validate our method: artificial images, generated automatically by a computer, and real image dataset, collected from patients with sickle cell anaemia.

1) OverArt Dataset: OverArt dataset consists of a set of 2000 synthetic images created especially for this work. To generate these 2000 images we overlap multiple ellipses. Each image contains a cluster with three ellipses. The use of three ellipses is a good trade-off between complexity and reality (see image 3).

The ellipses of each image are defined by three parameters: the rotation, the feret diameter size and its center position. The values of the parameters are generated randomly by a set of constraints.

The first ellipse position is the image center. The location of the other two of the ellipses depends on the position of the first one. These positions are selected to ensure that exists an overlapping area between them. The feret diameter and the rotation of the ellipse are random numbers between well defined ranges. The values of this constrains can be found in Table I.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maximum feret</td>
<td>100 px</td>
</tr>
<tr>
<td>Minimum feret</td>
<td>45 px</td>
</tr>
<tr>
<td>Minimum distance between centers</td>
<td>45 px</td>
</tr>
<tr>
<td>Maximum distance between centers</td>
<td>85 px</td>
</tr>
<tr>
<td>Minimum rotation</td>
<td>0°</td>
</tr>
<tr>
<td>Maximum rotation</td>
<td>360°</td>
</tr>
</tbody>
</table>

Table I: Parameters for the generation of the OverArt dataset.

To compare the methods we need to have a ground truth of the location of the concave points. A concave point is defined by the position where two or more ellipses intersects and must be located over the contour that defines the overlapping region.

The overlapped objects are defined by the equation of the ellipse (see equations 7 and 9). For each image of the dataset we obtain the exact position of the concave points that contain the image. The calculation of a concave point is done analytically, studying and solving the system of equation formed by the ellipses equations.

$$\lambda_1 = \frac{((x-h)\cos(A) + (y-k)\sin(A))^2}{(a^2)}$$ (7)

$$\lambda_2 = \frac{((x-h)\sin(A) - (y-k)\cos(A))^2}{(b^2)}$$ (8)

$$\lambda_1 + \lambda_2 = 1$$ (9)

The images we used for this first experiment are available at https://https://miquelim.github.io/ to enable future comparisons.

2) Real Dataset: The microscopic images of the blood smears used in this work were collected from erythrocytesIDB2 [8], available at http://erythrocytesidb.uib.es/ The images consist of prepared samples of patients with sickle cell anaemia classified by a specialist from “Dr. Juan Bruno Zayas” Hospital General in Santiago de Cuba, Cuba. The specialist’s criteria were used as an expert approach to validate the results of the classification methods used in this work.

The patients with sickle-cell disease (SCD), are characterized by red blood cells(RBCs) with the shape of a sickle or half-moon instead of the smooth, circular shape as normal cells have. WHO document “Global epidemiology of haemoglobin disorders and derived service indicators” [12] indicates that around a 5% of the world’s population carries trait genes for haemoglobin disorders, mainly sickle cell disease and thalassemia. The document also indicates that the percentage of people who carry these genes is as high as 25% in some regions and over 300,000 babies with severe hemoglobin disorders are born each year. SCD is spread among people whose ancestors are from sub-Saharan Africa, India, Saudi Arabia and Mediterranean countries. In order to confirm the SCD diagnose, peripheral blood smear samples are analyzed by microscopy to check for the presence of the sickle-shaped
erythrocytes and compare their frequency to normal red blood cells. The peripheral blood smear samples always include overlapped or clustered cells, and the sample preparation process can affect the quantity of overlapping erythrocytes in the images studied. Clinical laboratories typically prepare blood samples for microscopy analysis using the dragging technique. Using this technique, more cell groups are apparent in the samples due to the spreading process [8].

Each image was labeled by the medical expert. There are 50 images with different number of cells (see figure 5). The 50 images contains in total 2748 cells. These cells belongs to three classes defined by the medical experts. Those are circular, elongated and others (see figure 6).

B. Evaluation metrics

The evaluation of our method is performed comparing the proposed method with the state of the art. We used five metrics:

- **Mean of the Euclidean distance.** This metric is the Euclidean distance from one predicted point to the nearest one in the ground truth. One ground truth point can only be related to one predicted point. We set a minimum distance between a pair of points to be accepted as related points.

- **F1-Score.** It is a standard and widely used metric is the harmonic mean of the precision and the recall (see equation 12). The precision and the recall depends on the number of false positives, true positives and false negatives. The definition of these parameters depends on the nature of each experiment.

- **Sickle cell disease diagnosis support score (SDS-Score).** Proposed by Delgado et al. [5], the SDS-Score indicates the usefulness of the results for the diagnosis of sickle cell disease (see equation 13).

- **Matthew’s Correlation Coefficient (MCC).** Introduce by Matthew [11], is a correlation measure between the prediction and observation. We use the adaptation proposed by Mosley et al. [14] for multi class problems (see equation 14).

- **Class Balance Accuracy (CBA).** Introduced by Mosley et al. [14]. Represents an overall accuracy measure built from an aggregation of individual class metrics (see equation 15).

\[
\text{Precision} = \frac{\text{TruePositives}}{\text{TruePositives} + \text{FalsePositives}}, \quad (10)
\]

\[
\text{Recall} = \frac{\text{TruePositives}}{\text{TruePositives} + \text{FalseNegatives}}, \quad (11)
\]

\[
F1 = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}, \quad (12)
\]

\[
\text{SDS-Score} = \frac{\sum_{i=1}^{3} c_{ii} + c_{23} + n_{32}}{\sum_{i=1}^{3} \sum_{j=1}^{3} c_{ij}}, \quad (13)
\]
\[
MCC = \sum_{i,l,m=1}^{k} c_{il} \cdot c_{ml} - c_{il} \cdot c_{im}
\]

\[
\sqrt{\sum_{k=1}^{n} \left( \sum_{k=1}^{m} c_{ik}(\sum_{f=g=1}^{k} c_{gf}) \right) / \sum_{i=1}^{k} \left( \sum_{i=1}^{h} c_{ili}(\sum_{f=g=1}^{k} c_{fli}) \right)}
\]

(14)

\[
CBA - Score = \frac{\sum_{i=1}^{k} c_{il}}{\max(c_{i},c_{il})}
\]

(15)

Where \(c_{ij}\) are the number of element of class \(i\) predicted as the class \(j\) and \(k\) the number of classes.

In addition to these metrics, we use the Wilcoxon Test. Wilcoxon test is a non-parametric test presented by Wilcoxon [23]. This test is used to determine whether two dependent, and paired, samples were selected from populations having the same underlying distribution.

C. Experimentation

As we explained on previous sections we defined two experiments. Each one of them uses a different dataset. Both compare nine different methods studied on the state of the art section and the two proposed methods. Most of these methods are defined by a set of parameters. We get the values of the parameters from their respective articles when it is indicated. We calculated the parameters without an explicit value on its original through experimentation.

We do not consider all methods described in the state-of-art for the experimentation. The main reason for this decision is the similarity between the dismissed ones with some of the methods tested. For example Yeo et al. [25] and LaTorre et al. [10]. Another reason for the dismissal of some methods is the absence of information on the original paper to reproduce the algorithm and the lack of access to the source code.

We defined a baseline method. This method assumed that a concave point is the point that maximizes the distance between the contour and each of the convexity defect of the convex hull. This method is a naive approach used to compare it with the more sophisticated ones.

Song and Wang [20] is a no parametric method.

LaTorre et al. [10] used three parameters: the minimum concavity area, the minimum distance to the bounding box and the minimum concavity degree. For our tests, we used the parameters defined in the original paper: minimum concavity area equal to 20 pixels, minimum distance to the bounding box equal to 5 pixels and a 10 % of concavity degree.

Bai et al. [1] as Chávez et al. [4] have two kinds of parameters, parameters for the polygon approximation and parameters for the concave point detection. The original paper defined the value of the first type of parameters, the polygon approximation ones. The parameters for the concave point detection is the same from Chávez et al. [4] a threshold to determine if a point is of interest or not. We used the same value than the used in [4].

Chávez et al. [4] have two main parameters: the epsilon and a threshold for the angular change. The epsilon is a parameter of the Ramer-Douglas-Peucker algorithm. The second parameter is the minimum value of the curvature to consider a point as a concave point. We had to set these two parameters through experimentation, the epsilon value is set to 2 and the threshold value to 0.15.

Zafari et al. [29] have its method public available. We use its to do the experimentation.

We also used the source code of González et al. [8], we use the same parameters of the referenced paper.

Fernández et al. [7] used two parameters: the size of the environment to analyse, and a threshold to determine which point is concave. They set the first parameter, the size of the environment, in the original work by 5 pixels. They do not define the value of the second parameter, the threshold of the concavity, on the original work so we calculated it through experimentation. We obtained the best results with a threshold of 1.97.

Song and Wang [20] do not define the value of the parameters in the original paper. We determined that the best value of the main parameter of this method, the maximum distance between the medial axis and the concave points is a distance of 70 pixels.

Wang, Zhang and Ray [21] has as only one parameter, the number of objects in each cluster. They use an SVM to determine the value of this experiment for each cluster. We set this parameter constant with a value of three for each cluster on both experiments.

The concave point algorithm proposed in this work is a parametric method. The method has three parameters as explained in section [11]. These parameters are the \(K\), and the \(I_{min}\) and \(I_{max}\) with 5 and 50 respectively. The value of \(K\) depends on the size of the objects to study. Nevertheless, we used values in a range from 5 to 15 depending on the experiment.

Machine learning algorithm typically divides the available data into three groups: train, validation and test. The train set is used to fit the model and the validation dataset is used to evaluate the performance of the model propose. Finally, the test set is usually used for a final test of the model. Unfortunately, due to the limited amount of data, we can not divide the data into three subsets, instead, we have divided the data into two groups: train and validation. The first one is composed by thirty-four images selected randomly, while the test set is formed by sixteen images. All the experiments are done with the same test dataset.

1) Experiment 1: This experiment aims to detect the spatial precision for the concave point prediction. To do so the OverArt dataset is used. This dataset is used because contains the exact position of every concave point.

As a consequence of the goal of the experiment and the typology of the dataset, we used two different metrics. The first one is the mean Euclidean distance. We used this metric to evaluate the distance between the ground truth points and the prediction. We calculate its values as the mean of the distances between a predicted point and its nearest ground truth point. Secondly, we used the F1 Score to get a measure
for the number of correct predictions.

Both metrics, in a perfect scenario, are a bijective function between the prediction and the ground truth. We relate these pairs of points through the distance between them. We relate one ground truth point to the nearest predicted point. We considered as a false positive each predicted point with a distance higher than 7 pixels to its related ground truth point. We select this 7 pixel margin as a trade-off between the actual position and some valid amount of error.

2) Experiment 2: The second experiment allowed us to determine how the different methods to find concave points affects the results of an algorithm that use that information to segment overlapped cells and compare them to deep learning methods.

In this experiment, we use the method proposed by González et al.[8] for the division of objects through their concave points. After this division we compared the ground truth with the predicted objects. This experiment use the second dataset, erythrocytes1DB2. Unlike the OverArt dataset, this one only contains the position of the elements that are part of each cluster.

We use the F1-Score, SDS-Score, CBA and MCC as metrics for this experiment. This experiment has more than one class, for this reason, the false positive, false negative and true positive are calculated depending on the class of interest. The total results are obtained through the weighted average of the metrics per class. A false positive and a false negative are miss-classifications of the type of a cell, depending on the class to compare. Apart from these cases, there are two more possibilities: predict a cell that does not exist, and do not predict a cell that exists (see figure[7]). These two special cases are not considered for the calculation of the metrics, instead, we present the ratio between the occurrence of each type of error and the normal ones. Furthermore, we use harmonic mean to aggregate these two ratios and obtain a new metric. We called these situations over sample and under-sample, respectively.

This second experiment is designed to check how the differences detected in the previous experiment affect the subsequent division of the objects.

IV. RESULTS AND DISCUSSION

A. Experiment 1

First experiment aims to detect the spatial precision for the concave point prediction, as we already explained in the previous section[III]. To check this precision we compare the predicted position of the concave point to the ideal position of these points found in the ground truth. All the results of this experiment can be observed in table[II].

The first, the second and the third column of Table[I] depicts the results from Precision, Recall and F1-Score, the proposed method obtains the best score in the three metrics. Fourth and fifth columns show the precision in pixels of the concave point detection, these columns show the mean distance between the prediction and the ground truth its standard deviation.

From the results obtained on this experiment, we can analyse the different methods depending on their behaviour.
mean between these two values, to get the real performance
of the methods. Our method has the best under sample
proportion and very good over sample proportion, as a result,
the harmonic mean surpasses the rest of the methods.

The results obtained with the proposed method surpasses the
rest of the methods from the state-of-art. Nevertheless, presents
multiple limitations. The concave point-based method usually
makes over-segmentation, they found more elements than they
should. This problem is even bigger with non-circular objects.
Another problem of these approaches is the need to make a
previous segmentation. The quality of this segmentation has a
big impact on the ability to segment overlapped objects.

On this section, we have seen the results of our proposed
method and the different works studied on the state-of-art. We
tested two different experiments, in both of them, our method
has better results than the rest of concave points. These results
show that our methods are more precise and with a higher
detection ability. Furthermore, in the second experiment, we
have checked the difference of this precision on the final result.

V. CONCLUSIONS

The main goal of this work was the study of the existing
methods for the segmentation of overlapped objects and the
development of new methods to adapt the existing methods to
new scenarios and at the same time overcome its limitations.

In the introduction we discussed the difficulty of this task.
The existence of overlapped object reduces the information
available in some areas of the image. We analyzed the existing
state-of-art solutions to this problem. We found multiple pro-
posals from a more naive solution, as the Watershed algorithm,
to more complex ones as a neural network. We focused our
study on two different techniques. We selected concave point
methods and deep learning approaches. These methods exceed
the performance of the rest of the literature.

To do this study we adapted, in the case of concave point-
based methods, the taxonomy proposed by Zafari et al. [27].
The original taxonomy classifies the methods into four groups:
curvature, skeleton, chord and polygon approximation. We
added a new category that includes methods not considered

![Figure 7: Examples of the over and under segmentation of a cell using our new algorithm. In red under segmentation, in blue
over segmentation and in green normal segmentation](image-url)
by Zafari et al. [27]. This new category contained a set of methods without many similarities between them. We called this category other. Adding this new category we can consider a new set of methods. From this study of the state-of-art, we conclude that one of the most interesting methods is the work of González et al. [8], because its good results and the use of similar images than us (red blood smears).

From the original work of González et al. [8] we proposed a new method. Our main contribution was to improve the extraction of the concave point from the curvature. This contribution improves significantly the performance of the original method, increasing the precision of the predictions.

To check these our proposed method we tested it on two scenarios. We also compared our method with multiple methods from the state-of-art. The first experiment is designed to check the precision on the position of the predicted concave points. To do it we designed a new dataset consisting of 2000 images of overlapped objects, the OverArt dataset. We use this dataset because it contains a ground truth of the position of the concave points. The second experiment used concave point methods to segment overlapped objects on a real dataset consisting of red blood smears from patients of sickle-cell disease. This experiment aims to compare the results of the segmentation. We defined a set of metrics and we compared all the methods.

The objectives of this paper have been full filled. We fully developed a concave point-based method. The results of our method surpassed the state-of-art method. Finally, we also have defined an experimental framework that allows future comparison of segmentation methods. This framework contains the selected metrics, both datasets (the artificial dataset and the real dataset) and the design of two experiments.

VI. ANNEX

The datasets used for the experimentation can be found on [http://erythrocytesidb.uib.es/](http://erythrocytesidb.uib.es/) and [https://miquelmn.github.io/](https://miquelmn.github.io/) respectively. The second link also contains the code for the generation of OverArt dataset and the raw data of the results from the two experiments.

REFERENCES


