

# Unified Framework for Counting Agriculture-Related Objects in Digital Images

Jayme Garcia Arnal Barbedo  
Embrapa Agricultural Informatics  
Campinas, SP, Brazil  
jayme@cnpia.embrapa.br

**Abstract**—Counting objects is an important activity in the daily routine of many areas of industry. This is particularly true in agriculture, in which objects like cells, microorganisms, seeds and other structures have to be quantified as a source of relevant information. This paper proposes a framework that aggregates three different algorithms into a single tool able to tackle a wide variety of counting problems that exist in the agriculture industry. The factor that brings all those algorithms together is the input by the user of some templates for the objects, which allows the resulting method to select the best option for those particular conditions. As a desirable side effect, problems related to resolution and scale dependencies that plagued those previous algorithms are mostly solved by this new approach.

**Keywords**—Object Counting; Digital Images; Agricultural Applications

## I. INTRODUCTION

The counting of objects in the context of agriculture is very important, as many quantitative (and even qualitative) analyses depend on a reliable estimation for the number of certain elements. This is also a very diverse problem, as those elements may be as different as, for example, bacteria and soybean kernels. Those counting problems are still primarily tackled manually, that is, one or more individuals have to perform the counting manually, in a process that is often tedious and time demanding.

As a response to this situation, many automatic alternatives have been proposed in the literature, especially in the last decade. However, most of those proposals were developed to solve very specific counting problems, which means that they usually perform poorly when used in a context other than that for which they were trained.

The method proposed in this paper tries to provide a more general counting tool, focusing specifically in agricultural applications. It is important to emphasize, however, that the method's characteristics may make it suitable to be applied to other kinds of objects, but more tests are necessary before such a claim can be verified.

The method proposed here is based on three methods previously developed for specific counting problems [1], [2], [3], and on a step in which the user of the program provides some inputs that will ultimately reveal the best approach for each specific image submitted to the program. The user's participation is quick and simple, as will be seen in Section III, so the benefits provided by the automation of the counting process are not offset by an overly complicated operation.

The full scope of the method presented here is yet to be determined. However, the performance achieved for the three types of objects tested (microorganisms, root nodules and seed kernels) reveals that the strategy is suitable for most practical agricultural counting problems.

The paper is organized as follow. Section II presents a literature review containing some of the main publications in the subject of counting of agricultural object. Section III describes the proposed method. Section IV describes the tests and presents the main results. Finally, Section V presents some final remarks.

## II. LITERATURE REVIEW

As stated before, the method proposed here is based on three predecessors that tackled the problems of counting microorganisms, root nodules and seed kernels. While the first subject has been a major focus of research, the other two are largely untapped. As a result, this section briefly describes 12 works dedicated to microorganisms, and only one work for each of the other two subjects – to the author's knowledge, the only ones that exist in the literature. The methods proposed by the author itself are not presented in this section, as they will be described with some more detail in Section III.

Counting fecal coliforms to control the quality of water was the main motivation of the method proposed by Mukherjee et al. [4]. The method has a preprocessing stage, in which the image is modified to make the counting process easier, and a classification and counting stage, which is performed by applying a distance transform. This work was one of the first to propose an automatic method to count bacteria.

Cordiki et al. [5] proposed a method to count bacterial colonies that explores the properties of the surface of microbial colonies. The colonies found in Petri dishes are illuminated so those properties are highlighted. A multilevel threshold algorithm is employed to separate and count colonies. The authors reported good results and claim that the method can be applied to other problems.

Another colony counting technique is proposed by Marotz et al. [6]. The preprocessing stage is composed by the detection of the counting region, image scaling and thresholding. The recognition stage is composed by parameter calculation, application of fuzzy logic to determine the quality of the potential objects and identification of the center of the objects, which are used in the final counting.

In [7], Osowsky and Gamba propose a system to count bacterial colonies in which a program captures twenty images of one given dish, from which a mean image is inferred. After that, a background subtraction is applied in order to separate the colonies from the rest of the image and to attenuate small differences in illumination. Finally, thresholding is applied and the colonies are counted by an algorithm that is also capable of measuring their size. Chen and Zhang [8] present a method that is almost identical to that proposed in [7], containing only some subtle modifications.

Schönholzer et al. [9] proposed a strategy in which the images are captured separately for each RGB channel. The process has the following stages: (i) detection of all objects in the green channel, (ii) distinction between bacteria and debris using the green and blue channels, and (iii) elimination of the debris from the images. The counting is then performed using the clean image.

In [10], the authors present a program, freely available on the web, to count bacteria. The method begins by compensating background brightness variations. Then, the pixels related to the cells are separated using a global threshold, resulting in a binary image in which the cells are white. Merged cells are separated using the watershed technique. Finally, possible remaining artifacts are eliminated using some threshold rule.

The method proposed by Zhang et al. [11] deals with the problem of bacteria counting in food samples, in order to detect contamination. First, the image is thresholded. Then, impurities and other artifacts are removed using Support Vector Machines (SVM). In the following, morphological parameters are gathered and fed to the SVM, which performs the final recognition and counting of the patterns.

In its master thesis, Goyal [12] describes thoroughly many types of bacteria counting, the difficulties posed by each one of those problems, and a tutorial about machine vision. The author strongly emphasizes the hardware assembled for his research. More than proposing a method, the author analyses several features extracted from the images and discusses their utility in the context of counting bacteria colonies. Thus, this is more prospective rather than innovative.

The proposal by Ates and Gerek [13] has as main characteristic the absence of any shape-based transform, like Hough. Instead, they developed a two-step iterative method. First, a binarization using a threshold based on the image histogram is performed. Next, isolated binary objects are analyzed according to their size and compactness, in order to infer how close are the objects to ideal circular colonies. If the object does not meet the criteria of compactness, a watershed algorithm is applied in order to divide the object into new possible colonies. The algorithm divides the objects until all meet the conditions, obtaining the final count.

The method proposed by Shen et al. [14] is quite conventional, having a preprocessing stage, in which a median filter is applied to reduce noise, a thresholding stage, a step for removing the edges of the dish, and finally it uses a heuristic method to perform the final count.

To the author's knowledge, the only paper in a Western

language on the subject of counting seed kernels was written by Zhao and Li [15]. In their work, the authors proposed a vibrating mechanism to separate soybean seeds, and used a high contrast background to favor the estimates. They reported accuracy close to 100%. The method works well when the seeds are spread out and there is a high contrast between seeds and the background. If the contrast is low, both seeds and background will be bright, in which case the method tends to fail. Also, without external intervention, the seeds are more likely to be found clustered than spread, in which case the method is not effective.

As in the case of seed kernels, to the author's knowledge there is only one method designed to automatically count nodules using digital images, which was proposed by Lira and Smith [16]. Their method uses digital images in which the nodules are still attached to the roots. Also, the authors used sophisticated scanners to capture the images, possibly because digital cameras were still in their infancy when the research was carried out. The authors reported correlations between automatic and manual counting over 0.85.

### III. THE METHOD

Before beginning the description of the method, it is important to define two terms that will appear throughout the entire paper. The term *object* refers to an individual entity which, in this paper, can be a microorganism, a seed, or a root nodule. On the other hand, the term *element* refers to a blob detected by the program. Such a blob may comprise one or more objects, in case they are clustered. Therefore, every object is an element, but only some elements are objects. Clustered objects is one of the most problematic situations faced by the algorithm, and effective ways to separate and count each object are necessary, as will be seen later.

#### A. The Novel Procedures

Fig. 1 shows the general scheme used in the algorithm proposed here. Each box in the figure will be explained in this section.

In fact, the main contribution of this paper is represented by the four first boxes. The procedures in the left branch are mostly based on [1], but they have suffered some major modifications, deserving a more detailed description. On the other hand, apart from a few minor adjustments, all remaining boxes are described in previous papers [2], [3]. However, in order to make this paper as self-contained as possible, a less detailed description will be presented for each of those boxes.

The task to be performed by the user in the beginning is divided into two actions. First, he/she must identify in the image the largest and smallest objects among the entire set. It is important to emphasize that, in general, it is very difficult for the user to identify those extreme objects exactly, but the method was designed to be robust to small misidentifications. Fig. 2 shows the interface for this selection procedure.

The selection by the user reveals the region where the object is located, but not the object itself. Due to the wide variety of possible objects and backgrounds, the program



Fig. 2. Interface with the user (instructions in Portuguese).

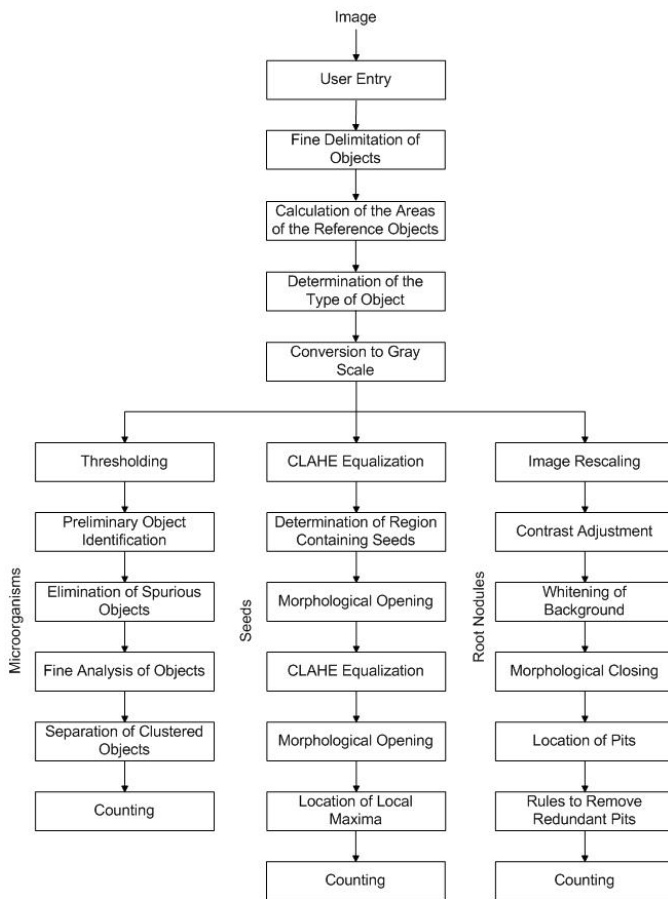


Fig. 1. Algorithm general structure.

uses five different methods to set the limits of the objects and, by varying some parameters, it produces 11 possible delimitations. Those possibilities are presented to the user (see Fig. 3), which chooses the one that better approximates the outlines of the objects. The five methods and their variations are presented in Table I.

In more than 90% of the cases, method 1 provides the best results. The remaining methods may be the best options for some specific cases and characteristics.

After the user chooses the reference objects, the program becomes completely automatic. The first task in this automatic phase is the calculation of the areas of the selected objects. Those areas will later act as thresholds for the sizes of the objects identified in the image.

The next step is the identification of the kind of object present in the image. This task could also be performed by the user, but increasing the complexity of the users participation would not be desirable.

The classes that were adopted are exactly those cited before: microorganisms, seeds and nodules. Seed and nodule images are, in general, very different among them. On the other hand, the variety of microorganism images is so vast that some of them have characteristics that are quite close to the other two kinds. It is important to emphasize, however, that identifying the correct class is not the main objective. The main goal is to apply the best possible strategy to the image at hand, so the counting is as correct as possible. Thus, if an image is mistakenly classified, it probably has characteristics of that other class, hence it is likely that the selected procedure is indeed the best option.

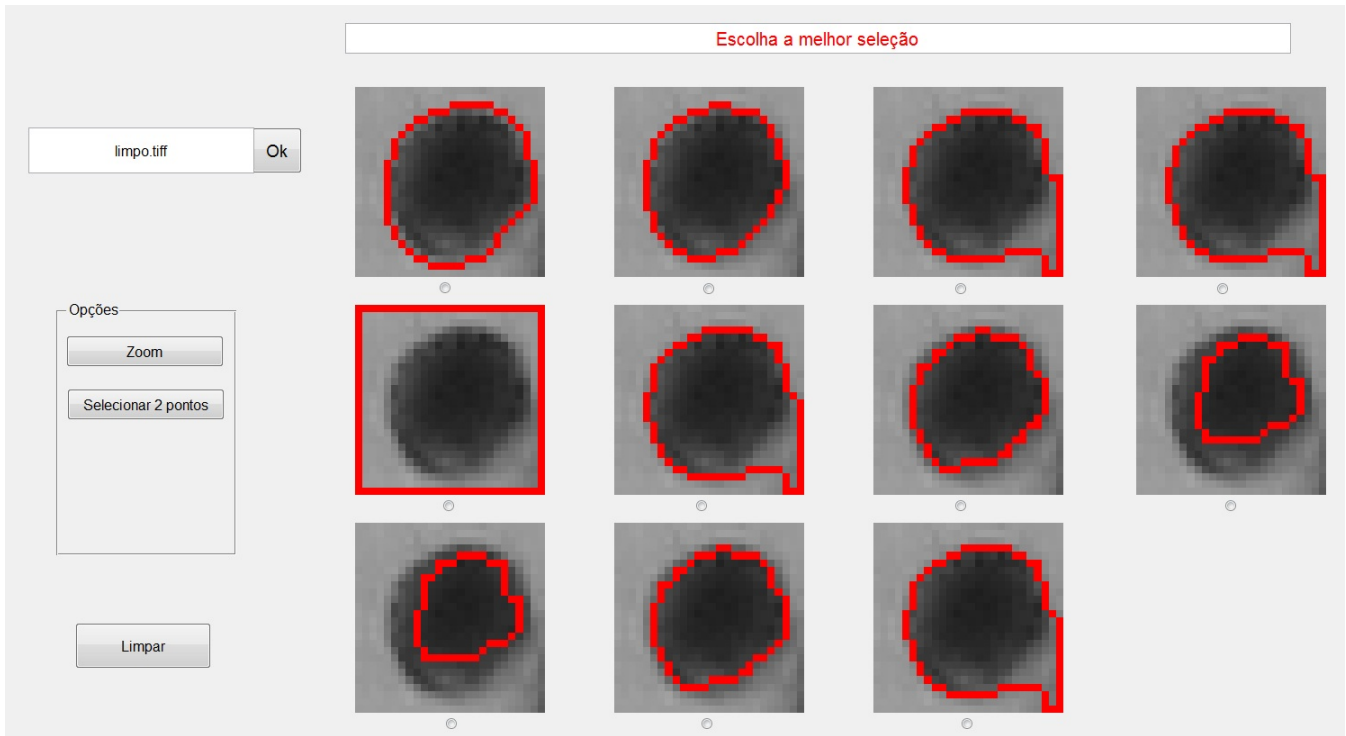


Fig. 3. Possibilities presented to the user.

TABLE I  
METHODS FOR DELINEATING THE OBJECTS.

Method	Descriptions	Variations
1	First, the Laplacian of Gaussian method for edge detection, using zero as threshold. That value was chosen so the detected edges have closed contours. In the following, the inner regions are filled (pixels are made equal to one) and all connected objects are identified. Since only one object should be present in that region, only the largest object is considered, and all other pixels are made equal to zero. The region containing the unitary pixels demarks the object.	No variations.
2	The only difference between this method and the first one is that this one uses the Canny method to detect the edges, instead of the Laplacian of Gaussian.	No variations.
3	This method simply applies binarization using three different thresholds. If the objects are darker than the background, the grey scale of the image is inverted by the operation $P_n = 1 - P$ , where $P$ e $P_n$ are the values of the original and modified pixels, respectively. All other stages, namely filling of inner regions and identification of the actual object, are identical to the previous ones.	Threshold = 0 Threshold = 0.5 Threshold = 0.7
4	This method is almost identical to the third, but instead of applying the binarization to the original region, this has its contrast modified by the technique of histogram equalization. In this technique, the image pixel values are modified in such a way the bins of the resulting histogram (in this case, 64) have the same amplitude.	Threshold = 0 Threshold = 0.5 Threshold = 0.7
5	This method uses the technique of region growing in which, from an initial position, its surrounds are filled until certain thresholds are reached. The initial position is always the central point of the region, and the threshold values are given as a percentage of the difference between maximum and minimum pixel values present in the image. The remaining procedures are identical to the other methods.	Threshold = 20% Threshold = 50% Threshold = 90%

Some methods for pattern recognition were tested, including neural networks and support vector machines (SVM). In the end, the best results were achieved using a simple decision tree, as will be seen in Section IV. Both objects selected by the user are used in the decision tree, together with the whole image binarized using the median of the pixels as threshold. Fig. 4 shows the whole decision tree.

As can be seen, there are four decision nodes, which are described in the following:

1. If the area of the largest object ( $A$ ) selected by the user is at least five times the area of the smallest one ( $a$ ), go to node

two, otherwise go to node three. This is a response to the fact that the areas of objects, in nodule images, vary widely.

2. The elements in the binarized image are identified. If the largest element ( $E$ ) has an area at least 1.2 times the area of the largest object selected by the user, it means that there are clusters, thus it is probably a root nodule image, otherwise it is considered that the image contains microorganisms.

3. The shape of soybean seeds is almost circular, but due to the tridimensionality and the angle of the illumination, parts of the seed may be shadowed, becoming black in the thresholding. In those cases, the detected object assumes the

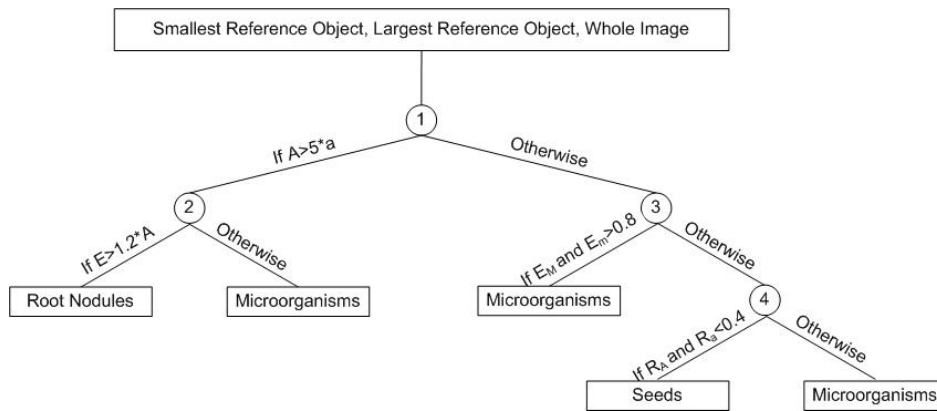


Fig. 4. Decision tree to determine the type of image.

approximate shape of an ellipse. Therefore, if the ellipticity of both selected objects ( $E_M$  and  $E_m$ ) is smaller than 0.8, it means that the objects do not have a shape close to an ellipse, thus being considered microorganisms. The ellipticity is obtained by fitting an ellipsis to the object and then dividing the area of the object by the area of the fitting ellipsis.

4. As said before, part of the seeds may remain unidentified due to shadows. As a result, the size of the object with respect to the background in the region selected by the user is reduced. If the area occupied by both objects ( $R_A$  and  $R_B$ ) is smaller than 40%, the image is considered as being of seeds, otherwise is considered as containing microorganisms.

All thresholds above were determined by means of practical tests with a set of training images. After the class of the image was determined, the image is converted to a gray scale if necessary, and the respective procedures are applied, as presented in the following.

### B. Procedures for Counting Seeds and Root Nodules

The strategies for counting root nodules and seeds (center and right branches in Fig. 1) have been thoroughly described in [2] and [3]. For that reason, they are only briefly described in the next few paragraphs. Possible differences between the original implementation and the version currently used are emphasized.

In the original version of the program for counting seeds [2], the algorithm was split into two versions, one for cases in which the seeds occupy the entire image, and other for cases in which the seeds occupy only part of the image. More recently, it was observed that the second version actually works for any kind of image, so that was the version implemented here. In that version, the following procedures take place:

- The contrast limited adaptive histogram equalization (CLAHE) [17] is applied.
- The region effectively containing seeds is determined by a combination of morphological mathematical operations.
- Image is morphologically opened using as kernel a disk with a radius of 1% of the image width.
- CLAHE equalization is applied once more.

- Image is morphologically opened once more, giving rise to local maxima in the places where the seeds are located.
- The number of local maxima provides the estimate for the number of seeds.

The method for counting root nodules comprises the following steps [3]:

- The image is rescaled so its width is exactly 1024 pixels.
- Contrast is adjusted.
- All pixel values above 128 are made white (value 255).
- The image is morphologically closed, giving rise to pits where the nodules are located.
- Some rules are applied to remove redundant pits.
- The final counting is given by the number of the remaining pits.

### C. The Branch for Counting Microorganisms

The method for counting microorganisms suffered several modifications, thus it will be described with a little more detail.

After the participation of the user, the image is binarized using as threshold half the maximum intensity of the image, and a preliminary identification of the objects is performed using method 3 described earlier in this section, because this is the best option when the entire image is considered.

Because the objects are supposed as not being clustered, and because the objects should be represented by white pixels, if the white pixels are the majority, indicating that this is how the background is currently represented, the binary image is inverted.

Some objects may have black *holes* within their boundaries. Those holes are filled by the algorithm. Also, small debris and artifacts are removed by the algorithm by eliminating any element that is smaller than 20% of the area of the smallest object selected by the user. A larger threshold was not adopted because it could potentially eliminate actual objects that were only partially detected by the thresholding procedure.

Each remaining element is identified and labeled by means of the connected component method. At this point, all elements are considered as containing at least one object. Each element is then submitted to a set of tests to determine the actual number of objects in each element:

- The process of thresholding may cause only parts of the objects to be detected. Because of that, it is necessary to apply a more effective delimitation procedure. First, the smallest box capable of encompassing each element is generated and, then, those boxes are expanded in all directions by  $\sqrt{a/\pi}$ , where  $a$  is the area of the smallest reference object. Such an expansion aims to allow the box to encompass parts of the element that were not detected before. As a collateral effect, parts of other objects may also be included in the region defined by the box. The box will work exactly as the boxes selected by the user in the beginning of the algorithm.

- The regions defined by the boxes are submitted to the method 1 described before, in order to delimit the elements more accurately. This strategy may fail in some cases, but the consequences are mild, as will be seen next section.

- After the fine delimitation, the algorithm has to determine if each element is composed by one or multiple objects. First, the minimum and maximum possible number of objects that can be present in each element are detected by the equations:

$$N_{min} = \left\lceil \frac{A}{1.1 \cdot A_{max}} \right\rceil, \quad (1)$$

$$N_{max} = \left\lfloor \frac{A}{0.9 \cdot A_{min}} \right\rfloor. \quad (2)$$

where  $A$  is the area of the element under analysis, and  $A_{min}$  and  $A_{max}$  are the areas of the smallest and largest objects chosen by the user, respectively. If  $N_{min}$  and  $N_{max}$  have the same value, this is taken as the definitive number of objects pertaining to that element. If they are different, other steps must be applied in order to determine the number of objects, as described next.

The main idea explored in this stage is the notion that, when two objects touch, they generate concavities that are not characteristic of the objects themselves. Thus, those concavities may be explored as indicatives of the presence of multiple objects. The strategy is simple: openings with increasingly larger kernels are successively applied to the region of interest, until the original element breaks into smaller ones. As the kernels are increased even more, the elements start to disappear. When an element disappears, its area is divided by the area of the smallest object chosen by the user, and the result is rounded to closest lower integer. This is the probable number of objects in that element. The kernels are increased until all objects disappear, and then all results are summed, giving the final number of objects in that area. For this strategy to work properly, the objects must be approximately convex, and the area of contact between objects cannot be too large. Those conditions are fulfilled by most microorganism images. After all elements are analyzed, the final counting is obtained by summarizing the results.

#### IV. TESTS AND RESULTS

This section presents the main results achieved by the method. Since the main objective here is to assess the impact produced by the participation of the user, and how that enabled

TABLE II  
OVERALL RESULTS AND COMPARISON WITH PREVIOUS METHODS.

Type/Method	Hits	Misses	False Pos.	Deviation
Microorganisms/New	90%	10%	9%	8%
Microorganisms/Old	93%	7%	9%	6%
Seeds/New	89%	11%	6%	7%
Seeds/Old	95%	5%	5%	3%
Nodules/New	88%	12%	5%	8%
Nodules/Old	90%	10%	5%	7%
Total/New	89%	11%	8%	8%
Total/Old	93%	7%	7%	5%

it to be used in a wide range of applications, the comparisons will be mostly with the results obtained by the three basic methods [1], [2], [3] in isolation. A comparison with other methods in the literature can be found in [1], [2], [3].

The images used in the tests were obtained from a number of sources, including Embrapa databases and the Internet (especially the CDC website - [www.cdc.gov](http://www.cdc.gov)). The images sizes vary from 500x300 to 3604x2376 pixels, they are in either RGB or grayscale format, and were captured in the visible spectrum by either consumer (seeds and nodules) or microscopy (microorganisms) cameras. The microorganisms, seeds and nodules sets contained, respectively, 31, 20 and 10 images.

Table II shows the general results obtained by the method for each kind of image, as well as a comparison with the results achieved by the original methods. The hits column indicates the ratio of actual objects correctly identified, the misses column indicates the ratio of actual objects not detected, the false positives column reveals the ratio of objects falsely detected (with respect to the actual number), and the deviation column is given by  $100|No - Ne|/No$ , where  $No$  and  $Ne$  are, respectively, the actual and estimated number of objects. This last column is the one that reveals the error in the estimated number of objects.

As can be seen, the overall performance dropped about 3% when compared to the specific methods. A drop in the performance was expected, as the classification performed after the user selects the reference objects is not perfect. However, a drop of only 3% is mild, especially considering the advantages of having a generic method. Three additional tests were performed in order to delve a little deeper into the results presented in Table II.

The first of those additional tests was designed to investigate what happens when the images are misclassified, which happens for about 16% of them. Table III shows the results when the images are correctly classified and when they are misclassified.

As can be seen, the only case in which the impact of misclassification is significant is for seeds. However, seed images are rarely misclassified (only 4% of the cases), thus limiting the damage.

The second additional test investigated how different users and choices would impact the results. All images were submitted to three different users, and the results among them did not vary by more than 3%. This is because the user inputs

TABLE III  
EFFECTS OF IMAGE MISCLASSIFICATION.

Type/Case	Hits	Misses	False Pos.	Deviation
Microorg./Correct	92%	9%	8%	6%
Microorg./Misclas.	88%	12%	10%	8%
Seeds/Correct	94%	5%	5%	3%
Seeds/Misclas.	65%	35%	3%	31%
Nodules/Correct	90%	10%	6%	7%
Nodules/Misclas.	87%	13%	5%	9%
Total/Correct	92%	8%	8%	6%
Total/Misclas.	83%	17%	7%	11%

TABLE IV  
EFFECTS OF OBJECT CLUSTERING.

Type/Case	Hits	Misses
Microorg./Non-Clustered	94%	6%
Microorg./Clustered	79%	21%
Seeds/Non-Clustered	90%	10%
Seeds/Clustered	89%	11%
Nodules/Non-Clustered	95%	5%
Nodules/Clustered	85%	15%
Total/Non-Clustered	92%	3%
Total/Clustered	83%	17%

are very simple and, if they are instructed properly, there is not much room for mistakes and poor choices.

The final additional test was performed specifically to determine how the method performs in discriminating clustered objects. Table IV shows the results considering separately clustered and non-clustered objects. The columns false positives and deviation do not have meaning in this test, so they do not appear in the table.

As can be seen, the counting for microorganism and nodule images is clearly impacted by the presence of clusters. The original method for counting seeds was designed to deal with clusters, so the impact, in this case, is negligible. Those results indicate that more has to be done in order to overcome this problem.

## V. CONCLUSIONS

This paper presented a method to count objects in digital images. It is based on three previous methods developed to tackle the problems of counting microorganisms, seeds and root nodules. In order to make it feasible to develop a method with such a generic scope, a module was included in which the user provides some relevant information that will aid in the next steps of the algorithm.

The performance achieved by the new method is a little below that achieved by the original methods. This was expected as a consequence of the generic nature of the algorithm, but the drop in accuracy was small enough to be easily offset by the flexibility offered. The advantages offered by such a flexibility are the reduction of the clunkiness associated to having multiple tools to tackle multiple problems, and an improved robustness to unexpected variations in the characteristics of the images to be analysed. It is important to highlight, however, that if someone is interested in only one specific type of counting problem, and if the conditions and characteristics

of the images are not expected to vary significantly, then a specific counting method may be the best option.

Despite the good results, there is still much to be done. First, the method is still not capable of properly dealing with clusters of objects, except in the case of seeds. The classification procedure, which determines which branch of the algorithm should be followed, can also be refined, and the number of branches may also be increased in order to accommodate more specific cases. Finally, despite its extended applicability, there is still much room to extend the algorithm's usability even further, to non-agricultural and non-biological applications. Some efforts are already underway towards such a goal.

## REFERENCES

- [1] J. G. A. Barbedo, "Method for counting microorganisms and colonies in microscopic images," in *Proc. International Conference on Computational Science and Its Applications*, 2012, pp. 83–87.
- [2] —, "Counting clustered soybean seeds," in *Proc. International Conference on Computational Science and Its Applications*, 2012, pp. 142–145.
- [3] —, "Method for automatic counting root nodules using digital images," in *Proc. International Conference on Computational Science and Its Applications*, 2012, pp. 159–161.
- [4] D. P. Mukherjee, A. Pal, S. E. Sarma, and D. D. Majumder, "Bacterial colony counting using distance transform," *International Journal of Biomedical Computing*, vol. 38, pp. 131–140, 1995.
- [5] G. Cordiki, R. Diaz-Urbe, J. L. Folch-Mallol, and J. Nieto-Sotelo, "CO-VASIAM: an image analysis method that allows detection of confluent microbial colonies and colonies of various sizes for automated counting," *Applied and Environmental Microbiology*, vol. 64, pp. 1400–1404, 1998.
- [6] J. Marotz, C. Lübbert, and W. Eisenbeiß, "Effective object recognition for automated counting of colonies in Petri dishes (automated colony counting)," *Computer Methods and Programs in Biomedicine*, vol. 66, pp. 183–198, 2001.
- [7] J. Osowsky and H. R. Gamba, "Automated system for counting colonies in Petri dishes (in Portuguese)," *Revista Brasileira de Engenharia Biomédica*, vol. 17, pp. 131–139, 2001.
- [8] W. B. Chen and C. Zhang, "Bacteria colony enumeration and classification for clonogenic assay," in *Proc. IEEE Int. Symp. Multimedia*, 2008, pp. 487–488.
- [9] F. Schönholzer, D. Hahn, B. Zarda, and J. Zeyer, "Automated image analysis and in situ hybridization as tools to study bacterial populations in food resources, gut and cast of *Lumbricus terrestris* L.," *Journal of Microbiological Methods*, vol. 48, pp. 53–68, 2002.
- [10] J. Selinummi, J. R. Sarkanen, A. Niemistö, M. L. Linne, T. Ylikomi, O. Yli-Harja, and T. O. Jalonen, "Quantification of vesicles in differentiating human SH-SY5Y neuroblastoma cells by automated image analysis," *Neuroscience Letters*, vol. 396, pp. 102–107, 2006.
- [11] R. Zhang, S. Zhao, Z. Jin, N. Yang, and H. Kang, "Application of SVM in the food bacteria image recognition and count," in *Proc. Int. Cong. Image and Signal Process.*, 2010, pp. 1819–1823.
- [12] M. Goyal, "Machine vision based bacteria-colony counter," Master's thesis, Thapar University, India, 2008.
- [13] H. Ates and O. N. Gerek, "An image-processing based automated bacteria colony counter," in *Proc. Int. Symp. Comp. Inf. Sciences*, 2009, pp. 18–23.
- [14] W. Z. Shen, C. L. Zhang, and Z. L. Chen, "Research on automatic counting soybean leaf aphids system based on computer vision technology," in *Proc. Int. Conf. Machine Learning and Cybernetics*, 2007, pp. 1635–1638.
- [15] P. Zhao and Y. Li, "Grain counting method based on image processing," in *Proc. Int. Conf. Information Engineering and Computer Science*, 2009.
- [16] M. L. Jr. and D. Smith, "Use of a standard TWAIN scanner and software for nodule number determination on different legume species," *Soil Biology & Biochemistry*, vol. 32, pp. 1463–1467, 2000.
- [17] K. Zuiderveld, *Contrast Limited Adaptive Histogram Equalization*. Academic Press, 1994, pp. 474–485.