An Image Enhancement Tool: Pattern Recognition Image Augmented Resolution[1,2]

M. Righi, M. D'Acunto, and O. Salvetti*
ISTI-CNR, via Moruzzi 1, 56124, Pisa, Italy
ISM-CNR, via Fosso del Cavaliere, 100, 0133, Roma, Italy
*e-mail: marco.righi@isti.cnr.it, mario.dacunto@ism.cnr.it, *ovidio.salvetti@isti.cnr.it*

Abstract—PRIAR (Pattern Recognition Image Augmented Resolution) is an innovative approach to single-frame super-resolution that combines common single-frame super-resolution with pattern-recognition algorithms. PRIAR uses the information gained through pattern-recognition to enhance resolution for low quality images, and to allow the end user to explore, recognize and super-resolve low-resolution images. In this paper, we present the basic functionality of the PRIAR algorithm that we have implemented. The program is modular and each module is easily combined. In addition, such modularity permits us to work on images where single modules can be changed in order to resolve different classes of problems. In this paper, we firstly present the features of the PRIAR program processing images reproducing animal cells recorded with a scanning probe microscope.

Keywords: pattern recognition, image analysis, image segmentation, boundary detection

DOI: 10.1134/S1054661816030160

1. INTRODUCTION

Image analysis is the investigation field devoted to extract meaningful information directly form images and to compute big data. The automation generates a high amount of data and its analysis requires the aid of the computer and suitable software. The impact of new software in big data analysis is able to improve laboratory activities: it can automatize or semi-automatize the data acquisition using modern device. One limiting problem of such automatic approach is the lack of information carried out from images that is commonly recognized as low resolution image. To overcome such problems, the scientific community is trying various solutions. Our proposal is the PRIAR program which features are presented in this paper. The problem statement faced by PRIAR is focused on information discovery: in a single image it is hard to get the information to overcome the information-gap between the low-resolution image and the high-resolution image.

The current PRIAR 1.1 program has been developed according to a previous method (PRIAR 1.0, described in detail in [1]) developed to aid the images analysis, in particular, to enhance low-resolution single frame 2D or 3D images, to recognize specific parts of an image and to substitute the recognized parts using an appropriate model. This enhanced image process is guided by a pattern-recognition algorithm, that takes advantage from the super-resolved image and the knowledge of the model that PRIAR explores.

In this paper, we describe the basic functionality of the PRIAR 1.1 algorithms focusing the attention on images recorded on biological systems, like animal cells. The images were recorded making use of an Atomic Force Microscope (AFM), and the patterns represented in the image are the complex plot of cytoskeleton components and organs. The accurate identification of such components could be of highest help in many branches of medicine.

2. PROBLEM STATEMENT

The super-resolution single-frame algorithms process $I'_{M_1 \times N_1 \times B_1}$ images where $M_1 \times N_1$ represents the row and column dimensions of the input image and B_1 is the number of bit used to represent the color of each pixel. The algorithm used in PRIAR elaborates the image using the schema represented in Fig. 1 (Sections 3 and 4 contain a detailed description of each step of the schema).

PRIAR methods consider as first to improve the image resolution using only local information: it super-resolve the image using a *blind* single-frame super-resolution that faces the blind super-resolution step without making assumptions on the problem. The blind super-resolved image is function only of the low-resolved input image.

---

[1] This paper uses the materials of the report submitted at the 9th Open German-Russian Workshop on Pattern Recognition and Image Understanding, held on Koblenz, December 1–5, 2014 (OGRW-9-2014).

[2] The article is published in the original.

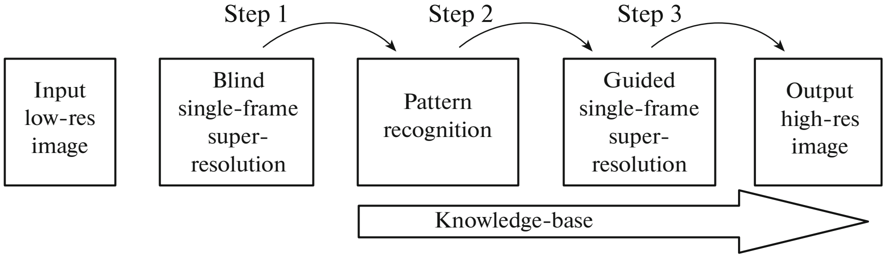

Fig. 1. The diagram illustrates the main modules of PRIAR.

PRIAR method enhances the image resolution performing a detailed analysis that are represented in the examined image. This functionality distinguishes PRIAR from other super-resolution methods. From a general point of view, the problem statement can be described as [2]:

$$i = (h(x, y) \circledast f(x - x', y - y')) + n(x, y), \qquad (1)$$

where

- f is the real scene;
- h is the PSF (Point Spread Function) [3–5];
- n is the noise;
- i is the signal related to the shot of the real analogic image;
- $\circledast$ is the convolution product.

The ideal sampling and quantization process of i generates the Eq. (2).

$$I = \psi_0(i), \qquad (2)$$

where

- I is the high-resolved discrete image;
- ψ_0 is the ideal sampling and quantization function.

Our images are captured in real-world conditions and not ideal condition so the equation becomes the 3.

$$I' = \psi_1(i) + N_1, \qquad (3)$$

where

- I' is the low-resolved discrete image;
- ψ_1 is the real sampling and quantization function;
- N_1 is the noise (we assume a Gaussian distribution for the noise).

The general problem resolved by the PRIAR method is summarized by Eq. (4).

$$S(I'_{M_1 \times N_1 \times B_1}) = I_{M_0 \times N_0 \times B_0}, \qquad (4)$$

where

- S is the super-resolution function, in this case it is the PRIAR function;
- I' is the low-resolution discrete image;
- I is the high-resolution discrete image;
- M_1 is the number of the rows in the low-resolved image, M_0 is the number of the rows in the high-resolved image and $M_1 \le M_0$ the constraint on the number of rows;
- N_1 is the number of the columns in the low-resolved image, N_0 is the number of the columns in the high-resolved image and $N_1 \le N_0$ the constraint on the number of columns;
- B_1 is the number of the bits that represent the color for each pixel in the low-resolved image, B_0 is the number of the bits that represent the color for each pixel in the high-resolved image and $B_1 \le B_0$ the constraint on the number of bits.

It is important to put in evidence that S is not a bijective function: it is obvious thinking that the subsampling of some different I_i images can generate the same I' image. The problem we have to solve is the calculus of I [6, 7] considering that ψ_0 is better than ψ_1: ψ_0 returns an image having spatial depth color resolution better than ψ_1, moreover during the real acquisition there is a N_1 noise that damage the I' image.

Considering that we transform matrix of digits into matrix of digits, the problem statement can be written as follows:

$$I' = G \cdot I + \Xi, \qquad (5)$$

where Ξ is the noise, G represent the PSF and subsampling distortion [8]. PRIAR resolves Eq. (5) [9] taking into account that does not exist an unique solution I because the problem is hill-posed.

3. PRIAR 1.1: MAIN STEPS

PRIAR 1.1 takes advantage by combining single-frame super-resolution with pattern-recognition methods.

This section describes the main PRIAR 1.1 steps that are detailed in the next paragraphs. First, PRIAR 1.1 reads a single image and performs a blind single-frame super resolution. The objective of this first step is an image improvement. The improved image provides a better handle for the following pattern-recognition work. It is important to mention that this first step does not take into account any information of the image (Fig. 1, step 1). As a consequence, it can use any general purpose super-resolution single-frame algorithm such as bicubic, b-spline, Kim-Kwon methods [10, 11]. Hence, the subsequent step inside PRIAR is devoted to analyze the obtained images applying on it a pattern-recognition approach. The role of the pattern-recognition procedure (Fig. 1, step 2) is equivalent to an a-prior function operating using a inferential approach. In fact, at this stage, the algorithm has to recognize the kind of the image to proceed and it must have recorded in its knowledge-base information allowing further proceeding into the image processing.

We have focused the application of PRIAR 1.1 to images recorded with AFM applied to biological systems (animal cells). In these microscopic techniques, an image represents the object as a matrix pixels (x, y) and assign to any pixel a z value with a gray scale. Nevertheless, the algorithm has been designed to be a platform applicable to a wide range of imaging techniques. As first, it classifies the image. Hence, the information acquired during the image classification is used during the reconstruction of the identified object. In fact, it permits to use the appropriate model to build the object in the image space. The third step (Fig. 1, step 3) regards the improved definition of image details, previously classified or simply detected, by increasing spatial (x, y) and depth (z) resolution. During this step various super-resolution methods are generally applied in order to obtain the best image and the best trade-off between image resolution and calculating time [12–17]. In turn, the third elaboration gets as input the super-resolved image and searches an object according to the model obtained during the first two previous steps [18, 19]. According to the recognized pattern and the model built consequently, the image is improved by increasing the spatial resolution, color depth and inserting objects that have been identified morphological properties. The pseudo-code 1 schematizes the main steps of PRIAR.

Algorithm 1 PRIARs algorithm

```
function PRIAR (low-resolution image, point of interest)
    class ← classificator (input image, point of interest)
    switch class do
        case grating
            segmentation ← seg method (otsu)
        case cell
            segmentation ← edge discover
    super resolved image ← blind super resolution (input image)
    initial path ← explore (seed, super resolved image)
    extended path
        explore extender (super resolved image,
        initial path, knowledge base)
    enhanced image ←
        build model (super resolved image,
        initial path, knowledge base)
end function
```

3.1. Classifier

The PRIAR classifiers distinguish two kinds of images: the first one represents a test image i.e., a simple and regular pattern (that we have named grating, a z two levels image, low complexity); the second one represents the object to be recognized (in our case the cytoskeleton as collected by an AFM of an animal cell, high complexity pattern). These two kinds of images represent a benchmark for our model to be built. In fact, the objective of this tool is to classify the kind of image in order to apply the appropriate pattern-recognition method. Once this is done, we have to merge the information acquired by blind super-resolution approach and pattern recognition strategy to enhance the image, substituting the recognized image components with their models (that can also be provided of meta-attribute that helps to integrate characterization in its contest). PRIAR is currently using a linear classifier. The classifier performs a segmentation of the image in order to identify each region [18, 19]. It is calculated for each region a set of features f_i: mean value along the Z axis, orientation of the segmented region [10, 11] and the distribution of the pixel-color in the segmented image [10, 11]. The algorithm approximates the features as independent-features so that the probability that an image falls in class C_i can be expressed eventually in an inferential way.

3.2. The Super-Resolution Method

PRIAR focuses on the problem of enriching the information that can be collected from a single input image. Firstly, in a $z = f(x, y)$ image, it is necessary to improve the spatial resolution and the color depth. In other words, it is necessary increase the image resolution and calculate a correct color value for each pixel. This can be made extending the Kim Kwon algorithm [12]. The single image super resolution algorithm uses only the information contained in the input image. In order to obtain the final super-resolved image it is necessary to calculate some intermediate images. The input image is interpolated, the result of the interpolation is an *X-image* that still contains low-frequency information (generally, it is a blurred image).

The high frequency information is calculated by combining the Laplacian of the X-image and other estimators that are calculated on different local observation of input image (each local observation get in output different partial information). A single image with enhanced resolution is finally obtained as a convex combination for each pixel of the set of candidate pixels based on their estimated likelihood. To improve the visual quality, the results are post-processed based on an appropriate estimated prior [13]. To calculate the high-frequency it is used a regression-based method that convex to the super resolved image. For each location (x, y), it is generated a set of patch $Z_i(x, y)$, and it is calculated a vector of differences

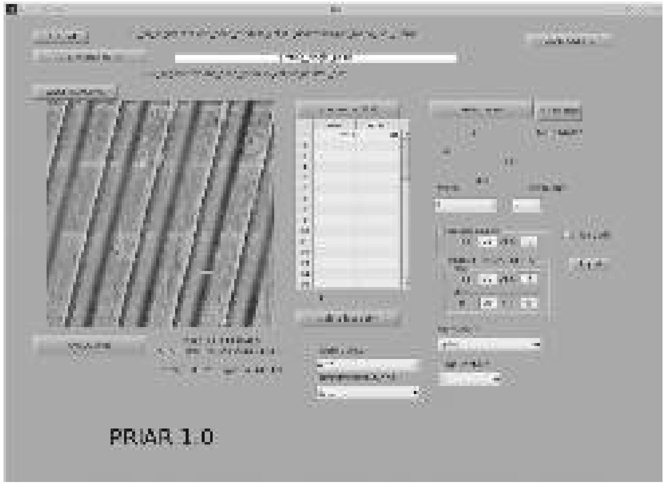

Fig. 2. This figure shows the graphic user interface of PRIAR.

$\{d_1(x, y), ..., d_N(x, y)\}$ between the output (that is not yet calculated) and each candidate. Each pixel is calculated using Eq. (6):

$$H(x,y) = \sum_{i=1,\ldots,N} P_i(x,y) \cdot Z_i(x,y), \qquad (6)$$

where $P_i(x, y)$ is the weight given to a certain patch. The function $P_i(x, y)$ is a Gaussian probability distribution.

3.3. Adopted Pattern-Recognition Method

The algorithm goal is recognize a specific area $I_0(x, y) \subseteq I(x, y)$ of the image I. Our algorithm accepts as input a coordinate $(x_0, y_0) \subseteq I_0(x, y)$ or a path that provides to the pattern-recognition method more information to match the structure. The algorithm uses one of the described input coordinates and expand the region using a method based on the gradient value pixel of the neighborhood Eq. (3). All the pixel in a neighborhood region are correlated and a local estimate of the correlation surface is made assuming $I_0(x, y)$ as the target image of size $I_a \times I_b$, and the $W(x, y)$ is a windowing function (of the same size of $I_0(x, y)$ or less) containing the object of interest, whose gradient goes to zero at the edges (a sort of boundary condition), then the normalized squared correlation is given by (for sake of simplicity in continuous form):

$$C^2(\rho,\theta) = \frac{\left[\iint I(x,y)\cdot(I_0W)\cdot(x-\rho,y-\theta)dxdy\right]^2}{\iint I^2(x,y)\cdot W(x-\rho,y-\theta)dxdy}. \qquad (7)$$

Taking the derivative of the normalized correlation we find that:

$$\begin{aligned} C^2(\rho,\theta) = -2\cdot\frac{\iint I(x,y)\cdot(I_0W)\cdot(x-\rho,y-\theta)dxdy}{\iint I^2(x,y)\cdot W(x-\rho,y-\theta)dxdy}, \\ \frac{\iint I(x,y)\cdot\nabla(I_0W)\cdot(x-\rho,y-\theta)dxdy}{\iint I^2(x,y)\cdot W(x-\rho,y-\theta)dxdy} \qquad (8) \\ +\frac{\left[\iint I(x,y)\cdot(I_0W)\cdot(x-\rho,y-\theta)dxdy\right]^2}{\iint I^2(x,y)\cdot W(x-\rho,y-\theta)dxdy}, \\ \iint I(x,y)\cdot\nabla(I_0W)\cdot(x-\rho,y-\theta)dxdy, \end{aligned}$$

that, at the least, leaves four term to be calculated. These equations can be transformed to the discrete domain, reducing the calculation of the correlation gradient at a central pixel p and the correspondent 8 neighbours [13, 20].

4. SUPER-RESOLVING IMAGE USING RECOGNIZED INFORMATION

During the last step (Fig. 1, step 4) of the algorithm PRIAR uses the computed information by pattern-recognition and classifying to super-resolve the image.

The information of the identified class and the information acquired by pattern-recognition algorithm are merged to create a new image where it is reconstructed the identified area.

The a-priori knowledge that is contained in the class can be of two different kinds: the first one is a geometrical description and it is used to super-resolve the image, the second one is used to mark the features of the classified object that are not representable by graphics.

Fig. 3. A low-resolution image of a microtubule obtained by an Atomic Force.

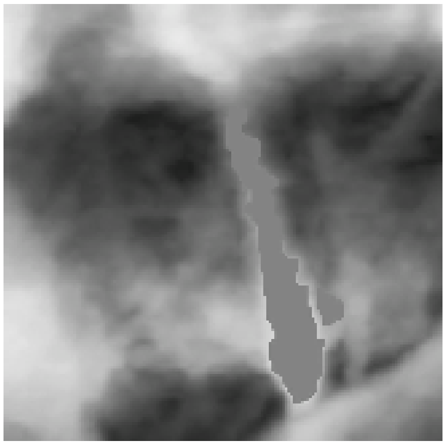

Fig. 4. The recognized area of a animal cell microtubule.

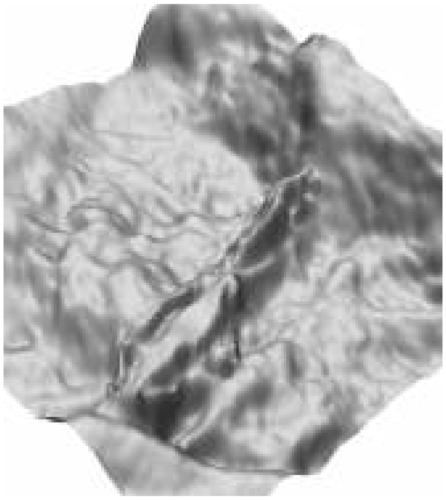

Fig. 5. 3D reconstruction of the enhanced image.

In our case the geometry of the objects is like a pipe so we simply minimizing the difference between the pipe and the data presents on the image itself. In turn, the GUI (Graphic user interface) guides the end-user to use the features of the tool. Figure 2 shows the main window of the GUI. It is possible use the GUI to manage basic information to choose the image to elaborate, to choose the directory that contains the results, to choose the area of interest, to choose the method used during the super-resolution step, to use the internal classifier or manually classify the image, to choose a single point where the pattern-recognition starts or track a path that guides the pattern-recognition process.

The tool has been developed to be remotely used by command line too. In fact, the core of the program can get the structure containing all parameters or a file that containing the variables to use during the computation. PRIAR tool shows intermediate results and the finale result in the form of images. The images are still saved in the chosen directory. Figure 3 shows the input images, Fig. 4 the tracked path.

In this paper, we have presented the features and functionality of the PRIAR algorithm. PRIAR is a tool designed to aid the images analysis, in particular, the improve low-resolution single frame 2D or 3D input images, recognize specific part of the image and match or substitute these parts with their appropriate models. The algorithm combines single-frame super-resolution and pattern-recognition methods. PRIAR works as follows:

(1) classification and identification of specific objects from single frame images recorded with a microscope;

(2) reconstruction of the identified object;

(3) Super-resolution of single identified objects according to the model obtained during the first two previous steps.

Figures 3 and 4 summarize the identification and improved resolution of cell components, filaments, micro-tubules of animal cells, the correspondent 3D reconstruction is shown if Fig. 5.

REFERENCES

1. M. Righi, Ph.D. Thesis, (Universita di Pisa, 2015).
2. M. Trimeche, Ph.D. Thesis (Tampere University of Technology, 2006).
3. K. Moore, Tech. Rep., ZEMAX (2005).
4. J. W. Goodman, Introduction to Fourier Optics, 3rd ed. (Ben Roberts, 2005).
5. W. J. Smith, Modern Optical Engineering, 4th ed. (McGraw-Hill, 2007).
6. S. Pelletier, Ph.D. Thesis (Department of Electrical and Computer Engineering, 2009).
7. S. J. van der Walt, Ph.D. Thesis in Engineering (2010).

8. S. S. Qureshi, X. M. Li, and T. Ahmad, in Proc. 14th Int. Conf. on Advanced Communication Technology (ICACT) (PyeongChang, 2012), pp. 642–647.
9. M. D'Acunto, G. Pieri, M. Righi, and O. Salvetti, in Proc. 4th Int. Workshop on Image Mining. Theory and Applications, IMTA2013 (SciTePress Digital Library, 2013), pp. 22–28.
10. R. C. Gonzalez and R. E. Wood, Digital Image Processing, 3rd ed. (Prentice Hall, Upper Saddle River, NJ, 2008).
11. R. C. Gonzalez, R. E. Woods, and S. L. Eddins, Digital Image Processing Using MATLAB, 2nd ed. (Prentice-Hall, 2010).
12. K. I. Kim and Y. Kwon, IEEE Trans. Pattern Anal. Mach. Intell. **32**, 1127 (2010).
13. M. D'Acunto, G. Pieri, M. Righi, and O. Salvetti, Pattern Recogn. Image Anal. **24**, 209 (2014).
14. M. Sonka, V. Hlavac, and R. Boyle, Image Processing, Analysis and Machine Vision, 3rd ed. (Thomson, 2008).
15. L. Ikonen and P. J. Toivanen, in ACIVS, Ed. by J. Blanc-Talon, W. Philips, D. C. Popescu, and P. Scheunders (Springer, 2005), pp. 308–315.
16. P. Getreuer, Image Processing on Line 1 (2011).
17. E. Ardizzone, R. Gallea, O. Gambino, and R. Pirrone, Fuzzy-Based Kernel Regression Approaches for Free Form Deformation and Elastic Registration of Medical Images (InTech, 2009), pp. 347–368.
18. M. Sezgin and B. Sankur, J. Electron. Imaging **13**, 146 (2004).
19. N. Otsu, IEEE Trans. Syst., Man Cybernet. **9**, 62 (1979).
20. S. Theodoridis and K. Koutroumbas, Pattern Recogni-