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Xiu xin Wang (✉ wangxx@cqupt.edu.cn)

CQUPT: Chongqing University of Posts and Telecommunications <https://orcid.org/0000-0003-2077-3505>

Hao wang

CQUPT: Chongqing University of Posts and Telecommunications

Guan Fu

CQUPT: Chongqing University of Posts and Telecommunications

Jiwei Ling

CQUPT: Chongqing University of Posts and Telecommunications

Methodology

Keywords: Computer Hologram, amplitude, Gerchberg-Saxton, microscope, biological cells

Posted Date: July 30th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-720181/v1>

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Application of Improved GS Algorithm in Cell Computing Holography

Xiu xin Wang^{1,2,*}, Member, IEEE, Hao Wang¹, Guan Fu¹, Ji wei Ling¹

¹Chongqing University of Posts and Telecommunications, Laboratory of Micro electronic Engineering; Medical Electronics and Information Technology Engineering Research Center; Chongqing engineering laboratory of digital medical equipment and system; Chongqing engineering research center of medical electronics and information technology, Chongqing, 400065, China.

²Key Laboratory of Opto-technology and Intelligent Control, Ministry of Education, Lanzhou Jiao tong University, Lanzhou 730070, China

* Wangxx@cqupt.edu.cn

Background: As an important research direction in cell image processing, Computer Hologram(CH) can quantitatively detect and analyze the amplitude and phase information of cells and holographic reconstruct the recorded images. Compared with the traditional optical microscope, CH reduces the complexity of operation, avoids the operation of cell staining and does not affect the physiological characteristics of cells in the recording process. It plays an important role in the field of cell morphology measurement and deformation analysis.

Results: An improved Gerchberg-Saxton (GS) algorithm is proposed to reconstruct cell hologram based on phase information. The cell image reconstructed by GS Algorithm with phase restricted conditions are analyzed and compared. Through the comparative experiments of different models, it shows that the improved GS algorithm is better than the traditional GS algorithm in cell image reconstruction based on phase information. With the improved algorithm of phase mapping and normalization conditions, the reconstructed image can distinguish the cell edge information and high signal-to-noise ratio information. The urine sediment image is taken as the experimental object. After reconstruction by this algorithm, other impurity cells can be filtered out, and the aberrant red blood cell image with clear edge can be obtained. This improved algorithm provides a new application for cell detection in clinical diagnosis.

Conclusions: The phase map reflects the temporal and spatial information of the image, determines the time or spatial position where different frequency signals appear, and describes the overall shape of the object. Due to biological cells generally for phase type or class phase objects, the improved GS algorithm in this paper can well describe the phase information of restored image, which is more suitable for the practical application of cell phase reconstruction.

1. Introduction

Traditional medical imaging instruments are optical microscopes which can zoom in on tiny objects that cannot be seen directly by the naked eye. But the traditional optical microscope can only detect the intensity of the light wave and obtain the two-dimensional distribution image of the light wave intensity of the object. It is difficult to give the three-dimensional space information of the object being imaged. There are some limitations in the application of the traditional optical microscope in the growing biomedical field. In order to improve the contrast of cell imaging, a fluorescence microscope [1,2] has been proposed, but before using this microscope, Rhoda mine, acridine orange, or green fluorescent protein and other substances need to be used to stain biological cells [3]. This pretreatment increases the complexity of the operation and inevitably affects the physiological characteristics of biological cells. It is an urgent need for the research of life science to develop new imaging analysis technology to realize undisturbed, dynamic and quantitative analysis of living, cell and subcellular samples[4-8].

Compared with the traditional optical holography[9-11], digital holography [12-14] has the advantages of low production cost, fast imaging speed, flexible recording and reproducing of phase information of the extract light field, etc. Digital holography uses photoelectric sensors (such as CCD or COMS) instead of a dry plate to record a hologram, and then stores the hologram in a computer. The computer simulates the optical diffraction process to achieve holographic reproduction and processing of the recorded object. Due to the high frequency of light waves, light intensity information can be easily recorded under existing optical equipment, but phase information is difficult to obtain or even directly lost during the acquisition process. However, the light wave phase contains more information about the imaged object, which may contain up to 80% of the information of the imaged object [15]. The phase recovery algorithm can improve the speed of the twin images in the X-ray band, which is effective not

only for the visible band, but also for the non-visible band [16, 17]. Now it has been successfully used in the fields of object shape measurement and deformation analysis [18], biomedical research [19], and three-dimensional dynamic measurement.

In this paper, the improved GS algorithm was used to encode the phase in the complex amplitude so as to obtain the appropriate transmittance function and complete the reconstruction of the contrapuntal phase information. Experiments have showed that the algorithm can clearly reconstruct the phase information of the image with high SNR, and retain the information of the image edge and the overall structure. Furthermore, this algorithm is applied to the detection of aberrant red blood cells in urine sediment. By using the characteristics of the GS algorithm and the improved GS algorithm to improve the quality of phase reconstruction, it is possible to reconstruct aberrated red blood cells with clear edges and achieve accurate cell detection.

2. Principle

Optical holography uses the principle of interference and diffraction of light and it combines the built optical path to achieve holographic recording and reproduction of objects. Holographic imaging schematic is as shown in Fig.1:

Fig.1. Holographic imaging schematic.

The light emitted by the laser passes through the beam splitter and is divided into two different directions of light. One beam is irradiated onto the object by the mirror as the object light wave, and the light wave projected by the object is incident on the CCD plane. The other beam passes through the acoustic-optic modulator as the reference light, and the beams with different frequencies are transmitted to the mirror and irradiated to the CCD recording plane. Two beams of light from the same light source go through different propagation paths, interfere with the CCD plane at the same time, record the hologram, and then restore the hologram by computer. Digital holography eliminates the light source and complicated optical path construction of optical holography and it stores the interference pattern formed in the traditional sense of optical holography as a digital image in a computer. By calculating the complex amplitude distribution of the light wave, the phase or amplitude is encoded, and the encoded function is plotted to obtain the reconstructed image in the optical hologram, so as to realize the diffraction propagation of the object light wave from the hologram plane to the object plane or the object image plane [20, 21].

The generation process of Digital holography is as follows:

- (1) Discrete sampling processing is performed on the images to be processed to obtain discrete digital image data;
- (2) Perform Fresnel or Fourier transform on the discrete data of the object light field;
- (3) Use the appropriate coding form to convert the intensity and phase information into the appropriate transmission expression form;

(4) Digitally reproduce the encoding function of step (3) by a drawing device to obtain a calculated hologram.

In the realization of digital holography, the imaging process and diffraction theory of optical holography are digitally imitated, scalar diffraction theory can well explain the propagation process of light. When the distance between the diffraction surface and the observation surface is expressed as z , $U(x, y, 0)$ represents the complex amplitude of the light wave on the diffraction screen, $U(x, y, z)$ represents the complex amplitude of the light wave on the observation screen. Then the Fourier spectra corresponding to the complex amplitudes of the diffractive surface and the observation surface are $F_0(f_x, f_y)$ and $F_z(f_x, f_y)$ respectively, as long the spectral distribution of the viewing screen light field is known, then the inverse Fourier transform is used to obtain the viewing screen light field, as shown in the following formula (1):

$$U(x, y, z) = \int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} F_z(f_x, f_y) \exp[j2\pi(f_x x + f_y y)] df_x df_y \quad (1)$$

Substituting it into Helmholtz equation [17] can get the relationship between $F_0(f_x, f_y)$ and $F_z(f_x, f_y)$ as (2):

$$F_z(f_x, f_y) = F_0(f_x, f_y) \exp[j \frac{2\pi}{\lambda} z \sqrt{1 - (\lambda f_x)^2 - (\lambda f_y)^2}] \quad (2)$$

Formula (1) becomes the following formula by substituting the above expression, where $\mathcal{F}$ represents the Fourier transform and $\mathcal{F}^{-1}$ represents the inverse Fourier transform.

$$U(x, y, z) = \mathcal{F}^{-1} \left\{ \mathcal{F}\{U(x, y, 0)\} \exp[j \frac{2\pi}{\lambda} z \sqrt{1 - (\lambda f_x)^2 - (\lambda f_y)^2}] \right\} \quad (3)$$

There are two methods of phase recovery: interference and non-interference detection, interference detection phase mainly includes holography and shearing interference [22], Non-interference detection methods mainly include iterative method and light intensity transmission equation method [23]. The iterative method is based on the GS algorithm [24]. GS algorithm was jointly proposed by Gerchberg and Saxton in the 1970s. It measures the light intensity distribution on the pupil surface and the imaging surface, and uses an iterative algorithm for phase recovery. GS algorithm is the most representative algorithm to solve the phase recovery problem in the current algorithm system. It can quickly converge and get the result with small error. Compared with original GS algorithm, we first normalize the phase, and then set a threshold value of the processed phase to achieve a reconstruction effect. The schematic diagram of the improved GS algorithm with computing holography steps is shown in Fig.2:

Fig.2. The schematic of the improved algorithm calculation hologram step.

Among them, the input light field wave fronts:

$$f(x, y) = |f(x, y)| \exp[i\varphi(x, y)] \quad (4)$$

The light wave fronts corresponding to the light field on the imaging plane:

$$g(u, v) = |g(u, v)| \exp[i\psi(u, v)] \quad (5)$$

Formula $|f(x, y)|$ and $|g(u, v)|$ represents the amplitude distribution of the input light field and the imaging plane respectively; $\varphi(x, y)$ and $\psi(u, v)$ represent the phase distribution on the input light field and the imaging plane; $f(x, y)$ and $g(u, v)$ satisfy the following relationship.

$$f(x, y) = F\{g(u, v)\} \quad g(u, v) = F^{-1}\{f(x, y)\} \quad (6)$$

(1) An initial phase $\varphi(x, y)$ distribution of the input light field is randomly generated as the initial iterative phase, it is continuously updated as the initial phase in subsequent iterations, and the input wave field amplitude distribution $|F(x, y)|$ forms the incident wave fronts $f(x, y)$, it is expressed as plural form $|F(x, y)|\exp[i\varphi(x, y)]$;

(2) Optimize the initial phase: the phase is first normalized and then multiplied by a factor value to achieve the reconstruction effect;

(3) Fourier transform $f(x, y)$ to $g(u, v)$;

(4) Construct a function $g'(u, v)$ from the phase portion of $g(u, v)$ and the desired amplitude distribution $g'(u, v)$ on the output surface;

(5) Perform inverse Fourier transform on $g'(u, v)$ to get the next iterative wave function $f'(x, y)$.

Set iterations to repeat the above steps to get the final phase ψ .

GS algorithm can converge quickly and get more accurate results in the case of analytic Fourier transform pairs between input and output surfaces. But in the actual calculation, especially when the distribution of the light intensity on the input and output plane provided by the computer model cannot find the strict Fourier transform matching, the convergence speed of GS algorithm will be greatly reduced, and sometimes even the operation of the GS algorithm will stagnate. Furthermore, when the number of iterations is too large, the iterative process sometimes falls into a local optimal situation, causing an increase in the amount of calculations and a waste of resources. In essence, GS is a kind of steepest descent algorithm that seeks extreme values by tracking the negative direction of the gradient of the high-dimensional variable function. The optimal value within the defined range will not be found if the initial value is not selected properly or the number of iterations is too small.

3. Method

In this paper, the improved GS algorithm was used to extract and reconstruct the wave front phase map of the urine sediment and the comparative analysis of the amplitude and phase information of the cell image is performed. The comparison experiment is used to illustrate the improved GS. The quality of the cell image reconstruction algorithm and the superiority of the traditional GS algorithm are more suitable for the practical application of cell phase reconstruction.

The urine sediment image was used as the experimental object. The basic process of digital holographic GS modeling is as follows:

(1) Input data; read an RGB cell picture whose pixel is $M \times N$ and preprocessed the original image, then intercepted the 256×256 pixel and performed gray scale processing, and read the object data sampled by the 256×256 pixel, so the original object is stored as a discrete data in a 512×512 pixel.

(2) Add phase information; the read image value contains amplitude information, so adding phase information was need. A random function was used to add a random phase, that is, multiply each pixel valued by the corresponding phase value.

(3) When the object function was given, the discrete spectral distribution function of the object can be obtained by using the fast Fourier transform (FFT), which is the holographic function $g(u, v)$ of the Fourier transform hologram, and found the amplitude and phase of $g(u, v)$. Any complex number can be expressed as $f(x, y) = |A(x, y)|\exp[j\varphi(x, y)] = f_R(x, y) + jf_I(x, y)$ by touch and angle. In the FFT process, translation is introduced in both the x and y directions. According to the translation theorem of the Fourier transform, an additional phase must be introduced in $g(u, v)$, which changes the distribution of $g(u, v)$. To this end, the `fftshift()` function was used to divide the frequency spectrum. The low frequency part moved to the center.

Based on the above principles, four models were established to demonstrate the superiority of the improved GS algorithm in cell image phase reconstruction through experiments. Model 1-GS amplitude

restoration; Model 2-GS Random phase restoration; Model 3-GS Random phase mapping restoration; Model 4-Improved GS phase restoration. Model 1 and Model 2 are not treated with phase mapping values. Phase mapping value is used in model 3, but the phase is random. Model 4 uses a combination phase mapping values with β factor, and the phases is normalized. A comparison of different Models in table 1.

Table 1. A comparison of different Models

The different models	Input	Phase Mapping Value	Output
Model 1	The amplitude of cell image	NULL	Cell images recovered by amplitude
Model2	Random phase of cell image	NULL	Cell images recovered by Random phase
Model 3	Random phase of cell image	$[-\pi, \pi]$	Cell images recovered by Phase Mapping Value
Model 4	Optimized phase of cell image	$[-\pi, \pi]$ $0 < \beta < 1$	Cell images recovered by Phase Mapping Value

In Model 1: original GS algorithm was used to extract the amplitude information of the image, and set the number of iterations to 20, 200, and 2000 comparisons respectively. This algorithm restored the amplitude information of the image during the processing of the image and compared restored image.

In Model 2, GS algorithm was used to extract the phase information of the image and set the number of iterations to recover the phase information.

In Model 3, The amplitude and phase of the image were normalized in Model 2, and mapped the image gray to 0 to 1, and then mapped the initial phase of the image $-\pi$ to π in order to extract the to-be-measured Phase to avoid the influence of phase shift amount deviation on measurement accuracy. Next we obtained the size of the image, changed the input image into a complex image form, and used a random function to generate a pair of images. Where phase is the preset estimated phase, and continuously adjusted to approximate the real phase in the loop, until the sought phase is very close to the real phase. The final estimated phase is mapped from $[-\pi, \pi]$ to $[0, 2\pi]$ and then to $[0, 1]$, finally, the extracted phase image is output. In the same way, the number of iterations is set to 20, 200 and 2000 for comparison, compared with model 1 and model 2 for comparison to recover the restored image and compared the final restored image.

In model 4, the phase is normalized and then multiplied by β factor value added to model 3. Setting the number of iterations to 20, 200, 2000, then compared the results of model 3 with the phase recovery graph.

4. Result

Fig.3 shows the urine sediment under observation. There are epithelial cells and urinary malformed red blood cells. Among the picture, urinary malformed red blood cells are also called pale shadow red blood cells, and phase dense vesicles are prominent at the cell membrane. The original picture type is a JPG color picture of 493×659 pixel.

Fig. 3 .Observed urine sediment image.

After preprocessing the JPG image, a 256×256 Matrix-sized gray scale image was obtained. As shown in Fig.4:

Fig. 4. Image of urine sediment after pretreatment.

Model 1: Fig. 4 was taken as the target image; the amplitude information of Fig. 4 was restored by using the GS algorithm. When the number of iterations was set as 20, 200 and 2000 respectively, the amplitude reconstructed image was shown in Fig.5(b),(c),(d).

(d)
Fig.5. (a) Original gray scale image (b) The amplitude information of restoration when the number of iterations was 20. (c) The amplitude information of restoration when the number of iterations was 200. (d) The amplitude information of restoration when the number of iterations was 2000.

By comparison, it can be concluded that iterating the amplitude of the image by the GS algorithm has little effect on the restored image. The reconstructed image only shows a change in brightness, with no change in the contour distribution of the cells. After the GS CGH algorithm is used to process the amplitude information of the image, the reconstructed images are not different with iteration times.

Model 2: Fig.4 was taken as the target image and GS algorithm was used to recover the phase information in Fig.6. When the number of iterations was also set to 20, 200, 2000, the phase reconstructed image obtained from three independent experiments was as shown in Fig.6(b),(c),(d).

Fig.6. (a) Initial random phase. (b) The recovered phase information when the number of iterations was 20. (c) The recovered phase information when the number of iterations was 200. (d) The recovered phase information when the number of iterations was 2000.

(c)

(d)

By comparison, it is concluded that the phase of the image is iterated by GS algorithm. When the phase was not normalized, the phase image would be fuzzy and chaotic, and different results would be obtained each time.

Model 3: Fig.4 was taken as the target image, and the input image was normalized in GS algorithm. When the number of iterations is also 20, 200, and 2000, the phase reconstructed image is shown in Fig.7(b),(c),(d).

(a)

(b)

Fig.7. (a) Initial random phase. (b) The recovered phase information when the number of iterations was 20. (c) The recovered phase information when the number of iterations was 200. (d) The recovered phase information when the number of iterations was 2000.

By comparing the phase restoration maps under different iterations, it can be clearly seen that as the number of iterations increases, the outline of the cells gradually became clearer, and the sharpness of the pictures also varied greatly. In the phase spectrum of the image, the information of the edge and the whole structures of the image are retained. The amplitude value described the light and dark distribution of the image, like the noise overlays on the original image, but did not affect the content of the image itself, while the phase had a greater impact on the image information.

Model 4: Fig.4 was taken as the target image, and the initial phase is restricted to a certain threshold value and processed iteratively. When the iterations are also 20, 200 and 2000, the phase reconstructed image is processed using the improved GS CGH algorithm as shown in Fig.8(b),(c),(d).

Fig.8. (a) Optimized initial phase. (b) The recovered phase information when the number of iterations was 20. (c) The recovered phase information when the number of iterations was 200. (d) The recovered phase information when the number of iterations was 2000.

Based on the algorithm of GS processing phase, the random phase was optimized, and a phase with good initial value was set for subsequent iteration. Compared with model 2, it is obvious that the improved process was better when the recovered phase information was iterated for the same number of times. Finally, the phase hologram and the reduction map were obtained the GS algorithm was used when the number of iterations was set to 2000. As shown in Fig.9.

Fig.9. Proved GS algorithm was used to obtain the phase hologram and restore graph when the number of iterations was set to 2000;
(a) Phase hologram. (b)Restore graph.

In order to quantitatively demonstrate the effect of phase retrieval, the root mean squared error (RMSE) is used to evaluate the results. The expression is as shown in the following formula (7):

$$RMSE = \sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - y_i')^2} \quad (7)$$

Where: n is the number of iterations; y_i is the phase division of the iteration ; y_i' is the phase distribution of the last iteration. To make the results easier to compare, we take the logarithm of RMSE to measure the indicators $RMSE' = \log_{10}^{RMSE}$, The indicators of different models in the case of 20, 200, and 2000 iterations are shown in Table 2:

Table2 RMSE based on different models and iteration numbers

The different models	RMSE (Iteration Numbers 20)	RMSE (Iteration Numbers 200)	RMSE (Iteration Numbers 2000)
Model 2	4.6841	4.6831	4.6631
Model 3	2.5037	2.5022	2.4991
Model 4	2.4994	2.4989	2.0863

The amplitude information processed by model 1 is not compared. Model 2 is the phase of unmapped original GS Algorithm, it can be seen that the phase peaks are disordered and small ; model 3 is the phase of mapped original GS Algorithm,the phase peak at the red blood cell at the target image is more obvious than Model 2, and model 4 is the phase of mapped improved GS algorithm Compared with Model 3, the phase peak at the position of the red blood cell is slightly higher, and the performance of the phase imaging image quality is slightly outstanding. Each model ultimately presents a phase energy diagram with 20,200, and 2,000 iterations.

(a)

(b)

(c)

Fig.10. Model 2 (a) phase energy diagram with 20 iterations. (b) Phase energy diagram with 200 iterations. (c) Phase energy diagram with 2000 iterations.

In order to prove that the optimized algorithm can produce better enhancement effect, the phase distribution maps of different models under different iteration times are generated. The phase distribution of model 2 at iterations of 20, 200 and 2000 is shown in Fig. 10(a),(b),(c).

(a)

(b)

(c)

Fig.11. Model 3 (a) phase energy diagram with 20 iterations. (b) Phase energy diagram with 200 iterations. (c) Phase energy diagram with 2000 iterations.

The phase distribution of model 3 at iterations of 20, 200 and 2000 is shown in Fig.11(a),(b),(c).

(a)

Fig.12. Fig.4. Model 4 (a) phase energy diagram with 20 iterations. (b) Phase energy diagram with 200 iterations. (c) Phase energy diagram with 2000 iterations.

The phase distribution of model 4 at iterations of 20, 200 and 2000 is shown in Fig.12(a),(b),(c). Model 2 is the complex amplitude form of the input image and the GS CGH algorithm without normalization processing. It can be seen that the phase distribution obtained by model 2 is disordered and the peak value is small; Compared with model 2, the peak phase of model 3 is more obvious in the target image; Compared with model 3, model 4 is a GS algorithm with optimized initial phase, the peak value of phase is slightly higher at the position of urinary malformed red blood cells, and the imaging quality of phase is outstanding.

5. Discussions

This paper focuses on the improvement of the phase reconstruction algorithm of the cell, in order to make it suitable for the practical application of cell phase reconstruction.

In the process of processing the phase information by the original GS algorithm, the phase is mapped and optimize, which solves the shortcomings of the randomness and chaos of the traditional recovery phase.

The research process adopted the research ideas of comparative analysis respectively. Through vertical comparison, the original algorithm can be compared more clearly, and the improved algorithm is more accurate. By setting different iteration times to compare the experiments within each model, the results are clearer.

By comparing Model 1 and Model 4, these results suggest that phase information is more important for image information restoration. On the basis of Model 3, the phase was mapped to $-\pi$ to π in order to extract the phase to be measured, so that the influence of the phase shift amount deviation on the measurement accuracy was avoided, finally clear phase was extracted. Normalization can limit the data that needs to be processed (through some algorithm) to a certain range you need. First of all, normalization can make subsequent data processing more convenient, and secondly, the convergence of the normalization program is accelerated. Because the value of the gray scale image has a range, while the value of the Fourier transform result (real part,

imaginary part or amplitude, phase) is arbitrary and unlimited, this requires that the data should be changed into the data required by the image when the two matrices are written into the image, generally using the method of mapping.

The initial phase and constraints were added to the model 4 to optimize the initial random phase. The accuracy of phase reconstruction can be greatly improved when the number of iterations is not large; Set the restriction conditions for iteration, take the correlation coefficient of the complex amplitude function and the initial input complex amplitude function after the inverse transformation reduction, when the correlation coefficient reaches the self-set value, the iteration cycle is broken out. It can avoid the waste of resources and greatly reduce the iteration times of GS algorithm.

This study further strengthens the clear contrast reduction degree of phase restoration, which can more easily and accurately distinguish the high signal-to-noise ratio information in some cell populations, and filter out the low signal-to-noise ratio information more effectively. It is more suitable for the practical application of cell phase reconstruction, and has a wider application in the detection of some cells and the clinical diagnosis of cytopathy.

In the process of horizontal comparison, when the number of iterations is too large, the problem that the iteration process sometimes falls into local optimality has not been properly resolved, and the algorithm will be further improved in the future.

6. Conclusion

The phase map reflects the temporal and spatial information of the image, determines the time or spatial position where different frequency signals appear, and describes the overall shape of the object. Due to biological cells generally for phase type or class phase objects, the improved GS algorithm in this paper can well describe the phase information of restored image, which is more suitable for the practical application of cell phase reconstruction, and can make up for the shortage of traditional optical microscope which can only provide amplitude image but is difficult to clearly distinguish cell edge, so it has better qualitative and two-dimensional microscopic imaging at present the effect.

The correct clinical evaluation of renal parenchymal disease under traditional microscope is firstly based on very careful microscopic observation of urinary sediment. The light intensity changes very little when light passes through the phase type sample of living cells, so the amplitude information of cells cannot clearly reflect the cell structure. In this study, the characteristics of the GS algorithm can be applied to the detection of aberrant red blood cells, use the improved GS algorithm to improve the sensitivity of phase detection, through the phase of urinary sediment image reconstruction, in addition to the other mixed cells in the urine sediment and isolates the aberrant red blood cells. It is convenient for the correct clinical diagnosis of renal parenchymal disease by the number and shape of aberrant red blood cells. It makes the detection of living cells and the clinical diagnosis of cell lesions more accurate, and has good development prospects in biomedicine. The further study will focus on how to record the various transient states of moving cells to improve the speed of image information processing and the accuracy of phase recovery.

Ethics approval and consent to participate

The experimental scheme does not violate ethics

Consent for publication

Agree to make a publication

Availability of data and materials

All data generated or analysed during this study are included in this published article

Competing interests

The authors declare that there are no conflicts of interest related to this article.

Funding

This work was supported in part by the National Natural Science Foundation of China (Grant No. 61605021); in part by Science and Technology Research Program of Chongqing Municipal Education Commission (No.KJQN202000624) in part by Opening Foundation of Key Laboratory of Opto-technology and Intelligent Control (Lanzhou Jiao tong University), The Ministry of Education (KFKT2020-08); in part by the ChongQing's technological innovation application development (No.cstc2019jscx-msxmX0079); in part by the Doctoral Foundation of Chongqing University of Posts and Telecommunications (Grant No. A2020-19); in part by Foundation of Chongqing University of Posts and Telecommunications (Grant No. A2018-89) and in part by the Foundation of Chongqing University of Posts and Telecommunications (No. X2020-53).

Authors' contributions

Wang xiuxin analyzed and interpreted the patient data regarding the hematological disease and the transplant. Wang hao performed the histological examination of the kidney, Fu guan and Ling Jiwei were major contributor in writing the manuscript. All authors read and approved the final manuscript.

Acknowledgements

We appreciated the Hospital that support the findings of this study .

Authors' information

Wang Xiuxin is a professor of Chongqing University of Posts and telecommunications, who mainly studies holographic technology. Wang Hao is a graduate student of Chongqing University of Posts and telecommunications, majoring in holographic technology. Fu Guan is a graduate student of Chongqing University of Posts and telecommunications, mainly studying image processing. Ling Jiwei is a graduate student of Chongqing University of Posts and telecommunications, mainly studying medical algorithms.

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