

Image Quality Assessment Using Self-Adaptable Bacterial Foraging Optimization Algorithm a Review

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Abstract—

There are number of successful image quality metrics that rely on the structural information in an image in order to assess its perceptual quality. It is a challenging task to extract the structural information that is perceptually meaningful to the visual system. The current research is motivated by the observation that there is no single metric that provides the best performance scores in all conditions. This paper presents a new approach for objective image quality assessment using self-adaptable bacterial foraging optimization algorithm (SA-BFOA). Moreover, multi-metric fusion approach is used for objective image quality assessment. BFOA is inspired from the social foraging behaviour of bacteria “*Escherichia Coli*”. BFOA, because of its efficiency to solve the real-world optimization problems, has drawn the attention of several researchers. The underlying biology behind the foraging strategy of *E.coli* has been emulated in an extraordinary manner and is used as a simple optimization algorithm.

Keywords—Image Quality Assessment (IQA), Bacterial Foraging Optimization Algorithm (SA-BFOA).

I. INTRODUCTION

The degradation of visual quality of an image is often occurring during its acquisition, compression, transmission, storage or reconstruction. It is important to many images and multimedia processing systems involving monitoring, controlling and improving the quality of the image, to automatically estimate the quality of an image. To measure the image quality degradations, the *mean squared error* (MSE) and the *peak signal-to-noise ratio* (PSNR) have been traditionally used. These metrics are mathematically convenient to use but they do not correlate well with human perception of image quality [6].

Visual image quality assessment method play important role in numerous image processing applications. Image Quality Assessment (IQA) methods can be classified as subjective assessment-evaluation of quality by humans, and objective assessment-evaluation of quality by algorithms. However, subjective evaluations are not only cumbersome and expensive, but also cannot incorporate into automatic systems that adjust themselves in real-time based on the feedback of output quality. So, objective image quality assessment research aims to design quality measures that can automatically predict perceived image quality.

Traditional object methods could be classified as full reference quality assessment (FRQA), reduced-reference quality assessment (RRQA), and no reference quality assessment (NRQA) as require full information, partial and none information in original images is needed for IQA, respectively. However FRQA methods need perfect original image which cannot always get. Progress on NRQA has been very slowly, because the blind image quality assessment method need to test or training the distorted information without reference. Alternatively, partial information about the reference can be made available. RRQA algorithms involve supplying minimal information (often the feature information) about the reference along with the distorted image that is useful in quality computation. Over the years, numerous IQA methods have been proposed and results in large human studies have shown that some perform well and robust relative to other methods. But the effective of image size change has rarely been discussed. However, we regularly need to assess images with different size, for example, imaging super-resolution, and the aim of IQA is to design quality measures that can automatically indicate how far have advanced in this condition. Mean-square error (MSE) and Peak signal-to-noise ratio (PSNR) are two extensively used objective quality measures among objective visual assessment approaches. But, they may not correlate with human perception very well.

With the increasing use of digital imaging devices such as digital cameras and camera phones, and the rapid development of the internet services, digital images have been becoming one of the most popular types of media in our daily life. For example, Google, Facebook and Flickr, etc. can provide us a huge amount of images. The quality of those images can be deteriorated due to noise corruption, blur, JPEG or JPEG 2000 compression, etc. However, in most scenarios we do not have the source of the distorted image, and consequently the evaluation of quality of an image has been becoming increasingly important [4].

To model the visual content of images based on certain significant properties of the *human visual system* (HVS), modern image quality estimation methods are attempted. One popular approach operates on the basis of an important aspect of the *human visual system* (HVS) - its sensitivity towards the image structures for developing cognitive

understanding. In this approach, the perceptual quality of a given distorted image is estimated by comparing its structures with those in its reference image.

The *structural similarity index* (SSIM) is an image quality metric which is representative of the class of structural information-based metrics. This method measures the visual quality of a patch in the distorted image by comparing it with the corresponding patch in the reference image, in terms of three components: luminance, contrast and structure. By combining the effects of the three components over all the image patches, a global quality score is computed. SSIM achieved much success because of its simplicity, and its ability to tackle a wide variety of distortions. SSIM is highly sensitive to geometric distortions like scaling, translation, rotation and other misalignments due to its pixel-domain implementation. multiscale extension, wavelet transform-based modification, gradient-domain implementation and various pooling strategies have been proposed to improve the performance of SSIM.

The key to the success of any structural information-based method lies in its efficiency in capturing the structures from the images. But it is a non-trivial task to obtain or analyze the structural information in a perceptually meaningful way. The wavelet transform is a widely used mathematical tool for analyzing image structures. The wavelet transform however uses a set of predefined, data-independent basis functions, and the suitability of capturing the structures of the signals under consideration has limited its success [6].

II. PREVIOUS WORK

Z. X. Xie, et.al., proposed a color image quality assessment (C-IQA) method based on the primary and fundamental image quality parameters perceived by human vision system. They established a comprehensive image quality assessment model, called as the best quality assessment function for the color image. The maximum of the function corresponded to the color image with the best quality. The function could be used either in FR-IQA or in NR-IQA. Not only it did not rely to any reference image but also could be used to assess the reference image quality. The method could also be used to acquire the color image with the best quality by means of a reference image through a gray transformation [1].

W. Xue et.al., presented blind image quality assessment (BIQA) approach, which was completely free of the human subjective scores in learning. They partitioned the distorted images into overlapped patches, and a percentile pooling strategy was used to estimate the local quality of each patch. After that, a quality-aware clustering (QAC) method was proposed to learn a set of centroids on each quality level, that were used as codebook to infer the quality of each patch in a given image, and subsequently a perceptual quality score of the whole image was obtained. The idea behind QAC was that with the normalized quality scores of a set of patches in hand, a set of patches were grouped into groups of similar quality, and then were clustered the same quality group patches into different clusters based on their local structures. The main advantages of this method were that the QAC achieved competitive spearman rank order correlation coefficient (SROCC) results with those state-of-art BIQA methods which exploited the human subjective scores in training, and QAC had good linearity to human perception of image quality, and at last, QAC provided a real-time solution to BIQA applications [2].

Y. Kang-long, et.al., presented an improved reduced-reference image quality assessment (RRIQA) method that was based on the structural similarity image metric (SSIM) and scale invariant feature transform (SIFT). The method was applicable to super-resolution image, and more than one reference image was considered. Super-resolution (SR) was the technique that constructs high-resolution (HR) images from low-resolution (LR) images [3].

S. A. Golestaneh, et.al., presented a no-reference quality assessment algorithm for JPEG compressed images (NJQA), in which quality was estimated by first counting number of zero-valued DCT coefficients within each block, and then quality relevance map was used to weight those counts. The quality relevance map for an image was a map that indicated which blocks were naturally uniform/non-uniform vs. which blocks had been made uniform/non-uniform via JPEG compression [4].

K. Gu, et.al., reported a dedicated contrast changed image database (CID2013) which was composed of four hundred contrast-changed images of fifteen original natural images and the mean opinion scores (MOSs) recorded from twenty-two inexperienced viewers. After that they proposed a novel reduced-reference image quality metric for contrast-changed images (RIQMC) using entropies and order statistics of the image histograms [5].

T. Guha, et.al., proposed a new quality assessment metric that relied on a sparse modelling approach to learn the inherent structures of the image which were learnt as a set of basis vectors, a linear combination of only a few of these basis vectors were used to represent these structures. This strategy was known to generate basis vectors that were similar to the receptive field of the simple cells present in the mammalian primary visual cortex. By comparing the structures of the reference and the distorted images in terms of the learnt basis vectors, the perceptual quality of the distorted images was estimated [6].

III. SA-BFO ALGORITHM [7]

Bacteria Foraging Optimization Algorithm (BFOA), proposed by Passino, was a new comer to the family of nature-inspired optimization algorithms. Locomotion is achieved by a set of tensile flagella during foraging of the real bacteria. Flagella help an *E.coli* bacterium to tumble or swim, which are two basic operations performed by a bacterium at the time of foraging. Each flagellum pulls on the cell when they rotate the flagella in the clockwise direction which results in the moving of flagella independently and finally the bacterium tumbles with lesser number of tumbling whereas in a harmful place it tumbles frequently to find a nutrient gradient. Moving the flagella in the counter clockwise direction helps the bacterium to swim at a very fast rate. The bacteria undergo chemotaxis in the above-mentioned algorithm,

where they like to move towards a nutrient gradient and avoid noxious environment. Fig. 1 depicts how clockwise and counter clockwise movement of a bacterium take place in a nutrient solution [8].

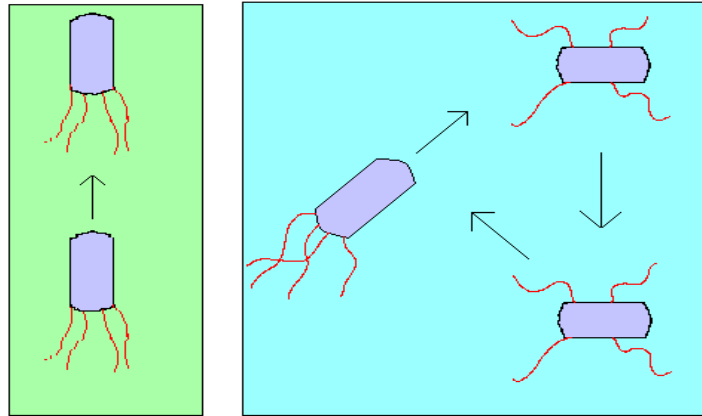


Fig. 1: Swim and tumble of a bacterium [8]

They are increased in length and in presence of suitable temperature they break in the middle to form an exact replica of itself, when they get food in sufficient amount. From this phenomenon Passino got inspired and introduced an event of reproduction in BFOA. The chemotactic progress may be destroyed and a group of bacteria may move to some other places or some other may be introduced in the swarm of concern due to the occurrence of sudden environmental changes or attack. This constitutes the event of elimination-dispersal in the real bacterial population, where all the bacteria in a region are killed or a group is dispersed into a new part of the environment

A. Step-by-step BFOA

[Step 1] Initialize parameters $n, S, N_c, N_s, N_{re}, N_{ed}, P_{ed}, C(i)$ ($i=1,2,\dots,S$), Θ^i . Where,

n : Dimension of the search space,

S : The number of bacterium,

N_c : chemotactic steps,

N_s : swim steps,

N_{re} : reproductive steps,

N_{ed} : elimination and dispersal steps,

P_{ed} : probability of elimination,

$C(i)$: the run-length unit during each run or tumble.

[Step 2] Elimination-dispersal loop: $l = l+1$.

[Step 3] Reproduction loop: $k = k+1$.

[Step 4] Chemotaxis loop: $j = j+1$.

[substep a] For $i=1, 2, \dots, S$, take a chemotactic step for bacteria i as follows.

[substep b] Compute fitness function, $J(i,j,k,l)$.

[substep c] Let $J_{last} = J(i,j,k,l)$ to save this value since we may find better value via a run.

[substep d] Tumble: Generate a random vector

$$\Delta(i) \in R^n$$

with each element $\Delta_m(i)$, $m = 1, 2, \dots, S$, a random number on $[-1, 1]$.

[substep e] Move: Let

$$\theta^i(j+1, k, l) = \theta^i(j, k, l) + C(i) \frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}} \quad (1)$$

This results in a step of size $C(i)$ in the direction of the tumble for bacteria i .

[substep f] Compute $J(i,j+1,k,l)$ with $\theta^i(j+1, k, l)$.

[substep g] Swim:

(i) Let $m = 0$ (counter for swim length).

(ii) While $m < N_s$ (if have not climbed down too long)

• Let $m = m+1$.

• If $J(i,j+1,k,l) < J_{last}$, let $J_{last} = J(i,j+1,k,l)$. then another step of size $C(i)$ in this same direction will be taken as equation (1) and use the new generated $\theta^i(j+1,k,l)$ to compute the new $J(i,j+1,k,l)$.

• Else let $m = N_s$.

[substep h] Go to next bacterium ($i+1$): if $i \neq S$ go to (b) to process the next bacteria.

[Step 5] If $j < N_c$, go to step 3. In this case, continue chemotaxis since the life of the bacteria is not over.

[Step 6] Reproduction:

[substep a] For the given k and l , and for each $i = 1, 2, \dots, S$, let J_{health} be the health of the bacteria. Sort bacterium in the order of ascending values.

$$J_{health}^i = \sum_{j=1}^{N_c+1} J(i, j, k, l) \quad (2)$$

[substep **b**] The S_r bacteria with the highest J_{health} values die and the other S_r bacteria with the best values split and the copies that are made are placed at the same location as their parent.

[Step 7] If $k < N_{re}$ go to step 2. In this case the number of specified reproduction steps is not reached and start the next generation in the chemotactic loop.

[Step 8] Elimination–dispersal: For $i = 1, 2, \dots, S$, with probability p_{ed} , eliminate and disperse each bacteria, which results in keeping the number of bacteria in the population constant. To do this, if a bacterium is eliminated, simply disperse one to a random location on the optimization domain. If $l < N_{ed}$, then go to step 2; otherwise end.

In order to get an insight into the behaviour of the virtual bacteria in BFO model, we illustrate the bacterial trajectories in a fitness landscape by tuning the run-length unit parameter $C(i)$, which can essentially influence the bacterial behaviours. The fitness landscape is defined by the 2-D Ackley function (Equation 3), which has one narrow global optimum basin and many minor local optima. It is a widely used multimodal benchmark with the global optimum (0, 0) and the minimum is 0.

$$f(x, y) = -20 \exp\left(-0.2 \sqrt{\frac{1}{2}(x^2 + y^2)}\right) - \exp\left(\frac{1}{2}(\cos 2\pi x + \cos 2\pi y)\right) + 20 + e \quad (3)$$

B. SA-BFO Algorithm

In the SA-BFO algorithm, an “individual run-length unit” to the i th bacterium of the colony was introduced and each bacterium can only modify the research behaviour of itself by using the current status of its own. In this way, not only the position but also the run length unit of each bacterium undergoes evolution. In SA-BFO evolution process, each bacterium displays alternatively two distinct search states:

(1) *Exploration* state, during which the bacterium employs a large run-length unit to explore the previously unscanned regions in the search space as fast as possible.

(2) *Exploitation* state, during which the bacterium uses a small run-length unit to exploit the promising regions slowly in its immediate vicinity.

By varying its own run-length unit adaptively, each bacterium in the colony permanently maintains an appropriate balance between *Exploration* and *Exploitation* states. This is achieved by taking into account two decision indicators: a fitness improvement and no improvement registered lately. The criteria that determine the adjustment of individual run-length unit and the entrance into one of the states are the following:

Criterion-1: if the bacterium discovers a new promising domain, the run-length unit of this bacterium is adapted to another smaller one. Here “discovers a new promising domain” means this bacterium register a fitness improvement beyond a certain precision from the last generation to the current. Following *Criterion-1*, the bacterium’s behaviour will self-adapt into *Exploitation* state.

Criterion-2: if the bacterium’s current fitness is unchanged for a number K_u (user-defined) of consecutive generations, then augment this bacterium’s run-length unit and this bacterium enters *Exploration* state. This situation means that the bacterium searches on an un-promising domain or the domain where this bacterium focuses its search has nothing new to offer.

In this case, S is the colony size, t is the chemotactic generation counter from 1 to max generation, i is the bacterium’s ID counter from 1 to S , X^i is the i th bacterium’s position of the bacteria colony, N_s is the maximum number of steps for a single activity of *Swim*, $flag^i$ is the number of generations the i th bacterium has not improved its own fitness, $C^i(t)$ is the current run-length unit of the i th bacterium, $\epsilon^i(t)$ is the required precision in the current generation of the i th bacterium, α and β are user-defined constants, $C_{initial}$ and $\epsilon_{initial}$ are the initialized run-length unit and precision goal respectively. As we can see, we embed the reproduction, elimination and dispersal events in each chemotactic generation. Hence, the algorithm convergence rate can be significantly improved.

IV. MULTI-METRIC FUSION APPROACH

Numbers of objective metrics have developed during last few years. It is observed that different metrics perform differently for different distortion types. For example, for contrast change type of distortion, FSIM gives better score than other metrics while for Lossy compression type of distortion, MSSIM provides better result. So, fusion of different metrics is suggested.

As shown in Figure 2, we first take a reference image and a query image. Both the images are selected from the TID2013 database. Secondly, scores of the existing metrics are evaluated for each image using a MATLAB algorithm. Then, new score is set with the help of proposed method.

Let n be the number of metrics and $i = 1, 2, \dots, n$ then

$$MMF \text{ Score} = \text{abs}(\exp(f_i) + (f_j - y)^{0.1}) \quad (4)$$

where $f_i = i_{th}$ number of metric, $y = \sum_{i=1}^{n-2} f_i$ and $f_j = j_{th}$ number of metric, $j \in i$.

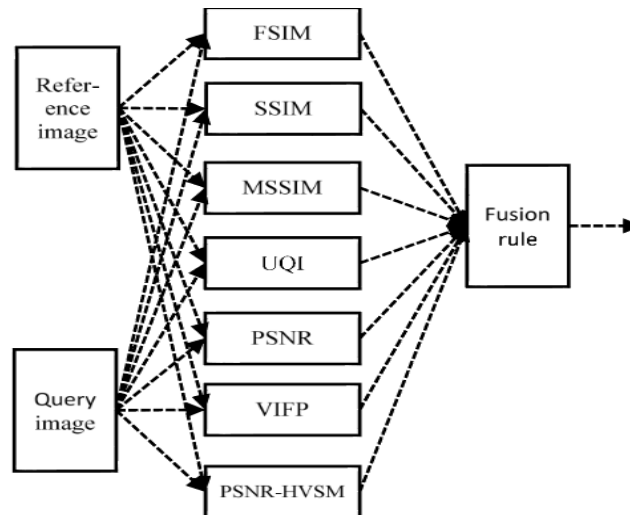


Fig. 2: Block diagram of multi-metric fusion approach IQA system

V. CONCLUSION

A multi-metric fusion (MMF) approach is used for visual image quality assessment. None of the single metric can be used to assess the quality of an image with respect to different performance measure. The Self-adaptive Bacterial Foraging Optimization algorithm is used for image quality assessment, which cast Bacterial Foraging Optimization into the adaptive fashion by changing the value of the run-length unit during the algorithm execution. This method outperforms rest of the quality metrics by a significant margin for each performance measure. The proposed approach is simple and flexible in including new metrics.

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