MEU جامعة الشرق الأوسط
MIDDLE EAST UNIVERSITY
Amman - Jordan عمان - الأردن

The Color Image Enhancement
Using SSGA Steady State Genetic Algorithm

تحسين الصورة الملونة باستخدام الخوارزمية الجينية المنتظمة

By

Ala'a Abdullah Al-Sabbah

Supervised by

Prof. Dr. Reyadh Naoum

A Thesis Submitted to Middle East University - Faculty of Information Technology, in Partial Fulfillment of the Requirements for the Master Degree in Computer Science

إقرار تفويض

أنا الاء عبدالله عوض الصباح أفوض جامعة الشرق الأوسط بتزويد نسخ من رسالتي للمكتبات أو المؤسسات أو الهيئات أو الأفراد عند طلبها.

التوقيع:

التاريخ: ٤/٩/ ٢٠١٢

Authorization Statement

I am Ala'a Abdullah Al-Sabbah, Authorize the Middle East University to supply a copy of my Thesis to libraries, establishments or individuals upon their request.

Signature:

Date: 4/9/2012

COMMITTEE DECISION

This thesis (The Color Image Enhancement Using SSGA Steady State Genetic Algorithm) was successfully defend and approved on August 7th 2012.

<u>Examination committee signatures:</u>

Prof. Dr. Reyadh Naoum.
Head of Department of Computer science.
(Middle East University)

R NaouM

Dr.Abd al-lateef abu- Dalhoom.
Professor in Department of Computer Science.
(Jordanian University)

Dr. Mohammad al-hreabat.
Asistance professor in department of Computer Information System.
(Middle East University)

DECLARATION

I do hereby declare the present research work has been carried out by me under the supervision of Prof. Dr. Reyadh Naoum, and this work has not been submitted elsewhere for any other degree, fellowship or any other similar title.

Signature:

Date: 4/9/2012

Ala'a Abdullah Al-Sabbah

Department of Computer Information System

Faculty of Information Technology

Middle East University

DEDICATION

(وَإِذْ تَأَذَّنَ رَبُّكُمْ لَئِنْ شَكَرْتُمْ لَأَزِيدَنَّكُمْ)

Almighty Allah says “And remember! Your Lord caused to be declared (publicly): "If ye are grateful, I will add more (favors) unto you”.

So all praise is for Allah, the exalted, for His favors that cannot be counted.

I dedicate this work to my parents, my brothers, my sisters, my relatives, my friends, and for all those who helped, supported, and taught me.

Acknowledgments

Thanks to almighty God for His blesses which enabled me to achieve this work. I would like to thank everyone who contributed to this thesis. This work would not be accomplished without them.

I would like to thank my parents, my brothers, and my family for their support during my study, encouragement and the extreme freedom they gave me.

Needless to say that I am indebted to my advisor Prof. Dr. Reyadh Naoum, for the outstanding motivation, guidance, support, and knowledge he provided me throughout this work. He gave me the trust to work freely on things I like. He became a good friend where his feedback has greatly improved this thesis. I consider myself extremely lucky to have Prof. Dr. Reyadh Naoum as my supervisor. He is an excellent scientific advisor and a great man. I wish him all the best in his years to come as a great professor.

I would like to thank the Information Technology Faculty members at the Middle East University.

I would like also to thank my colleagues for their help and advice in specific topics. My appreciation is extended to my family members specially my best friend my brother Awad. So are all of my friends specially Heba, , Shima Joudeh, Dareen, and Umaia

Finally, I thank everyone who criticized me either negatively or positively.

Abstract

This thesis presents a model for enhancing the color image using the steady state genetic algorithm. We modified the fitness function to get more accurate result and less noise.

In this research we will use the Hue saturation intensity (HSV) color model, after enhancing the S, H and V components, the transformation will be made to RGB color model. We have developed three models contrasts, brightness and saturation for enhancing the colourful and chromaity of the image with different types of input - output and different type of parameter.

The three models are compared based on their ability to train with lowest error values. To use these models the input RGB color image is converted to an intensity image using Space Variant Luminance Map SVLM. The 2D gamma correction used to enhance the Luminance component.

We enhanced Luna image using SSGA method then we compare the enhanced image performance with previous methods images by calculating the PSNR peak signal noise ratio and MSE mean square error .

The saturation enhancement is done by two phases : finding the most saturation color and adjusting the saturation ratio, where the contrast component enhanced using the adaptive factor.

The results in this thesis enhanced the previous results due to the combination of color and chromaity of the image. We used the Matlab ver. (7) with C^{++} language.

Three image quality metrics are applied to the color enhanced images. They are PSNR (Peak Signal-to-Noise ratio), RMSE (root mean square error) and MSE (mean square error). The comparison is made with PSNR, RMSE and MSE values. Finally it has been observed that our model, SSGA, yields better results than the previous results for enhancing the color image.

الخلاصة

هذا البحث يقدم نموذج جيني لتحسين الصورة الملونة باستخدام الطريقة الخوارزمية الجينية المنتظمة, الهدف من هذا البحث هو تحسين الصورة الملونة باستخدام طرق تحسين الصورة المقترحة وتطوير الطريقة الخوارزمية الجينية المنتظمة باستخدام اقتران معدل لإعطاء نتائج أدق واقل تشويش.

هذا البحث سيستخدم نموذج شدة تشبع كثافة بعدين لتحسين مكونات النموذج حيث يتم التحويل إلى نموذج احمر–ازرق – اخضر.

لقد طورنا ثلاثة نماذج لتحسين مكونات التلوين باستخدام أنواع مختلفة من المدخلات والمخرجات وأنواع مختلفة من المعايير, هذه النماذج تقارن بالنسبة لقابلية التمرين مع أقل نسبة خطأ.

لاستخدام هذه النماذج يتم تحويل الصورة الملونة إلى شدة الصورة باستخدام خريطة فضاء تغير الإضاءة , سوف نستخدم معيار التصحيح من نوع جاما.

تم تصحيح الشبع بمرحلتين: إيجاد نقطة التشبع العظمى وتعديل نسبة التشبع, بينما تم تعديل التباين باستخدام معامل التباين المطور .

النتائج في هذا البحث كانت أفضل من نتائج الطرق السابقة من حيث مكونات اللون التي تحسنت إضاءتها و تباينها و تشبعها , لقد استخدمنا الماتلاب (7) مع لغة++C.

List of Abbreviations

Abbreviation	**Stand for**
AC	A spatial domain coefficients
AGA	Adaptive Genetic Algorithm
AINDANE	Adaptive and integrated neighborhood dependent enhancement approach for nonlinear
BTR	Binary Tournament Replacement
CZP	Circular Zone Plate
DC	Compressed domain coefficients
DCT	Discrete cosine transform (DCT)
DRO	Dynamic range optimization
DSC	Dice Similarity Coefficients
FCM	Fuzzy C means algorithm
FPN	Fixed pattern noise
GA	Gentic algorithm
HIS	Hue Saturation Intensity
HSV	(hue, saturation, value) colour model
IAGA	Improved Adaptive Genetic Algorithm
IE	Image Enhancement
ISODATA	integrated self-organizing data
JPEG	Joint Photographic Experts Group
LSGA	level set genetic algorithm,
MAE	Mean absolute error

MPEG	Moving Picture Experts Group
MSE	Mean Squared error
PCM	Possibilistic C means algorithm
PDVE	Peak detection and valley extraction
PSNR	Peak signal to signal noise ratio
RBF-GA	Radial Basis Function Genetic Algorithm
RBFNN	Radial Basis Function Neural Network
RGB	Red Green Blue
RMSE	Root Mean squared error
RWS	Roulette wheel Selection
SGA	simple genetic algorithm
SNR	signal to noise ratio
SOM	Self Kohenen Map
SSGA	steady state gentic algorithm
SUS	Stochastic Universal Sampling
SVLM	space-variant luminance map
TSOM	Thresholding self-organizing map (SOM)
TSP	Travelling Salesman Problem
U V Y	color image pipeline
CIE XY	CIE primary color coordinate system
UIQI	Universal Image Quality Index
YCbCr	Prior to scaling and offsets to place the signals into digital form

Table of contents

Chapter One : Introduction

Chapter Two : Literature Survey and Related Work

Chapter Three : Genetic Algorithm

Chapter Four : Methodology

Chapter Five : Results of the Enhancement

List of Figures

List of tables

Chapter One 1

Introduction

1.1 Overview

Image enhancement, IE, is required mostly for better visualization or rendering of images to aid the visual perception. As seen in Figure (1.1) Images Processing is composed of image acquisition, preprocessing, feature extraction, segmentation and image understanding [41].

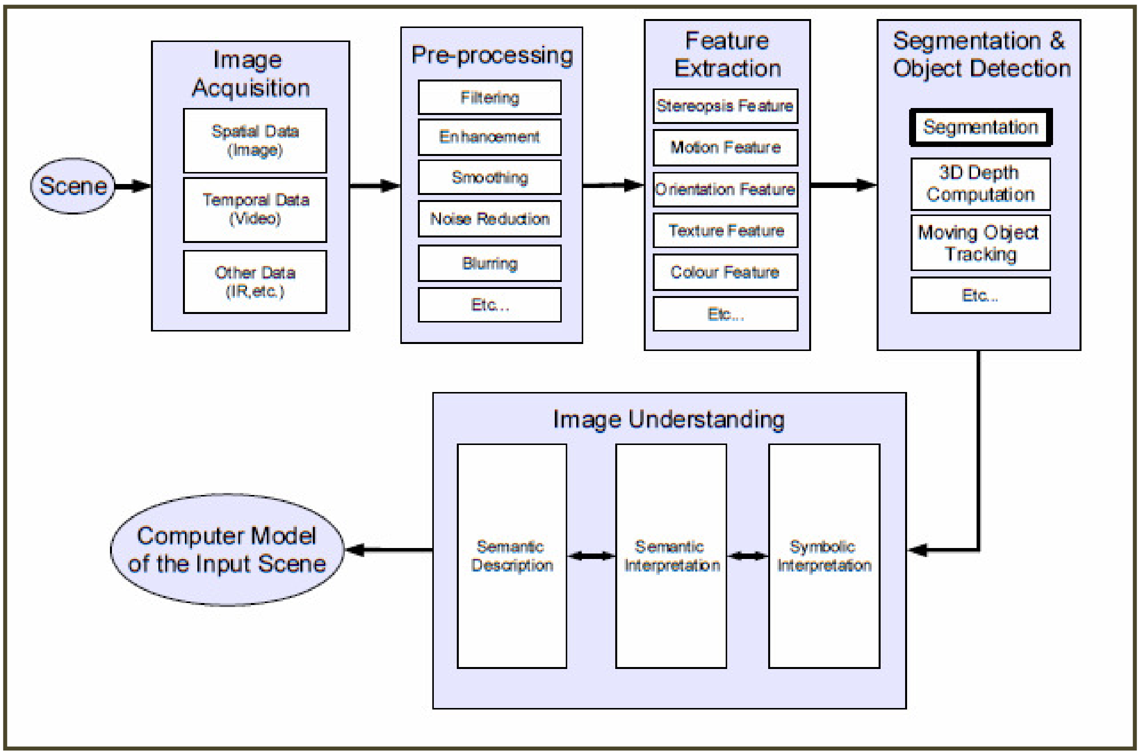


Figure (1.1): Representation of image processing

Images enhancements mean adjusting the brightness, changing the tone of the color, sharpening the image and reducing noise. The process of editing or modifying the images is, in general, called Image Processing.

Image Enhancement (IE) transforms images to provide better representation of the subtle details. It is an indispensable tool for researchers in a wide variety of fields including medical imaging, art studies, forensics and atmospheric sciences.

The IE method suitable for one problem might be inadequate for another. For example forensic images and videos employ techniques that resolve the problem of low resolution and motion blur while medical imaging benefits more from increased contrast and sharpness. Image enhancement methods may be categorized into two broad classes: transform domain methods and spatial domain methods [7].

The techniques in the first category are based on modifying the frequency transform of an image. However, computing a two-dimensional (2-D) transform for a large array (image) is a very time , consuming task even with fast transformation techniques and is not suitable for real time processing [7]. The techniques in the second category directly operate on the pixels. Contrast enhancement is one of the important image enhancement techniques in spatial domain. Other than the two popular methods, histogram equalization and histogram specifications, this thesis is concerned with the spatial domain methods.

Improvement of image quality has been highly demanding for users in digital imaging systems including HDTV, LCD display, and digital photography. The image quality is mostly deteriorated by several reasons such as: the limited bit resolution, the narrow dynamic range, and the insufficient acquisition time [15].

There are various reasons, why a raw image data requires processing before display, the dynamic range of the intensity values may be small due to the presence of strong background illumination, and insufficient lighting.

It may be the other way also; the dynamic range of the original image may be too large to be accommodated by limited number of bit-planes of a display device. The problem gets more complicated when the illumination of the scene widely varies in the space.

These affect the human visual perception in terms of over-saturation and under-saturation, the blurring, and color distortion.

Image enhancement algorithms including homomorphic filtering methods, histogram based techniques, and transform based techniques (Arich and Dikbas 2009, [16]) have been studied to provide better quality for users.

(a) **(b)**

Figure (1.2) :An example of enhance image processing

In some places , the scene appears to be too dark while in some other places it is too bright. An example of such an image is shown in Fig. 1.2(a). It can be seen that the brightness of the blue sky affects the display of the reflection on the glass window of the car, where many details are not visible. In such images it is necessary to improve the local contrast. The result of processing (Mukherjee and Mitra2008, [14]) with improved display is shown in Fig. 1.2(b).

Image enhancement very often deals with such improvement of image contrast as it is related to the sharpness of the details.

In order to improve the visual quality of the input image captured in dynamic illumination environments, luminance and color information is characterized in terms of the spatial frequency. This characteristic leads complexity and performance tradeoffs between the global and the local in the spatial perspective. In particular, the transfer function design that increases the visual perception is an important key to perform the image enhancement.

The above mentioned enhanced methods are designed on the principle of amplifying the local intensity or color variations within an image to increase the visibility of texture details and other features. A majority of techniques advanced, so far, have focused on the enhancement of gray level images in the spatial domain. Also, these methods include adaptive histogram equalization, unsharp masking, constant variance enhancement; homomorphic filtering, high-pass, and low-pass filtering. However, new approaches for enhancing color images have taken into account the chromatic information as well.

In many such algorithms the RGB color coordinates are transformed into a different space such as HSV or YCbCr (Talebi (2009) [25],Pei& Chang (2009) [17] and Tang(2010) [26]) where chromatic components are more uncorrelated from the achromatic component. This allowed the representation of the color in terms of hue, saturation, and intensity in closer agreement with the physiological models which describe the color processing of the human visual system.

There are also a few researches reported in the RGB space, for example, Jabarouti (2011) [9] has used retinex theory leading to excellent quality of the enhanced images. However, their technique is computationally intensive as it requires filtering with multiscale Gaussian kernels and post processing stages for adjusting colors.

There are also techniques reported using equalization of the 3-D histograms in the RGB space [14] to enhanced images.

However, increasingly images are being represented in the compressed format for efficient storage and transmission [17]. Hence, it has become imperative to investigate compressed domain enhancement techniques to eliminate the computational overheads for carrying out the inverse transform to the spatial domain and back into the compressed domain by forward transform.

In particular, processing in the DCT domain has attracted significant attention of researchers due to its adoption in the JPEG and MPEG compression standards [14,6].

There are also other advantages of using compressed domain representation. For example, due to the spectral separation, it is possible to enhance features by treating different frequency components differently.

Different algorithms have been advanced for both color and grey level images in the block DCT domain, such as alpha rooting and multi contrast enhancement by processing the AC coefficients and its modified form by processing both DC and AC coefficients etc. However, there are also some disadvantages in processing images in the block DCT domain. As in most cases , blocks are independently processed, blocking artifacts may become more visible in the processed data. Sometimes superfluous edges may appear in the image boundaries due to the sharp discontinuities of the distribution at its boundaries.

The major objective for processing the data in the compressed domain is to reduce the computational complexity and storage requirements. Hence, these two requirements should be taken into account in designing the pertinent algorithms. For many spatial domains processing, an equivalent computation in the DCT domain could be developed by using the properties of the DCT such as its linear and orthogonal property, sub-band relationship [45], spatial relationship [46] and convolution-multiplication property [47].

The achievable performance depends on the optimal gamma value which is non-trivial task. Given the non-uniform illumination , the gamma correction challenges the over-saturation / under-saturation. In order to combine with the local characteristic on the gamma correction, the dynamic range optimization (DRO) was developed based on a bilateral filter [11]. Due to the significant computational complexity of the filtering, the DRO may not appropriate for real-time applications [11].

1.2 Problem definition

Noise in digital images has always been one of the most troubling dilemmas photographers have to deal with. Noise can be seen as low-frequency irregular arrangements of color patches and can also be more bothering if combined with other image color artifacts.

Causes of image noise are numerous, and some of them cannot be easily identified. Those causes, however, fall mainly into two categories: Fixed Pattern Noise (FPN), and Temporal Noise. Fixed pattern noise is seen as a spatially-fixed pattern across the whole image, and can be caused by three main factors:

1. Dark conditions: fixed pattern noise can be introduced in dark conditions, when there is no sufficient lighting and the photographed subject or scene is not well illuminated.
2. Long exposure: fixed pattern noise can also be introduced to your images when the exposure time is long, such as in night or low light photography.
3. High sensor temperatures.

The dark photographic conditions can also significantly reduce the available image sensor's dynamic range. For those of you not familiar with Dynamic Range, you can check it out and learn more about it in my earlier post Photography and Dynamic Range right.

Temporal noise is a variation in image noise from one image to the next. Pixel values vary randomly over time. Main factors that contribute to image temporal noise are as follow:

1. Shot Noise: Shot noise is most problematic under low-light conditions, where the SNR ratio is rather high. At high-light intensities, SNR ratio is high and shot noise is subsequently negligible.
2. Reset Noise: reset noise occurs at the sensor level, before the signal is converted from analogue to digital. Most camera and image sensor manufacturers are actually able to completely control reset noise by using a special signal processing circuitry.
3. Read Noise: read noise is noise added to the signal when it's being read out of the sensor and converted from analogue to digital. Read noise is independent of

exposure time. Slower analogue to digital converting and data processing cameras introduce higher levels of read noise.

4. Dark Current Shot Noise: dark current shot noise, which is noise associated with dark conditions previously discussed in FPN or fixed pattern noise can be largely controlled. The shot noise component of this kind of noise however, cannot be reliably controlled or removed.

These are measured by the ratio between signals to noise, known as signal to noise ratio or alternatively called SNR.

If the SNR value is high, the image quality is good and noise is at a relatively low level. If the SNR value is low, image noise is at high levels that are more visible, degrading the image quality.

Conventional color to gray algorithms achieved much but share one or more of three particular drawbacks. Firstly, some of them do not produce gray-scale images that satisfactorily render the levels of contrasts and detail that can be perceived in the original color images, for example they may not preserve important visual cues because there are no clear definitions of visual cues. Secondly, some may have very heavy computational costs and are not ready for practical applications; and finally, better quality results may depend upon adjustments to free parameters by human operators, which is not user friendly.

To solve these problems of enhancement , we propose the color model in this thesis.

1.3 Objective

In this research we try to enhance images, to have more visible, more accurate and less noise. The proposed model combined the color component enhancement and the robustness enhancement.

The model aimed to increase Chroma and reduce lightness. Chroma enhancement includes the luminance, saturation and contracts enhancement.

The model has genetic algorithm part, but doesn't use the simple traditional genetic algorithm, it used SSGA steady state genetic algorithm. SSGA depends on the fitness function, we use enhanced and modified fitness function.

1.4 Significance of the research

The objective of contrast enhancement is to increase the visibility of details that may be obscured by deficient global and local lightness. The goal of color enhancement can be either to increase the colorfulness, or to increase the saturation.

Increasing the lightness can give a perception of increased colorfulness ; however in this case perceived saturation reduces for a given Chroma. On the other hand, perceived saturation can be increased by increasing Chroma, reducing lightness and hybrid (both of them).If Chroma is increased moderately while slightly reducing the lightness, both saturation and colorfulness in an image can be enhanced. This method is also likely to avoid out-of-gamut or unrealizable colors.

This research develops an automatic image enhancement technique based on the real coded SSGA.

The task of the SSGA is to adapt the parameters of a novel extension to a local enhancement technique similar to statistical scaling, as to enhance the contrast and detail in the image according to an objective fitness criterion. In what follows an evolutionary Algorithm for automatic contrast enhancement has been proposed having the following advantages:

a) It uses a local enhancement technique,based on a variation of the statistical scaling method.
b) It uses no interaction with the user, during running stages of the algorithm, therefore the method is automatic.
c) It uses an objective fitness criterion with no additional external parameters.

In addition, the color constancy must be considered because of the color distortion caused by the contrast enhancement in the luminance space.

Retinex based algorithms considering the lightness and color in the human visual perception perspective have been advanced in terms of local contrast enhancement and lightness color rendition [51].Current contrast enhancement algorithms based on spatial domain techniques can be Global, local and hybrid [51].

Also, in our research we used the Local enhancement methods to enhance the image for each pixel according to the information (luminance, saturation, and Retinex) of its own and its neighbor. Global enhancement methods enhance the image from the luminance information of an entire image. Local enhancement methods enhanced the image for each pixel according to the information (luminance, saturation, and Retinex) of its own and its neighbor.

When these images are blurred, out of focus or not adequately bright which makes their examination difficult, although such problems may be fixed by using IE techniques.

The purpose of this research is to evaluate if IE techniques to improve the visualization of these images with the study of effect of such an approach, are useful (helpful).

Also, in this thesis we used SSGA algorithm to search the parameters of the Multi-Scale Retinex model and eleven parameters (e.g., seven for Retinex, four for SSGA) are needed to be set.

Chapter two 2

Literature Survey and Related Work

2.1 Overview

The display of a color image depends upon three fundamental factors, namely its brightness, contrast, and colours. Interestingly, all the previous work has considered either the brightness (such as adjustment of dynamic ranges) or the contrast (such as image sharpening operations), and even in some cases a combination of both attributes. But none of these algorithms have considered the preservation of colors in the enhanced image.

2.2 Literature Survey related to art field

Pei and Chang (2009) [17] presented a novel algorithm using color contrast enhancement and lacuna texture synthesis is proposed for the virtual restoration of ancient Chinese paintings.

Color contrast enhancement based on saturation and desaturation is performed in the U V Y color space, to change the saturation value in the chromaticity diagram, and adaptive histogram equalization then is adopted to adjust the luminance component. Additionally, this work presented a new patching method using the Markov Random Field (MRF) model of texture synthesis.

Pei and Chiu (2009) [21] presented a color enhancement scheme to virtually restore ancient Chinese paintings in electronic form. Two degradations result in color contrast loss in ancient Chinese paintings: paper aging and pigment fading. The proposed enhancement scheme comprises two subsequent methods: background adjustment and saturation enhancement. The former method, based on the Von Kries color conversion in the CIE xyY color space, retrieved the original color of the paint paper by modifying colors based on their similarity to the background color. Their proposed saturation enhancement method made colors more vivid and bright, and also improved the image contrast.

2.3 Literature Survey related to artificial neural networks

Mohammad Awad (2010) [48] designed artificial neural networks , ANN , for image segmentation, the new method is developed using unsupervised artificial neural network that combined both Self Kohenen Map, SOM, and thresholding method.

They segmented different image using five clusters and compared TSOM method with ISODATA method by using two different types of satellite images.

The disadvantage of the above method is that the efficiency depends on the selected number of iterations and threshold values, which makes it more depending on human.

2.4 Literature Survey related to DCT method

Mukherjee and Mitra (2008) [14] enhanced color images in the block DCT domain by scaling the transform coefficients. The unique feature of this algorithm is that it treats chromatic components in addition to the processing of the luminance component improving the visual quality of the images to a great extent.

Pei, Zeng and Chang (2009) [17] dealt with non-uniform scaling of DCT coefficients in a block. For example, in the scale factors are computed for every coefficient (both the DC and AC coefficients) by taking their roots. In the relative contrast between a pair of successive bands of AC coefficients is scaled by a factor, which remains constant for every block. This eventually requires computation of different scale factors for different bands of AC coefficients.

Sangkeun Lee (2007) [49] presented a simple and efficient algorithm for dynamic range compression and contrast enhancement of digital images under the noisy environment in the compressed domain.Its proposed approach also introduces a simple scheme for estimating and reducing noise information directly in the DCT domain. The main advantage of its proposed algorithm enhanced the details in the dark and the bright areas with low computations without boosting noise information and affecting the compressibility of the original image since it performs on the images in the compressed domain. In order to evaluate the proposed scheme, several base-line approaches are described and compared using enhancement quality measures.

2.5 Literature Survey related to histogram method

The Histogram method:

Image editors have provisions to create an image histogram of the image being edited. The histogram plots the number of pixels in the image (vertical axis) with a particular brightness value (horizontal axis). Algorithms in the digital editor allow the user to visually adjust the brightness value of each pixel and to dynamically display the results as adjustments are made. Improvements in picture brightness and contrast can thus be obtained.

Sural, Qian and Pramanik (2009) [35] developed a method that combined both HSV color space and a framework for extracting features that can be used both for image segmentation and color histogram generation. This approach makes use of the Saturation value of a pixel to determine if the Hue or the Intensity of the pixel is closer to human perception of color than pixel represents. The K-means clustering of features combines pixels with similar color for segmentation of the image into objects.

They are also able to generate a histogram that enables us to perform a window-based smoothing of the vectors during retrieval of similar images. While it is well established that color itself cannot retain semantic information beyond a certain degree, they have shown that retrieval results can be considerably improved bya better histogram.

Delon, Desolneux, Lisani, and Petro (2009) [3] designed a new method for the segmentation of color images is presented. This method searches for an acceptable segmentation of 1D-histograms,according to a “monotone” hypothesis. The algorithm uses recurrence to localize all the modes in the histogram. The algorithm is applied on the hue, saturation and intensity histograms of the image. This algorithm hasn't the simplicity of the system which wastes the time on the complexity of the additional parameter.

Xu& Yu (2010) [30] introduced a new hybrid image enhancement approach driven by both global and local processes on luminance and chrominance components of the image. This approach, based on the parameter-controlled virtual histogram distribution method, can enhance simultaneously the overall contrast and the sharpness of an image. That method increased the visibility of specified portions and aspects of the image whilst better maintaining image color. But this method ignored the chromatic and the luminance components.

Han and Yang (2011) [6] proposed a novel 3-D color histogram equalization method that produces uniform distribution in gray scalehistogram by defining a new cumulative probability density function in 3-D color space. This result was limited to the grey images and didn't enhance the brightness of the color images.

Duan and Qiu (2011) [19] divided the luminance range [0, 255] into 256 intervals using a hierarchical division procedure and used a control parameter to control the mapping. They proposed a dynamic specific histogram algorithm to do contrast enhancement for a real-time system due to its simplicity.

2.6 Literature Survey related to fuzzy method

Dutta and Chaudhuri (2009) [3] designed an unsupervised color image segmentation method. Color image segmentation is an important but still open problem in image processing.

At first, FCM is applied to the image and the cluster centers are obtained. Quite similar to the famous TSK fuzzy control model, we form several rules (IF-THEN like) for pixel classification. The results obtained from the rules are plotted as a histogram. An effective histogram peak detection and valley extraction (PDVE) algorithm is applied to the histogram and thresholds are extracted from the histogram for segmentation.

Hanmandlu and Jha (2006) [7] designed technique that has a visible improvement in the image quality for under exposed images, as the entropy of the output image is decreased. The terminating criterion is decided by both the visual and quality factors. For over exposed and under plus over exposed images, the proposed fuzzification function needs to be modified by taking maximum intensity as the fourth parameter. Fuzzy method ignored hue and saturation components.

Sowmya and Sheelarani (2009) [14]designed technique for the segmentation using Fuzzy C means algorithm, FCM, Possibilistic C means algorithm ,PCM, and competitive neural network. By comparing result for different images they conclude that soft computing techniques are found to be more accurate and reliable than traditional hard C means technique.

2.7 Literature Survey related to GA genetic algorithm

Praveena & Vennila (2010) [16] designed a new segmentation method that combined both K-means and genetic algorithm to have more reliable and accurate result. They segmented brain images using K-mean method using RGB (Red Green Blue) and HIS (Hue Saturation Intensity) and then used the GA genetic algorithm. They used the SGA simple genetic algorithm without any modification ;they focused on colors model more than the modification of GA.

Raghad (2010) [22] tried to solve the problem of image with multilevel noise. They used wavelet thresholding to minimize Mean Squared error (MSE),with Quad tree Construction to encode a given chromosome , and the fitness of a given chromosome is done by energy function. They invited a new crossover method called graft crossover.

Their experimental results suggested that their proposed approach is flexible, efficient with acceptable segmentation result. However the computational costs of their algorithms are high.

Wang and Tingzhi (2010) [23] have developed an Improved Adaptive Genetic Algorithm (IAGA) based on Simple Genetic Algorithm (SGA) and Adaptive Genetic

Algorithm (AGA). Their experiments show that IAGA has better segmentation than the SGA,IAGA.

Mahia and Izabatene (2011) [24] merged the Radial Basis Function Neural Network (RBFNN) with Genetic Algorithm, their work developed and tested successfully. They verified that the RBF-GA is an appropriate approach in satellite imagery segmentation and performs better than RBF network using conventional K-means algorithm. They claimed that the neural network and RBF-GA is advised when we use different data with different distribution. Also, they noted that time processing for GA algorithm increases with the size of the input data. The advantage of RBF-GA neural network over traditional segmentation algorithm is that it's not a parametric model.So it does not need the normal distribution assumption in the input data.

Payel and Melanie (2011) [28] designed a new method ,depending on the genetic algorithm, GA; they used thermography images of hands. They performed segmentation using several method, Gabor wavelet method, Chan-Vese method and level set genetic algorithm, LSGA.

The drawback of this research is the small population size N.

2.8 Literature Survey related to color model

Naik and Murthy (2009) [15] applied their image enhancement method to each R, G, B component image of RGB color images. They also tried to enhance RGB color images by transforming input RGB color images into HSV color images and enhancing only the V component image.

The enhanced RGB color image is finally obtained by transforming the enhanced V component image along with the original H and S component images into RGB color images.

Rahman (2010) [29] reported the multi scale retinex with color restoration(MSRCR) that makes use of the logarithmic transfer functions associated with the spatial convolution performing at individual R G B spectral bands.

Lin, Su, Huang, and Fan (2011) [33] proposed a novel colour segmentation algorithm that can work in various illumination circumstances. The proposed colour segmentation algorithm operates directly on RGB colour space without the need of colour space transformation and it is very robust to various illumination conditions. This approach can be employed in various domains such as human skin colour segmentation and the maturity of tomatoes; their parameters weren't familiar to compare with other method, HSI was more familiar and can be easily compared.

2.9 Literature Survey related to segmentations

Ning and Zhang (2009) [30] designed a method for region segmentation which didn't need a preset but depended on the initial mean shift. This method adds to the overload of statical approach.

Tarnos and Oluday (2011) [31] presented a comparative study about image segmentation; they use Edge-based method to solve the problems such as less edge image very noisy, boundary that are very smooth and texture boundary. They suggested an evaluation method technique that combined machine evaluated and human evaluated.

2.10 Literature Survey related to space-variant luminance map

Lee & Kang (2010) [11] presented a color image enhancement method that makes use of a space-variant luminance map (SVLM) for the local brightness characterization.

Two-dimensional gamma correction combined with the SVLM is developed to increase the intensity at the dark region and vice versa at the bright region in the luminance domain. The enhanced luminance information is applied to the adaptive contrast enhancing process and the linear color restoration. The proposed algorithm reveals details of the input image and minimizes loss of the edge sharpness in the non-uniform and low illumination conditions. The developed enhancement process depended on the SVLM with its ability to get errors.

2.11 Literature Survey related to unsupervised method

Akram, Moustafa and Alqadi (2009) [1] developed unsupervised and no prior knowledge of number of regions to be segmented is required. This method designed a new color model for digital image, which can be used to separate low, and high frequencies in the image without losing any information from the image. The proposed model can be used in different application but it has given notable errors.

Meylan and Susstrunk (2010) [32] used a Retinex-based adaptive filter to enhance natural color images, and their results showed that the color image with halo area could be enhanced. However, it needed to choose the appropriate filter size to reduce halos images and to introduce global tone mapping for extremely high dynamic range images.

Tao and Asari (2010) [33] reported the adaptive and integrated neighborhood dependent approach for non-lineaer enhancement (AINDANE) for low and non-uniform illuminance conditions. The separated adaptive luminance and contrast enhancement processes are developed to maintain the dependency of image brightness.

Although the combined method is useful to refine the image quality, the performance is focused on the low luminance condition. The transfer function has the lack of the local characteristic as well as the lack of the bright region improvement.

Rabin and Gousseau (2011) [18] developed technique concerned with the modification of the gray level or color distribution of digital images. This method tries to overcome the common drawback of classical methods aiming at such modifications is the revealing of artefacts and the attenuation of details and textures.

In this work ,they proposed a generic filtering method enabling, given the original image and the radio metrically corrected one, to suppress artefacts while preserving details.

The approach relies on the key observation that artefacts correspond to spatial irregularity of the so-called transportation map, defined as the difference between the original and the corrected image. The proposed method draws on the nonlocal Yaroslavsky filter to regularize the transportation map. The efficiency of the proposed method is shown on various radiometric modifications: contrast equalization, midway histogram, color enhancement, and color transfer [18].

Chapter three 3

Genetic Algorithm

3.1 Overview

Genetic Algorithm (**GA**) is an adaptive heuristic search algorithm premised on the evolutionary ideas of natural selection and genetics. The basic concept of GA is designed to simulate processes in a natural system necessary for evolution. As such, they represent an intelligent exploitation of a random search within a defined search space to solve a problem.

GA is a form of a randomized search where strings are chosen and combined in a stochastic process. This is a radically different approach to the problem solving methods used by more traditional algorithms which tend to be more deterministic in nature.

GA exploits the idea of the survival for the fittest and an interbreeding population to create a novel and innovative search strategy. A population of individuals (strings, or chromosome), representing solutions to a specified problem, is maintained by the **GA**.

The **GA** iteratively creates new populations from the old ones by selecting methods to select strings and interbreeding the fittest to create new ones, which are, hopefully, closer to the optimum solution of the problem at hand. So, in each generation, the **GA** creates a set of individuals from previous individuals , regardless of the type of used encoding.

The idea of survival for the fittest has a great importance in **GA;** it uses what is termed as a fitness function in order to select the fittest string which will be used to create new individuals, and conceivably better populations of individual. The fitness function takes a string and assigns a relative fitness value. These values will be used to select the fittest strings in order to be a member on the next generation.

Traditional methods of the problem optimization have suffered a set of problems which encourages researchers to use **GA** properties as a suitable technique. The reasons behind that are:

1. **GA** works with a coding of parameters set, not which the parameters themselves.
2. **GA** searches for a population of points, not for a single point. The search is carried out from generation to generation until convergence.
3. **GA** uses payoff information, not derivative or other auxiliary knowledge. The value of an objective function feeds back to direct a search.
4. **GA** uses probabilistic transition rules, not deterministic ones. The best fitness function value is not guaranteed to be found, but GA usually makes a significant progress.

In addition to the reasons mentioned above, problem solving technique suffers from different problems during implementation. These problems are:

1. Reaching an optimal solution highly depends on an initial state.
2. Most of these methods are aimed to find a local optimal solution, not a global optimal one.
3. Insufficient when dealing with problems which use discrete variables.

4. Slow Convergence for finding problem solutions. In many cases, it is difficult to determine error tolerance rate.

GA has been used to find solutions for most of the complex problems in different fields. **GA** uses genetic concepts to encode the problems into a generation (a group of individuals) and then simulates the generation evolution by applying mathematical genetic operators (selection, crossover and mutation) to determine the best solution (individual) over multiple iterations of a finite number of generations. The definition of "best" comes from a fitness function which defines whether a given individual is better or worse. Termination condition is not satisfied, GA will repeat its operation.

3.2 Basic GA Operation.

In Fig.(3.1), we summaries the basic operation of the GA or in other words the evolutionary algorithm.

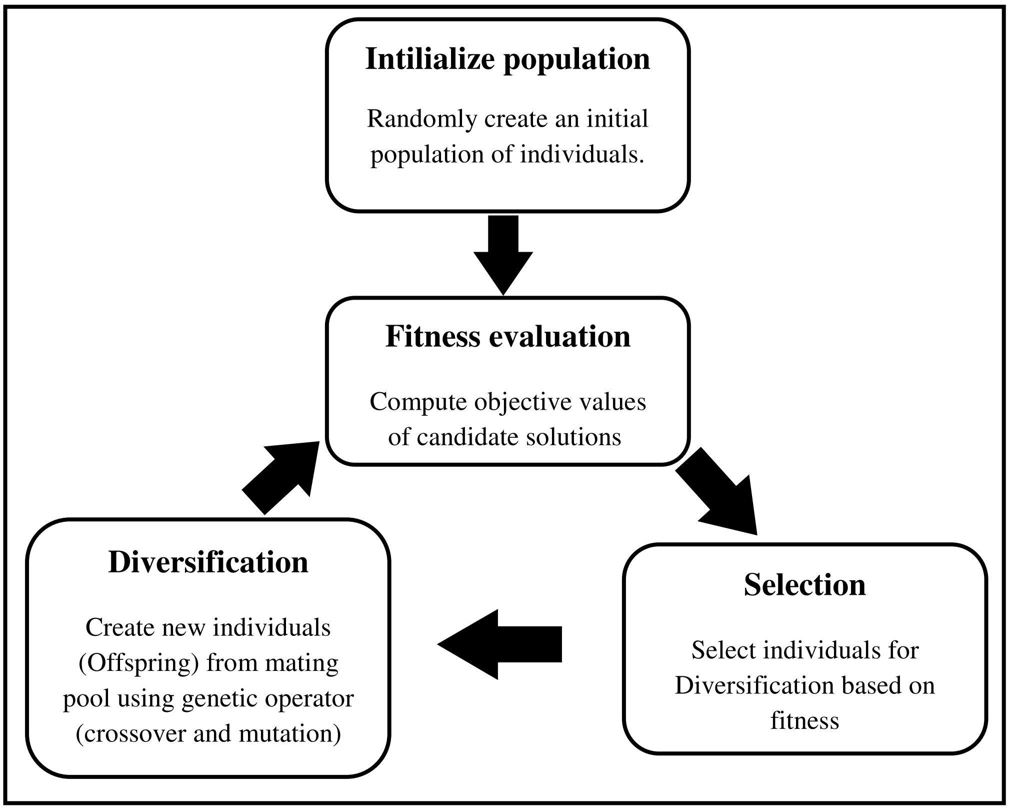


Figure (3.1): The basic algorithm of evolutionary process.

To find a solution for a specific problem, we can apply **GA** to solve the problem. The basic **GA** is comprised from the following steps:

3.2.1 **Initiation** is the creation of an initial population of chromosomes, that consists of the random selection of the demanded number of chromosomes (individuals) which have a determined length. In addition, we can use population from a similar problem to be as good seeds for the problem rather than randomness in population initialization which improves the goodness of this modification.

3.2.2 **The evaluation of the fitness of chromosomes in a population** is measured by calculating the value of the fitness function for each chromosome of this population. The higher value of the fitness function is the better "quality" of the chromosome. The form of the fitness function depends on the type of the solved problem. It is assumed that the fitness function always takes nonnegative values and, furthermore, the solved optimization problem is a problem of searching for the maximum of this function. If the initial form of the fitness function does not meet these assumptions, then an appropriate transformation is made (e.g. the problem of searching for the minimum of the function may easily be reduced to the problem of searching for the maximum).

3.2.3 **Checking the stopping criterion**, the determination of the criterion for stopping the GA processes depends on a specific application of this algorithm. In optimization issues, if the maximum (or minimum) value of the fitness function is known, the stopping of the algorithm may occur after obtaining the desired optimum value, possibly with specified accuracy. The stopping of the algorithm may also occur if its further operation no longer improves the best obtained value. The algorithm may also be stopped after the lapse of a determined period of time or after a determined number of generations. If the stopping criterion is met, then the last step is taken, that is the presentation of the "best" chromosome. Otherwise the next step will be a selection.

3.2.4 **The selection of chromosomes**, the selection of chromosomes consists of selecting, based on the calculated values of the fitness function. These chromosomes will take part in the creation of offspring until the next generation. This selection takes place in accordance with the natural selection rule, i.e., the chromosomes with the highest value of fitness function have the most chances in the participation of the creation of new individuals. There are many selection methods which will be discussed in the next sections.

3.2.5 **Applying / Using genetic operators**, applying genetic operators to chromosomes which are selected with the selection method leads to the creation of a new population constituting the offspring population derived from parents population. In the classical GA, two basic genetic operators are used: crossover operator and mutation operator. It should, however, be emphasized that the mutation operator has a definitely secondary role in comparison with the crossover operator. This means that in the classical GA, crossover is almost always present while mutation occurs quite rarely. The probability of crossover is usually assumed to be high (generally $0.5 \leq Pc \leq 1$), and, in turn, a very small probability of the occurrence of mutation is assumed (often $0 \leq Pm \leq 0.1$). This also results from the analogy to the world of living organisms where mutations rarely occur.

3.2.6 **Creating a new population.**

3.2.7 **Presentation of the "best" chromosome.**

GA steps will be presented in more detail in the next section.

3.2.8 Genetic Algorithm Elements

GA consists of a set of elements:

3.3.1 Population

We speak about a population of individuals $\mathbf{N_{pop}}$, where $\mathbf{N_{pop}}$ is suggested to be between 25-500 individual. The basic terms are **gene, chromosome, genotype, phenotype,** and **allel**. The terms corresponding to them and coming from the technical vocabulary are also used, such as **chain, binary sequence**, and **structure**.

- Population is a set of ***individuals*** of a specified size.
- Individuals of a population in genetic algorithms are sets of ***task parameters*** coded in the form of chromosomes, which means solutions otherwise called *search space points*. ***Individuals*** are sometimes called ***organisms.***
- Chromosomes: otherwise *chains* or *code sequences* – are ordered sequences of ***genes*** has length (L) $\mathbf{Chromosome_i = Gene_1\ Gene_2 \ldots.\ Gene_L,\ 1 \le i \le N_{pop}}$ If we use Binary encoding , then gene, $\mathbf{Gene_{1 \le j \le L}}$ **is {1,0}** [71] **.**
- Gene: also called ***a feature***, ***sign, or detector*** constitutes a single element of *the genotype*, of the chromosome in particular.
- Genotype: otherwise ***structure*** is a set of chromosomes of a given individual. Thus, individuals of a population may be *genotypes* or single chromosomes(if a genotype consists of only one chromosome, and such is often the assumption).
- Phenotype: is a set of values corresponding to a given genotype, which is a ***decoded structure***, and thus, *a set of task parameters (a solution*, *search space point).*
- Allel: is the value of a given *gene*, also specified as ***the feature value*** **or** ***the feature variant.***

- Locus: is a ***position*** indicating the place of the location of a given gene in *the* ***chain*****,** which is in the chromosome (its plural form, that means “positions”, is loci).

After determining the population size and the length of chromosome, individuals are generated randomly to represent initial values for current generation which represent initial search space for GA.

The next step will be evaluating these individuals.

3.3.2 Evaluation

Each individual has a calculated fitness value related to the objective (evaluation) function regardless of whether individuals are generated previously or reproduced later. Therefore, we must pay attention when designing an evaluation function which distinguishes between better and worse solution. If the fitness function is chosen poorly or defined imprecisely, the genetic algorithm may be unable to find a solution to the problem, or may end up solving the wrong problem.

In maximization problems, the fitness value will be equivalent to objective function value. In contrast, for minimization problems we aim to get the lowest value for objective function.

3.3.3 Encoding

Encoding is one of the most important processes in GA to represent suitable solutions. Choosing suitable representation method enhances the effectiveness of GA in solving problems. Also it depends on the type of problem which will be solved. There are different ways for encoding. But we must take into account that the selected method depends on the problem itself. There are different methods for encoding such as:

a. Binary Encoding:

Binary encoding is the most common encoding method which has been used in GA. This method is preferable for three reasons :

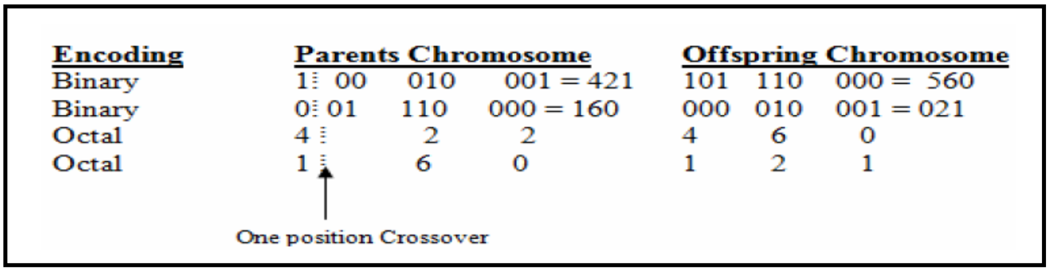
Firstly, for historical cause; original work of GA uses binary representation for individuals. Secondly, by applying the principle of selecting small size of genes, this will enable the nature representation of the problem to avoid memory problem. Finally, both crossover and mutation will be implemented easily on strings.

Binary encoding converts the value of parameters (features) into binary values {0,1}, e.g., chromosome= 10000101.

In binary encoding, the value of parameters will be transformed into binary representation. After that, the resulted values will be decoded into real ones. In this case, the speed of GA simulation will drop down. Moreover, it will be suitable to use natural (real) value for parameters rather than using binary method to be close to problem search space. This encourages researchers to find out other methods to be used.

b. Integer Encoding:

By this method, string (Chromosome) is represented by using integer numbers. After performing one-position crossover on binary chromosome, new individuals (offsprings) will be produced disrupting the original individual (solution). New offsprings will differ in their structure from the original solution. In integer encoding, there is no need to transform (encoding, decoding) parameters into binary representation which will have positive impact on speeding up simulation process for GA, figure (3.2) clarifies the reason of using this method in encoding.



Encoding	Parents Chromosome	Offspring Chromosome
Binary	1⁝ 00 010 001 = 421	101 110 000 = 560
Binary	0⁝ 01 110 000 = 160	000 010 001 = 021
Octal	4 ⁝ 2 2	4 6 0
Octal	1 ⁝ 6 0	1 2 1

Figure (3.2) : Comparison between Binary and Integer (Octal in this example)

c. Real Encoding:

This method differs from other encoding methods by using actual real values of Figure chromosome as shown in figure (3.3).

1.2	**2.2**	**0.4**	**.....**	**0.672**

Figure (3.3) : Real value encoding of chromosome.

In addition, this method avoids tearing the structure of chromosome when it happenes in binary encoding. As a result, there is no need for decoding chromosomes. Other strength points of real encoding are: Firstly, precision of real encoding since binary method needs a long chromosome to give a high precision such as 13 bit will give 0.001 precision. However, it is less than real encoding method. Secondly, the size of mutation in real can be controlled by adding a random value from Gauss-Poisson distribution (this is what is done by a revolution strategy).

3.3.4 Selection

We are going to present several selection methods which are used frequently in GA. Selection is a process of choosing individuals from current populations as parents are implementing crossover and mutation on them to reproduce new individuals (offsprings or Childs). This process comes directly after encoding population.

However, all selection methods are distinguished through using selection pressure. Selection pressure represents the number of a better individual. As for the methods which use a high selection pressure, they will suffer from Premature Convergence or Slow Finishing. One of the big concerns in keeping these factors balanced is to feed our space by new bloods and to be able to explore different situations and circumstances. There are different common selection methods which can be used. They are:

a) ***Roulette wheel Selection (RWS):***

RWS is a selection method used in **SGA** for selecting high probability parents with high fitness value.

RWS works by adding all individual fitness value (denoted by $\sum F_i$) then calculating the expected probability for each individual "e_i" (the expected number of times for selecting individual for crossover) by dividing its fitness value, over cumulative fitness values for all individuals as shown in equation (3.1):

$$\begin{cases} \bar{F} = \frac{\sum Fi}{n} \\ e_i = \frac{Fi}{\bar{F}} \end{cases} \tag{3.1}$$

WhereF_i: Individual fitness,

$\bar{F}$: Average fitness,

n : number of individuals in generation.

In RWS, each individual takes a slice from roulette wheel. The slice size depends on the individual fitness value. After that, spin the wheel for N_{pop} times, where N_{pop} is the number of individual in current generation. On each spin, the individual under the wheel's maker is selected to be in the matting pool to reproduce next generation.

The ***Roulette wheel Selection*** can be implemented as follows [50]:

1. Sum the total expected (fitness) value of individuals in the population. Call this sum T.
2. Repeat N_{pop} times

a. Choose a random integer (**r**) between 0 and T.

b. Loop through the individuals of the population, and calculate the summation of their expected values until it becomes greater than or equals (**r**).

After that, select the individual whose expected value puts the sum over the specified limit. It is obvious that the roulette wheel method can be applied if the values of the fitness function are positive.

In general, this method of selection suffers from different problems such as: Premature convergence where premature convergence happens at the beginning of GA simulation process.The individual with highest fitness value will be dominant on others. Furthermore, the dominant individuals will sustain in next generation too. In other words, individuals of a very low fitness value will be eliminated early from the population, so we cannot learn from weak individuals.

Slow finishing; slow finishing happens at the end of GA simulation process. At the end of the execution, there will be a large number of individuals who have similar fitness values. In this case, which one will be selected? and cannot be able to discriminate between them.

Finally, there is no guarantee to keep the best individual for next generations. To overcome this problem, we can use Elitist selection method.

b) ***Elitist Selection*****:**

The idea behind this method is getting over the problem of RWS. Elitist method keeps a finite set of best individuals in each generation since these individuals may not be selected or disrupted during crossover and mutation. However, elitism finds a solution for RWS problems but still suffers from problems too. For that reason we use another method called Ranking Selection.

c) Ranking selection:

Ranking selection is an alternative method which prevents too-quickly convergence and slow finishing problems. There are different ways to perform this method, but the simplest is linear ranking method. Linear ranking method is proposed by Backer in 1985, where individuals of a population are ordered descending (from 1 to N_{pop}) according to their fitness value. An individual with the highest fitness value takes the rank = 1, the next individual takes rank = 2 and so on.

The new fitness value for individuals is computed as shown in equation (3.2), [71]:

$$\mathbf{F' = max - (max - min) [(rank\text{-}1)/ (N_{pop} -1)]} \qquad (3.2)$$

Where :

$$\mathbf{1 < max \leq 2 \ \ \& \ \ rank \in \{1, 2, \ldots, n\} \ \& \ min = 2 - max}$$

Rank-based fitness overcomes the scaling problems of the proportional fitness assignment. Ranking method does not give a high portion of fitness to a small number of individuals who have high fitness value. In this case, the selective pressure will be reduced if there is a high difference in fitness values of population individuals where the probability select individual with i^{th} and $(i+1)^{th}$ rank will be the same. While the absolute difference in their fitness can be low or high. Value Ranking introduces a uniform scaling across the population and provides a simple and effective way of controlling selective pressure.

d) ***Stochastic Universal Sampling (SUS):***

RWS suffers from another problem where the actual probability of selecting each individual highly differs from the expected value of that individual.

Baker, in 1987, suggested a method called SUS in order to reduce the difference between an actual value and the expected one. In SUS spins the wheel only once and individuals are mapped to contiguous segments of a line, where each individual's segment is equal in size to select N_{pop} parents. Thus, the probability of selected individuals must be within the expected and actual value of that individual as mentioned in equation (3.3), [71] :

$$c_i \geq probability\ of\ i \geq e_i \tag{3.3}$$

Where :

e_i : actual value for i.

c_i : expected value for i.

SUS method still suffers from premature convergence and slow finishing problem such as RWS. To avoid these problems, we can merge another method with SUS such as Ranking selection where F′ is calculated by using Linear ranking and performing the selection by using SUS.

Contiguous segmentation and centralization make SUS improper for a parallel selection. Naturally, all individuals have the ability to move freely and easily from one location to another and compete on crossover and resources on parallel. To avoid the SUS problems we can use other methods such as the Tournament Selection method.

e) ***Tournament selection:***

In the tournament selection, individuals are organized implicitly. Individuals with low fitness value have the chance to be selected. The simplest and most common way to perform this method is Binary Tournament Selection.

Binary Tournament Selection has been used in SSGA where two individuals are selected randomly and the best one will be added to the mating pool for reproduction causes. If those individuals have the same fitness value, then one of them will be chosen randomly. Those steps are repeated until we reach the required number of individuals.

We can formulize this method as shown in equation (3.4), [71]:

$$select_n = \begin{cases} ind_i , & if(f(ind_i) > f(ind_j)) \\ ind_j , & otherwise \end{cases} \tag{3.4}$$

Where:

$select_n$: selected individual that has number n,

$f(ind_i)$: fitness of individual i,

$f(ind_j)$: fitness of individual j.

There are different ways to perform this method. One of these ways is to select two individuals randomly and generate random number ($0 \leq r \leq 1$). If $r \leq k$ (k is parameter e.g. 0.75) then we select the individual with highest fitness value else we select the individual with lowest fitness value [50].

We notice that a large number of competitive groups will increase the selection pressure where the individuals with fitness value lower than average will have low selective pressure value. In contrast, individuals with fitness value higher than average will have a high selective pressure value.

Tournament method has some advantages over other methods. There is no need to perform additional computation, e.g. F_i, Average fitness. Also, there is no need to transform fitness value as described in equation (3.1). In figure (3.4) we present, in briefly, Tournament Selection Method.

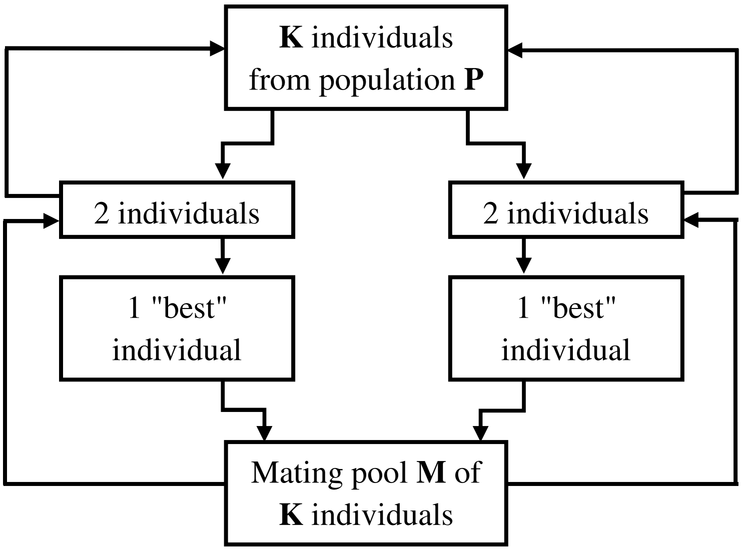


Figure (3.4) : Tournament Selection.

3.3.5 GA Operator

GA has two main types of operator which are used to reproduce new individuals in the next generations. These operators are: Crossover and Mutation.

Crossover is one of the main characteristics which distinguishes GA from other revolution techniques. It is a process of exchange of genes between two individual (chromosomes) to reproduce new individuals with inherent parent's behavior.

Crossover is used firstly to represent the search in the parameters space. Secondly, it is concerned in finding a way to keep the information stored by parents chromosomes because they are considered good chromosomes resulted from selecting process. All crossover methods depend on encoding method and problem type. There are many common crossover strategies such as:

a) Single crossover position(1x):

Single crossover position is the simplest method for crossover and it is used in SGA. Crossover is accomplished by using crossover probability Pc ($0.6 < Pc < 0.9$) and selecting random position k ($k \in \{1, 2, \ldots, l-1\}$, l = is chromosome length) to produce new two Childs (chromosomes) by intersecting parents chromosomes at k position.
K genes from first parent (second parent) transfer to first child (second child) , while k-*l* genes from first parent (second parent) transfer to second child(first child), as shown in figure (3.5).

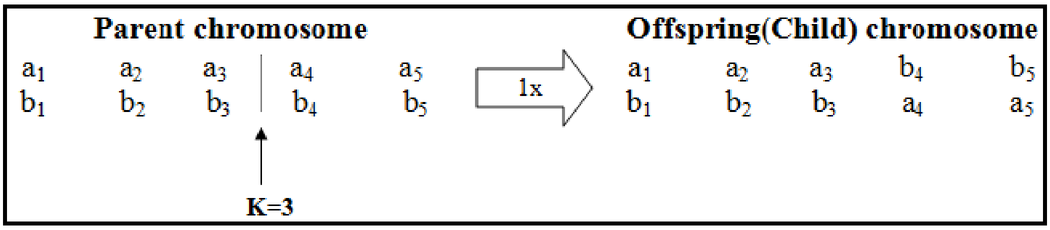


Figure (3.5) : 1x crossover.

Single point crossover still suffers from a shortage in diversity within the community, and it tears up the edge of one parent's chromosome. To get over these problems, researchers suggest using an alternative method called Two-point crossover. Single point crossover still suffers from a shortage in diversity within the community, and it tears up the edge of one parent's chromosome.

To get over these problems, researchers suggest using an alternative method called Two-point crossover.

b) Two-point crossover(2x):

Two-point crossover is different in its high probability for not tearing up the edge of chromosome. Instead, it has an exceptional ability in tearing genes of chromosomes since there are two crossover points. Two-point crossover (2x) has better performance than 1x or at least they are equivalent. Two-point crossover (2x) is used widely in SSGA.

Crossover is accomplished by using crossover probability Pc ($0.6 < Pc < 0.9$) and selects random position k_1, k_2 ($k_1, k_2 \in \{1, 2, ..., l-1\}$, $k_1 < k_2$) where the genes between k_1 and k_2 are switched. Figure (3.6) shows how 2x works.

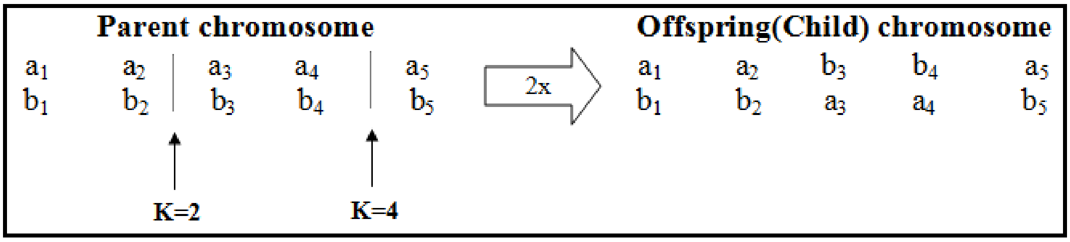


Figure (3.6) : Tow-point crossover 2x.

c) Uniform crossover:

Uniform crossover differs from other methods where genes are randomly exchanged by using probability (e.g., 0.5) as shown in figure (3.7).

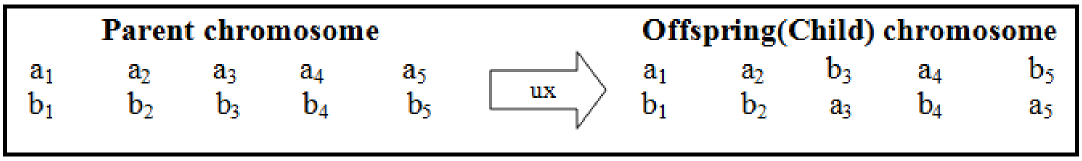


Figure (3.7) : Uniform crossover.

This method has a great influence on tearing chromosomes in order to gain a high diversity in populations. However, it has a high performance on a real world problem. In addition, genes are inherited from the first parent (the remaining genes come from another parent). Accordingly, uniform crossover is used frequently in GAs. This type of crossover may be applied on different types of the encoding of the chromosome. Only one condition must be met. The chromosomes must be of the same length. This method has been adapted in SSGA inherited from the first parent (the remaining genes come from another parent). Accordingly, uniform crossover is used frequently in GAs.

3.3.6 Replacement

Replacement is described as a deletion process performed on the worst individuals in order to be replaced by better new individuals. There are two famous methods of replacement:

a) ***Binary Tournament Replacement (BTR):***

BTR is intended for binary sets of chromosomes to replace them by the worst chromosome from previous generations which have been selected randomly. The following equation (3.5) explains BTR, [71].

$$replace_n = \begin{cases} ind_i & if(f(ind_i) < f(ind_j) \\ ind_j & otherwise \end{cases} \tag{3.5}$$

$$For\ n = \{1, 2\}, random\ numbers\ i, j \in \{1, 2, \dots\dots\dots, N_{pop}\}, i \neq j$$

Where: $replace_n$: $individual\ n\ that\ will\ be\ replace$d,

$f(ind_i)$: fitness of individual i,

$f(ind_j)$: fitness of individual j.

BTR sustains better individuals by performing replacement always with better individuals. Furthermore, the best individual will never be replaced. To enhance the probability and to sustain the best individuals, we can use other methods of replacements.

b) Triple Tournament Replacement (TTR):

This method looks like the ones, but it differs in the number of individuals which will be replaced by the number of individuals equals 3. The following equation (3.6) explains the TTR [71].

$$\boldsymbol{Replace_n} = \begin{cases} \boldsymbol{ind_i} & \boldsymbol{if\ F(ind_i) < F(ind_j)\ and\ \ F(ind_i) < F(ind_k)} \\ \boldsymbol{ind_j} & \boldsymbol{if\ F(ind_j) < F(ind_i)an\ \ F(ind_j) < F(ind_k)ind_j} \\ \boldsymbol{ind_k} & \boldsymbol{otherwise} \end{cases}$$

(3.6)

$$\boldsymbol{For\ n = \{1, 2\}, random\ numbers\ i, j, k \in \{1, 2, \ldots \ldots \ldots, N_{pop}\}, i \neq j, i \neq k, j \neq k}$$

$Where:\ \boldsymbol{replace_n}\ : individual\ n\ that\ will\ be\ replace$d,

$\boldsymbol{F(ind_i)}: fitness\ of\ indivual\ i$

$\boldsymbol{F(ind_j)}: fitness\ of\ indivual\ j$

This method of replacement is aimed to keep the best individuals in order to produce at least two elite size equals (the best two individuals will never be replaced).

- ***Other Replacement methods:***

There are additional ways which can be used for replacement in Genetic Algorithm such as:

- **Worst replacement**: where we always replace a new individual with the worst one in populations.
- **Random Replacement**: where we replace a new individual with an individual selected randomly from population.
- In addition, there is a replacement strategy which considers the fitness and the similarity among individuals in the same population in order to select an individual which will be deleted if it has the lowest fitness value and a similarity with a new one.

3.3.7 Stopping Criterion

Stopping Criterion can be considered as an indicator to a GA convergence.

There are numbers of criteria such as:

On-line performance:

This method is a measurement of GA performance depending on individual fitness, the mathematical equation (3.7) is as follows, [71]:

$$On-line\ (T) = \frac{1}{T}\sum_{t=1}^{T} F(T) \tag{3.7}$$

Where :**T**: number of times to find fitness,

F(t): binary evaluation for fitness values.

During GA process, on-line (T) converges to constant value. In this case, GA simulation will be terminated. Furthermore, stopping criterion can be selected from the list below:

- The maximum number of generations has been reached.
- Average of generation fitness converges to the maximum value.
- Maximum fitness value is not improved during the next specific number of iteration.
- Similarity between all generation individuals in chromosome level or fitness value level.
- If the fitness value of one of the individuals exceeds the determined threshold value.

3.4 GA Forms

Here, we will focus on two forms of GA; Simple Genetic Algorithm (SGA) and Steady State Genetic Algorithm (SSGA).

A) Simple Genetic Algorithm (SGA)

This form of GA has been suggested by Holland after studying Fruit fly community. This form of GA focuses on the reproduction of a new generation which replaces the whole previous one. As a result, there is no intersection between generations. SGA works as follows:

Algorithm of SGA:

```
Begin
t = 0
Initialize P (t) // P(t) = Population
Evaluate P (t)
 While (Termination condition is not satisfied) do
Selection P(t+1) from P(t)
Perform Crossover on P(t+1)
Perform Mutation on P (t+1)
Evaluate P (t+1)
t = t+1
end
```

B) Steady State Genetic Algorithm (SSGA)

SSGA is another form of GA where the generation is changed gradually by performing partial replacement of individuals (unwanted individuals), where a part of the population is transferred to the next generation without any changes.

In this case, we have intersected communities where a set of individuals is replaced by a new one as it happens in Elephants evolution. SSGA works according to the following algorithm:

Algorithm of SSGA:

```
Begin
t = 0
Initialize P (t) // P(t) = Population
Evaluate P (t)
While (Termination condition is not satisfied) do
Selection P(t+1) from P(t)
Perform Crossover on P(t+1)
Perform Mutation on P (t+1)
Evaluate P (t+1)
Replacement (P(t), P(t+1))
t = t+1
end
```

SSGA has a set of characteristics which excels SGA. A number of these characteristics are:

- The ability to find solutions by using small samples contrary to SGA, whereas SSGA can select a new good individual as soon as they are generated , while SGA must examine all population to select good individuals.
- SSGA avoids repeating the same individual in population, so generation will contain plenty of different solution. In addition, Smith, in 1996, suggests performing mutation continuously on new individuals until we gain individual which differs from the rest of populations.
- SSGA has more steadiness against genetic divergence or unlinearity (Epistasis). For example, if we suppose that an individual is constructed from good genes, this individual has a high fitness value. These individual genes will be torn up by using crossover operator to produce new individuals. The original individual (the parent) will still be a part of a current generation and can be selected to cross over again unlike SGA.

Chapter Four 4

Methodology

4.1 Overview

Our developed model has advantage that it combines the colorful and chromaity of the image, it enhances the Saturation, Contrast and Luminance of the image.

4.2 Phase (1) Preprocessing phase

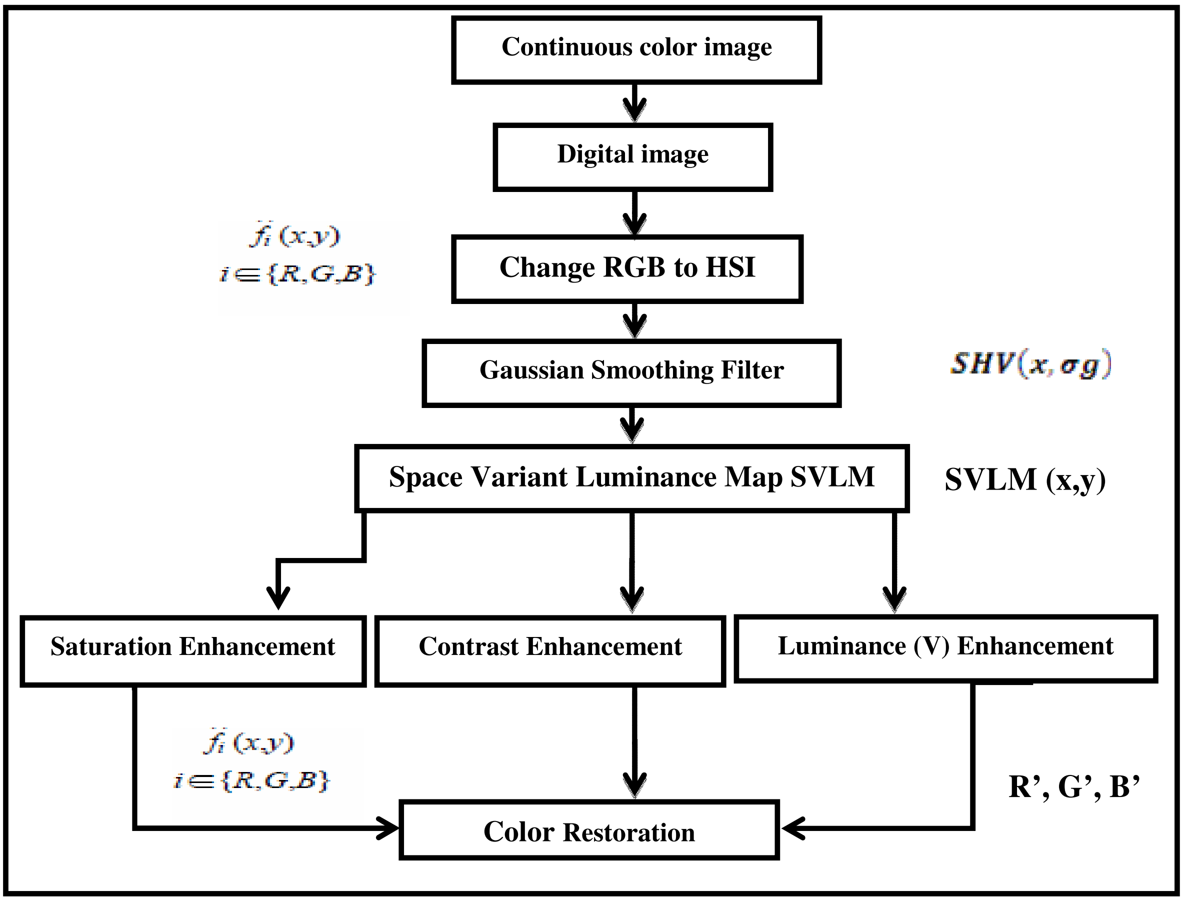


Figure (4.1) : Representation of phase (1).

This phase will represent three conversions for the image, first the continues image will be converted to digital image ,then it will be converted from RGB to HSI model, after

SVLM will be calculated, then each component R,G,B will be enhanced through its algorithm, SVLM, as shown in figure (4.1), after that R', G' and B' will be restored.

4.2.1 Color transformation:

There are many color models. In this thesis the input color image with **RGB** color model is adopted. Next, the **RGB** color model is transformed to **HSV** color model; the reasons of using **HSV** color model are summarized below.

First, the value **V (luminance)** and color information **(Hue and Saturation)** are decoupled. Second, the **HSV** color model describes perceptual color relationships more accurately than **RGB** color model. Third, transforming **RGB** color model to **HSV** color model is easy. The transformation from **RGB** to **HSV** is described as follows in equations (4.(1-3)) [30]:

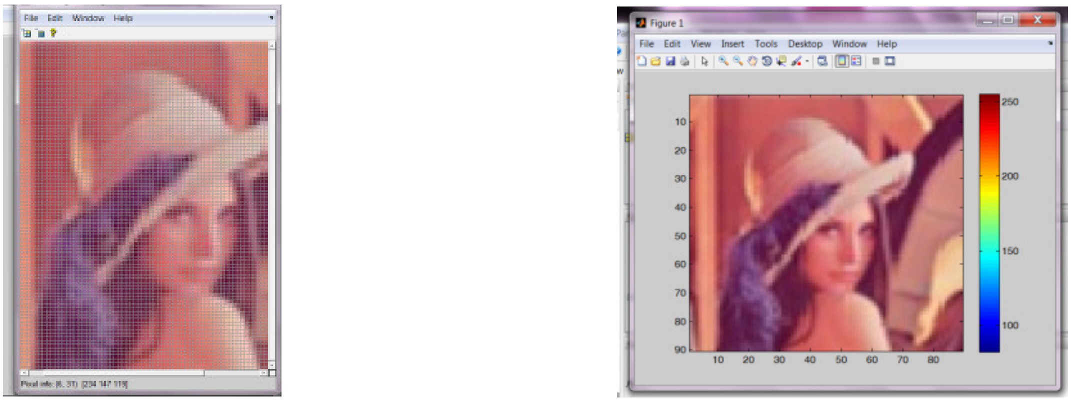
$$S = \begin{cases} 0 & , \quad if \max = 0 \\ \dfrac{max - min}{max} \times 255 & , \quad otherwise \end{cases} \tag{4.2}$$

$$V = max \times 255 \tag{4.3}$$

$$H = \begin{cases} undefined & , \quad if\ max = min \\ 60^o \times \frac{g-b}{max-min} + 0^o & , \quad if\ max = r \quad , g \geq b \\ 60^o \times \frac{g-b}{max-min} + 360^o & , \quad if\ max = r \quad , g < b \\ 60^o \times \frac{b-r}{max-min} + 120^o & , \quad if\ max = g \\ 60^o \times \frac{r-g}{max-min} + 240^o & , \quad if\ max = b \end{cases} \tag{4.4}$$

Where r red pixel value ,g green pixel value , b blue pixel value.

As shown in figure (4.1) the image should be digitized then converted RGB to HSV image as done to luna image in figure 4.2(B).



A **B**

Figure (4.2) : RGB representation of Luna image in our proposed model.

As shown in figure 4.2(A) the pixel mask of image has been used in the enhancement method. When the mask is over an area of constant or slowly varying gray level, the result of convolution will be close to zero.

4.2.2 Gaussian Smoothing Filter

The Gaussian convolution of a luminance histogram $H_L(x)$ depends upon both x and σ_g, namely, the Gaussian standard deviation. The convolution function $S_{HL}(x,\sigma_g)$ is provided by equation(4.4) [50].

$$S_{HL}(x,\sigma_g) = H_L(x) * g(x,\sigma_g) = \int_{-\infty}^{\infty} H_L(u)\ g(x-u,\sigma_g)\ du$$

$$= \int_{-\infty}^{\infty} H_L(u) \frac{1}{\sqrt{2\pi}\sigma_g} e^{\frac{-(x-u)^2}{2\sigma_g^2}}\ du \qquad (4.4)$$

Where "*" denotes the convolution operator and $g(x-u, \sigma_g)$ is the Gaussian function. The degree of smoothing is controlled by the standard deviation of the Gaussian function. The larger the standard deviation σ_g, the smoother the function $S_{HL}(x\sigma_g)$ is [50]. Notably, in Tsai [51] the smoothing parameter is predetermined. In Tsai and Lee, they proposed the standard deviation is decided automatically. This method is briefly statesd as follows [52]:

Standard deviation σ_g is based upon the majority of the widths within the luminance histogram. In a histogram

$$H_L(x)\ ,\ \text{if}\ H_L(x) < H_L(x-1)\ \text{and}\ H_L(x) < H_L(x+1),$$

then luminance x is a valley. The highest point between two successive valleys is a peak, which identifies a distribution. Therefore, the widths between two successive valleys are computed and thus, the maximum width, W_{max}, among the widths is determined. Next, the width histogram for all peaks from **0** to W_{max} is computed. After the highest point in the width histogram is located, which is regarded as the standard deviation σ_g of the widths, Eq. (4.4) is employed to convolute the histogram $H_L(x)$that provides smoothing histogram.

The objective of choosing the standard deviation is to smooth the most frequent “ripples” of the histogram and to leave the significant modes [54]. That is, the major peaks in the original histogram can be distinguished. The number of peaks in the smoothed histogram is considered as the number of peaks in the original histogram.

4.2.3 Selection of Luminance Distributions

Each color image can be represented by Gaussian mixtures – a more capable model to describe image illumination distributions. To reduce the computation time, the image illumination distribution at luminance domain is analyzed. Herein, each single Gaussian distribution is expressed as one peak and two valleys at luminance component. The luminance of a color image is computed first. Then, the luminance histogram $H_L(x_k)$ is computed. The histogram of an image with brightness levels in the range [0, 255] is a discrete function $H_L(x_k) = n_k$ where x_k is the ***kth*** brightness level and n_k is the number of pixels in the image having brightness level x_k. Finally, Gaussian smoothing filter is applied to smooth the original histogram to obtain the reliable peaks and valleys. Thus the unreliable peaks and valleys are removed.

We assumed that luminance distributions in images are multi-Gaussian. After the small peaks and valleys have been removed, the average differences are employed as the first derivation with which to determine the major peaks and valleys. The average difference at point *x* is defined by [54]:

$$S'_{HL}(x) = \frac{1}{\sigma_g - 1} \sum_{i=1}^{\sigma_g - 1} \frac{S_{HL}(x+i) - S_{HL}(x-i)}{2 \times i} \qquad (4.5)$$

A peak is defined as a positive to negative crossover in the first derivation of the smoothed histogram. Furthermore, a valley is defined as a negative to positive crossover. All peaks and valleys from the first derivation of the smoothed histogram are discovered. In cases where the peaks and valleys are too close, they will be removed if the distance between a valley and a peak is less than the standard deviation σ_g.The remaining peaks are the candidates of the luminance distribution in the image.

4.2.4 Space Variant Luminance Map (SVLM) :

The input RGB color image is converted to an intensity image as shown in equation (4.6), [11] :

$$I(x,y) = 0.299 \times R(x,y) + 0.587 \times G(x,y) + 0.114 \times B(x,y) \qquad (4.6)$$

Where: **R(*x*,*y*), G(*x*,*y*)**and **B(*x*,*y*)**represent the **Red**, the **Green** and the **Blue**, respectively, for the pixel at location **(*x*,*y*)**. ***I*(*x*,*y*)** represents the intensity (luminance) value of the each pixel of the intensity image.

The intensity image is low-pass filtered using a 2-D discrete Gaussian filter to estimate its illuminance as expressed in equation (4.7), [11] :

$$L(x,y) = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} I(x,y) Gaussian(x+m, y+n) \tag{4.7}$$

Where: ***L*(*x*,*y*)**represents the estimated illuminance value and the ***Gaussian(x,y)*** the 2-D Gaussian function with size m by n.

The ***Gaussian(x,y)*** is defined as shown in equation (4.8), [11] :

$$Gaussian(x,y) = q.e^{(\frac{-(x^2+y^2)}{c^2})} \tag{4.8}$$

Where ***q*** is used to normalize the Gaussian function by equation(4.9), [11] :

$$\iint q.e^{(\frac{-(x^2+y^2)}{c^2})} dxdy = 1 \tag{4.9}$$

c is the scale (Gaussian surround scale constant) that determines the size of the neighborhood.

Figure (4.4) illustrates a block diagram of the multiple Gaussian masking used for the SVLM.

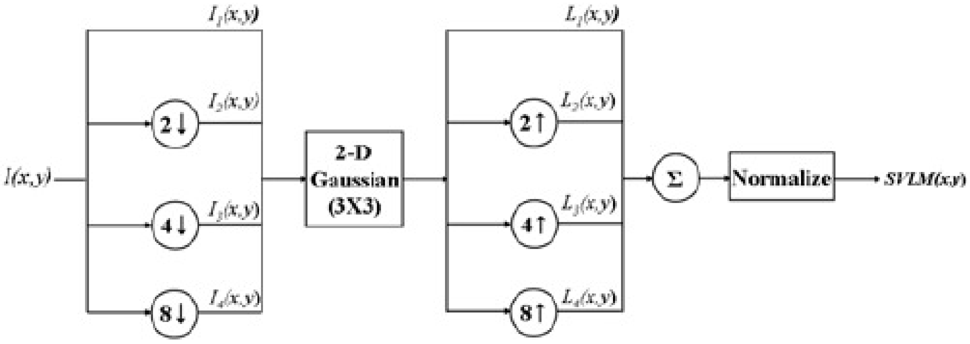


Figure (4.3) : A block diagram of the single Gaussian mask used for SVLM calculation [11].

For the computation efficiency, we used the single Gaussian mask to extract the local characteristic of the input intensity instead of employing several down-scaled sizes of the input intensity image such as 1/2,1/4,1/8 each width and height.

The normalization is obtained from equation (4.10), [11] :

$$\boldsymbol{SVLM}(x,y) = \frac{\boldsymbol{L_1}(\boldsymbol{x},\boldsymbol{y}) + \boldsymbol{L_2}(\boldsymbol{x},\boldsymbol{y}) + \boldsymbol{L_3}(x,y) + \boldsymbol{L_4}(x,y)}{4} \qquad (4.10)$$

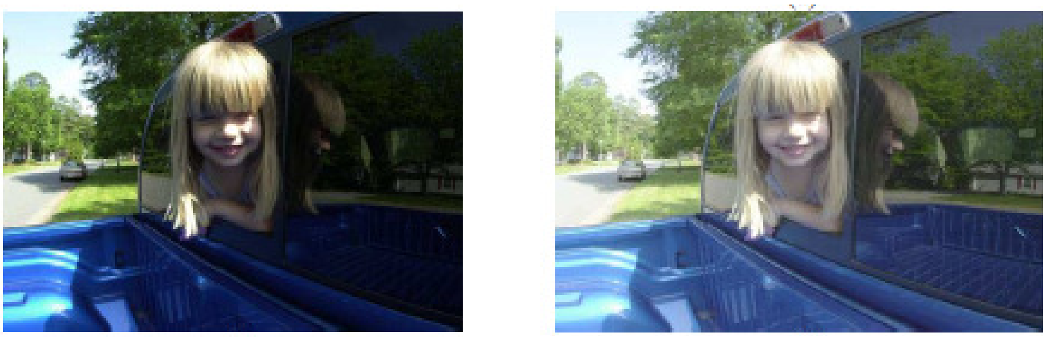
We characterized the performance of the **SVLM** in the frequency response perspective. The**2-D** Circular Zone Plate (CZP) method was employed as the input signals. The resolution of the input signals is 2048 x 2048.

4.2.5 Luminance Enhancement

The luminance enhancement has been proposed using the combination of the 2D exponential gamma correction fed by the SVLM. The pertinent local dependency obtained from the SVLM effectively enhances the luminance of the input image. Combining the input intensity $I(x,y)$ with the power factor of the **SVLM**, the 2D gamma correction can be expressed as shown in equation (4.11) [11] :

$$\boldsymbol{O}(\boldsymbol{x},\boldsymbol{y}) = 255\left(\frac{I(x,y)}{255}\right)^{\gamma} \;,\quad \gamma = \alpha^{\left(\frac{128-SVLM(x,y)}{128}\right)} \qquad (4.11)$$

Where $O(x,y)$ represents the luminance enhancement intensity value, and γ represents the exponential value including the dynamic local characteristic for the luminance enhancement.



(a) (b)

Figure (4.4) : The performance comparison of Gamma correction.
(a) The input image, (b) Conventional gamma correction ($\gamma = 0.5$) [11].

4.2.6 Contrast Enhancement

Using the enhanced luminance information above, we enhance the contrast. The visual quality improvement is accomplished using the ***SVLM(x,y)*** in the adaptive contrast enhancing process as show in equations (4.(12-14)) [11]:

$$S(x,y) = 255\left[\frac{O(x,y)}{255}\right]^{E(x,y)} \tag{4.12}$$

Where ***E(x,y)*** is :

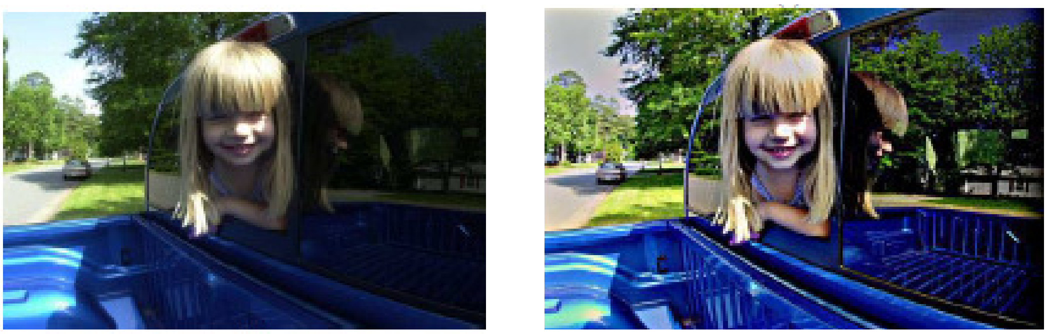
$$E(x,y) = r(x,y)^{P} = \left[\frac{SVLM(x,y)}{O(x,y)}\right]^{P} \tag{4.13}$$

and the adaptive factor P is

$$\mathbf{P} = \begin{cases} 2 & for\ \sigma \leq 40 \\ -0.025\sigma + 3 & for\ 40 < \sigma \leq 80 \\ 1 & for\ \sigma > 80 \end{cases} \tag{4.14}$$

In (4.13), ***r(x,y)*** is the ratio, and the ***P*** is an image-dependent parameter containing the standard deviation of an image to tune the contrast enhancing. The standard deviation $\boldsymbol{\sigma}$ is calculated from the ***I(x,y)*** indicating the contrast level of the input intensity image. The customized factor in (4.14) empirically obtained in our experiments.

The contrast enhancing process in equations (4.12)-(4.14) produces the output image pixels depending on their neighboring pixels. The luminance of the dark regions becomes boosted and the luminance of the bright regions becomes attenuated. Therefore, the image contrast and fine details are effectively enhanced without degrading the image quality as shown in figure (4.6).



(a) (b)

Figure (4.5) :The performance contrasts comparison [3].
(A) The input image (b) contrast image enhancement

4.2.7 The saturation enhancement

The best way to enhance the saturation contrast of a given image is to histogram equalize the saturation distribution of the image. However, the image resulting from applying saturation histogram equalization could be rather unnatural.

The color enhancement methods proposed [55] and [56] are implemented by saturating all the chromatic colors and then desaturating them using the center of gravity law for color mixture. Clearly, not all the producible colors at any luminance level cover the whole color gamut triangle. Consequently, for a specific fully saturated color, a color at the edge of the gamut triangle in the CIE xyY space might be outside the producible parallel epiped.

In [55] and [56],mixing a fully saturated color with a neutral color (white) does not always yield a producible color and an extra gamut clipping process. This problem mainly produces artifact pixels in the resultant image.

The above problem primarily arises from the incomplete separation of chromaticity and luminance components. Thus, our research proposes a color enhancement which considers the physical constraints of displays.

The two steps mentioned below achieve the proposed color enhancement. First, the enhancement procedure finds the most saturated color, which is producible while preserving the hue and the luminance. Second, the saturation ratio of color is defined and adjusted according to a specified saturation ratio transfer function.

a) *Step 1 : Finding the Most Saturated Color*

Saturating a color $\boldsymbol{C = (x, y, Y)}$ to $\boldsymbol{S = (x_s, y_s, Y_s)}$ while preserving its hue can be expressed as shown in equation (4.15) [21].

$$\begin{pmatrix} x_s \\ y_s \end{pmatrix} = \begin{pmatrix} x \\ y \end{pmatrix} + k \begin{pmatrix} x - x_w \\ y - y_w \end{pmatrix} \tag{4.15}$$

The scalar $\boldsymbol{k}$ is termed the saturation gain here. It is generally accepted that as $\boldsymbol{k}$ increases, the saturation of the resultant color also increases. Since no luminance components are modified, $\boldsymbol{Y_s}$ equals $\boldsymbol{Y}$. The saturated color $\boldsymbol{S}$ is converted back to the RGB space through equation (4.16) [21].

$$\begin{pmatrix} R_s \\ G_s \\ B_s \end{pmatrix} = T^{-1} \begin{pmatrix} X_s \\ Y_s \\ Z_s \end{pmatrix} = T^{-1} \begin{pmatrix} X_s \\ Y \\ Z_s \end{pmatrix} = T^{-1} \frac{Y}{y_s} \begin{pmatrix} x_s \\ y_s \\ z_s \end{pmatrix} \tag{4.16}$$

Where $\boldsymbol{T}$ represents the conversion matrix from **RGB** to $\boldsymbol{XYZ}$ and $\boldsymbol{z_s = 1 - x_s - y_s}$.

The dynamic range of the red, green, and blue channels of a given display is assumed to be constrained in **[0, 1]**. Consequently, given a color $\boldsymbol{C}$, the most saturated color of the same hue and with the same luminance must satisfy equation (4.17) [21].

$$\mathbf{0} \leq \begin{pmatrix} R_s \\ G_s \\ B_s \end{pmatrix} = T^{-1} \frac{Y}{y_s} \left(\begin{pmatrix} x \\ y \\ z \end{pmatrix} + k \begin{pmatrix} x - x_w \\ y - y_w \\ z - z_w \end{pmatrix} \right) \leq \mathbf{1} \tag{4.17}$$

Otherwise, this saturated color cannot be correctly produced on the display. The producible color with the largest saturation has $\boldsymbol{k}$ equal to the maximum value in the intersection of the three solution intervals of the inequalities in equation (4.17).

Replacing the largest ***k*** satisfying the inequalities(4.17) into (4.15) yields the most saturated color $S = (x_s, y_s, Y)$, which is producible.

b) *Step 2* : Adjusting the Saturation Ratio:

Step 1 obtains the most saturated color S, which can be displayed without hue shift. Adapted from the definition of colorimetric purity, in figure (4.6), we define an argument called the saturation ratio of a color *C* as shown in equation (4.18),

$$r = \frac{\overline{CW}}{\overline{SW}} \tag{4.18}$$

,where ***W*** denotes the reference white of the display in the CIE xy diagram.

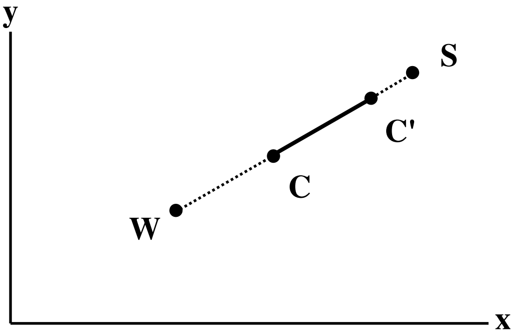


Figure (4.6) : C and C' have the same hue and luminance. C is enhanced to C' with larger saturation ratio than C by using the color gamut constraint.

While the colorimetric purity of a color indicates the amount of white mixed with the spectral color, the saturation ratio represents the quantity of white mixed with the color which could be displayed on a given display device with the maximum saturation of its hue.

The saturation ratio of an achromatic color is close to zero. While Mean colors which are almost saturated have saturation ratios very close to one. Hence, the saturation of a color is altered by tuning its saturation ratio. By increasing the saturation ratio, the color becomes more saturated [21].The adjustment over the saturation ratio ***r*** is somewhat arbitrary. However, reversing or changing the saturation relationship among pixels of a painting is undesirable. For instance, after the saturation enhancement is applied, a pixel that is originally pale blue should not be more saturated than a pixel that is originally blue. A monotonically increasing saturation ratio transfer function is used to maintain the saturation relationship among image pixels. Besides, it is not advisable to saturate colors close to the reference white, since such achromatic colors belong to a region of hue ambiguity. Figure (4.7) shows the suggested saturation transfer function.

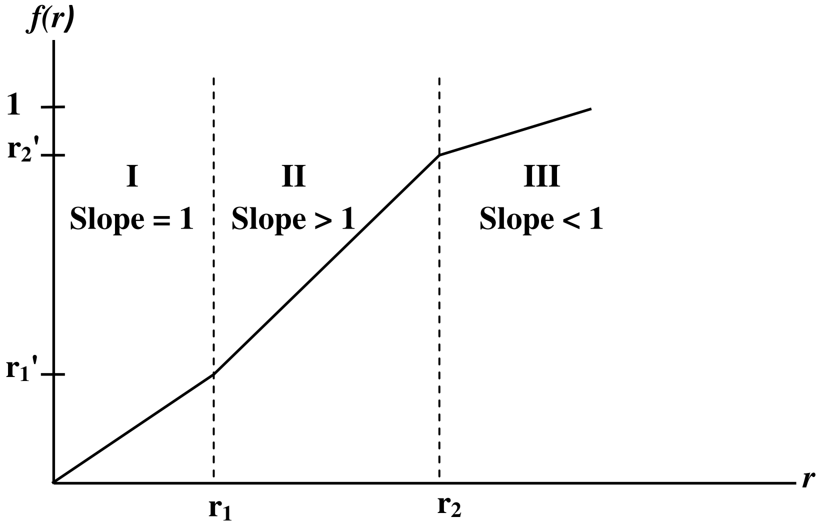


Figure (4.7) : Possible choice of the saturation ratio transfer function for saturation enhancement.

For colors with small saturation ratio, below the threshold $\mathbf{r_1}$, the saturation remains unchanged owing to hue ambiguity at low saturation, the colors in the middle saturation region, with saturation ratio below $\mathbf{r_2}$, but larger than $\mathbf{r_1}$, are enhanced more than the colors with low or high saturation. Resorting to a certain saturation transfer function ***f(r)***, saturating a pixel $C = (x\ ,\ y\ ,\ Y)$ with original saturation ratio r to $C' = (\ x'\ ,\ y'\ ,Y\ )$can be represented as shown in equation (4.19) [21].

$$\begin{pmatrix} x' \\ y' \end{pmatrix} = \left(1 - f(r)\right) \begin{pmatrix} x_s \\ y_w \end{pmatrix} + f(r) \begin{pmatrix} x_s \\ y_s \end{pmatrix} \tag{4.19}$$

where **(x_s, y_s)** is the most saturated color from step 1.The proposed saturation enhancement can be easily controlled by ***f(r)*** as seen in figure (4.8), the effect of saturation enhancement as done in the acient painting.

(A) **(B)**

Figure (4.8) :The saturation performance [6].
(A) The original image (B) the enhanced saturation image.

4.3 Phase (2) The SSGA enhancement algorithm:

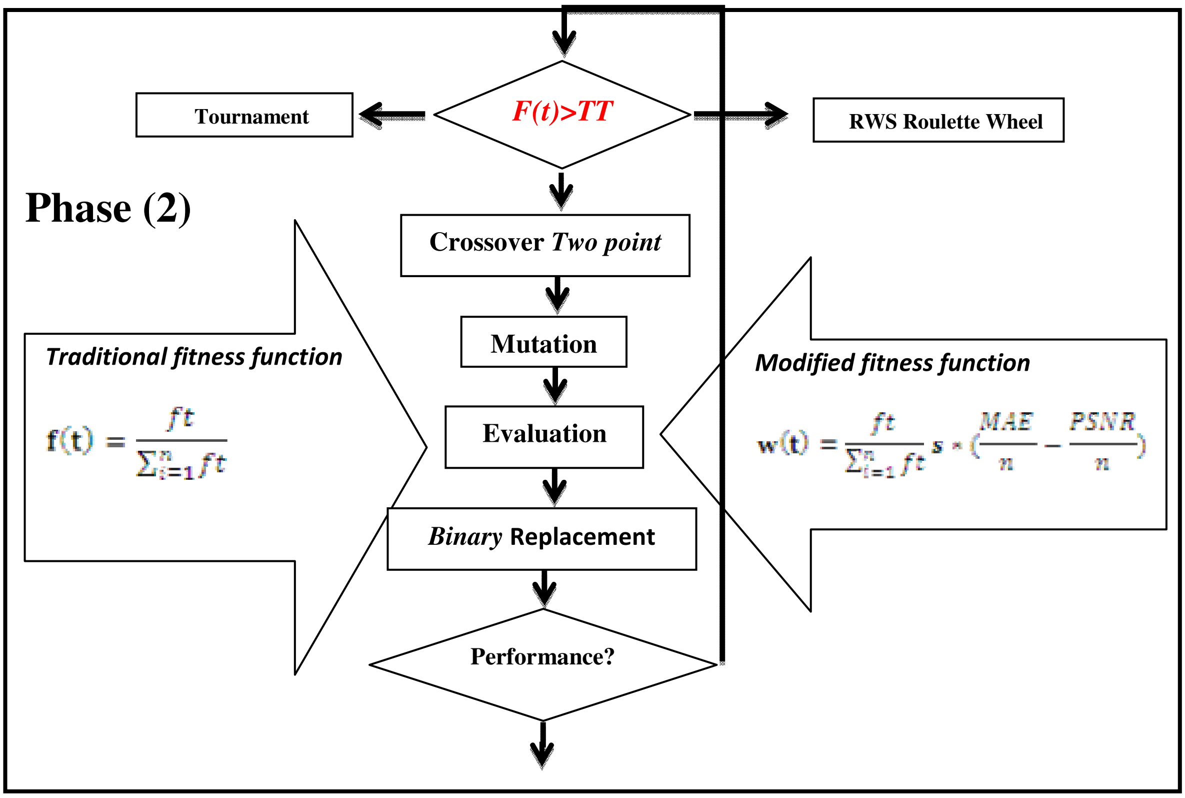


Figure (4.9) : SSGA enhancement model.

Before proceeding with the description of our SSGA-based enhancement Algorithm, let us briefly review the basic strategies for image enhancement. Image enhancement techniques can be classified in four main categories as follows (Jabraouti2011) [9]: point operations, spatial operations, transform operations and pseudocolouring methods.

Point operations which include contrast stretching, window slicing, histogram modeling, are zero-memory operations that remap a given input gray-level into an output gray-level,

According to a global transformation these methods have the disadvantage of (1) treating the image globally, (2) not being able to differentiate between several areas of the image that might require different levels of contrast enhancement. In these techniques, linear contrast stretching and histogram equalization are the most widely used. Linear contrast stretching employs a linear transformation that remaps the gray-levels in a given image to fill the full range of values.

Histogram equalization applies a transformation to the input image so that the output image will have a uniform histogram (that is, the gray-levels have a relative frequency that is uniformly distributed). Spatial operations include noise smoothing, median filtering, unsharp masking, low pass, band pass and high-pass filtering.

In this category of methods, spatial operations are performed in local neighborhoods of input pixels, these operations being often convolutions with Finite Impulse Response filters (FIR), called spatial masks.

Spatial operations might suffer from excessively enhancing the noise in the image or conversely by smoothing the image in areas that need sharp details .Transform operations include linear filtering, root filtering, homomorphic filtering.

These are techniques in which zero-memory operations are performed on a transformed image followed by the inverse transformation, the result being the enhancement of the image in particular spatial frequency domains.

Pseudocolouring methods include false colouring and pseudocolouring, and are based on the fact that humans can distinguish many more colours than gray-levels, therefore gray scale images are artificially “coloured” using a proper colour map.

The disadvantage of these methods comes from the non-uniqueness of the colour mappings, extensive interactive trials being required to determine an acceptable mapping.

Our model of image enhancement takes into account several factors: locality and adaptability of the method to the given image, as opposed to classical global enhancement methods; automation of the image enhancement process; robustness, that is producing good enhancement results on a large category of images.

For previous reasons, we use the SSGA-based image enhancement method. Before starting the SSGA processes we should convert the image to the chromosomes and this can be done by the Block processing algorithm and Objective enhancement criterion.

4.3.1 Block processing algorithm and chromosome representation

Local enhancement methods apply transformation functions that are based on the color level distribution, or other properties, in the neighborhood of every pixel in a given image (Gonzales 1987) [58].

An example of a local enhancement method is adaptive histogram equalization where each pixel is assigned a value according to a histogram equalization transform performed in the $n \times n$ neighbourhood of that pixel. Adaptive histogram equalization has shown good results in medical imaging [59]. This approach is computationally expensive as histogram equalization is a time consuming strategy, and if it is applied to each pixel in the image it becomes even more time consuming.

We have chosen to use a less time consuming method similar to statistical scaling presented in(Gonzales 1987) **[58]**. The method applies to each pixel at location (x, y) using the following transformation[34]:

$$g(x,y) = \left\{k \frac{M}{\sigma(x,y)+b}\right\}.[f(x,y) - c.m(x,y)] + m(x,y)^a \tag{4.27}$$

$$0.5 < k < 1.5; a \in \psi_1, b \in \psi_2, c \in \psi_3 \; with \; \psi_1, \psi_2, \psi_3 \subset R^+$$

Where $m(x, y)$ and $\sigma(x, y)$ are the gray-level mean and standard deviation computed in a neighbourhood centered at(x, y) and having $n \times n$ pixels. **M** is the global mean of the image, $f(x, y)$ is the gray-level intensity of input image pixel at location (x, y),while $g(x, y)$ is the pixel's output gray-level intensity value, at the same location and **a**, **b**, **c**, k are the parameters of the method. The original method Gonzales 1987) [58] allowed only for a reduced range of possible output transformation, as constants in equation (4.27) where taken as $b = 0$, $c = 1$, while the last term k was not present.

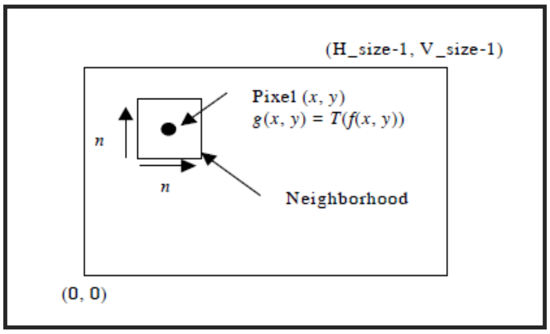


Figure (4.10) : Block processing applying to each pixel in the image the operation T (●) in the neighborhood.

We have broadened the spectrum of the transformation output range by modifying the original method as shown in equation (4.27). In our modified method $b \neq 0$ allows for zero standard deviation in the neighbourhood, $c \neq 0$ allows for only a fraction of the mean $m(x, y)$ to be subtracted from the original pixel gray-level, while the last term may have a brightening and smoothing effect on the image. The quantities $m(x, y)$ and $\sigma(x, y)$ depend on the neighbourhood of the pixel, therefore they are dependent on the local information. The parameters of the method a, b, c and k are the same for the whole image.

The task for the GA is to find the best combination of the four parameters, a, b, c and k , according to an objective criterion that describes the contrast of the image. The representation of the chromosomes is therefore a string of 4 real genes denoting the four parameters. This representation is given in figure (4.11), where T(●) designates the operation given in equation (4.27).

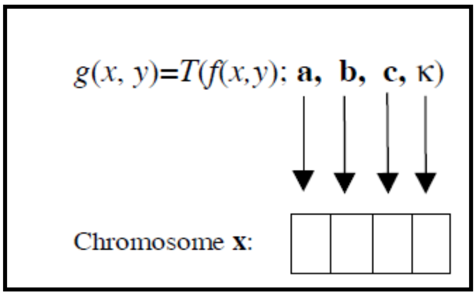


Figure (4.11) :Chromosome representation.

4.3.2 Objective enhancement criterion and fitness function

In order to apply an automatic image enhancement technique, which does not require human intervention, and no objective parameters given by the user, a criterion for enhancement method should be chosen. This criterion will be directly related to the fitness function of the GA. Let us proceed by noting that a good contrast and enhanced image has a high number of edgels (that are pixels belonging to an edge). Also, an enhanced image has a high intensity of the edges compared to a non-enhanced variant of the same image [60]. The number and intensity of edgels are not enough to describe a valid fitness criterion for a more *naturally* enhanced image.

The problem is that an image can have an extreme contrast with sharp transitions from white to black (or conversely, from black to white), and a relatively small number of gray levels (histogram of the image with two peaks: each one placed at the extremities of the gray-level intensity interval).In this case , the image will have a relatively high number of edges and a very high intensity of edges. A criterion that is proportional to number and intensities of edgels might give an oversized credit to an image that doesn’t have a natural contrast. What is needed is a quantification of the number of gray-levels present in the image, or equivalently the histogram of the image should approach the uniform distribution, as in the case of histogram equalization techniques.

It has been found that the following fitness (to be maximized) is a good choice for an objective criterion [34]:

$$F(x) = \log\left(\log\left(E(I(x))\right)\right) . \frac{n\_edgels(I(x))}{H\_size \times V\_size} . H(I(x)) \tag{4.28}$$

In equation (4. 28), function ***F*(x)** denotes the fitness function applied to chromosome **x**, ***I*(x)** denotes the original image ***I*** with the transformation ***T*** applied according to equation (4.27),where the respective parameters ***a*, *b*, *c*, *k*,** are given by the chromosome **x = (*a b c k*)**. ***E*(*I*(x))** is the intensity of the edges detected with a Sobel edge detector [61], where the detector is applied to the transformed image ***I*(x)**, ***n_edgels*** denotes the number of edgel pixels as detected with the Sobel edge detector. The term ***H(I(x))*** is a measure of the entropy in the image ***I(x)***. ***H_size***, ***V_size*** are the horizontal and vertical sizes (number of pixels in each direction) of the image. The Sobel detector used is an automatic threshold detector [62].

The sum of intensities of edges ***E*(*I*)** included in the enhanced image is calculated by the following expression (4. 29) [34]:

$$E(I) = \sum_x \sum_y \sqrt{\delta h_I(x,y)^2 + \delta v_I(x,y)^2} \tag{4.29}$$

Where :

$$\delta h_I(x,y) = g_I(x+1,y-1) + 2g_I(x+1,y) + g_I(x+1,y+1) -$$

$$g_I(x-1,y-1) - 2g_I(x-1,y) - g_I(x-1,y+1)$$

$$\delta v_I(x,y) = g_I(x-1,y+1) + 2g_I(x,y+1) + g_I(x+1,y+1) -$$

$$g_I(x-1,y-1) - 2g_I(x,y-1) - g_I(x+1,y-1)$$

As the SSGA tries to find the solution **x_sol** that maximizes the fitness, it means that we perform the operation described in equation (4.27), as to : a) *increase the relative number of edgels* in the image; b*) increase the overall intensity of edgels*, and c) *increase the entropic measure* in the image. Increasing the measure of entropy means, equivalently, transforming the histogram of the image to one that approximates a uniform distribution. According to the definition of histogram equalization (Jain 2009)[63], this means we actually perform histogram equalization by maximizing the measure of entropy. The model has chosen the entropic measure because it is easy to integrate into the fitness function. Note that we used a log-log measure of the edge intensity not to over emphasize this parameter when compared to the others in the fitness function. Large values for edge intensity might produce extreme contrast, and un-natural images [34].

Initial Population Generation

In our model we start the steady state genetic algorithm by building an initial population, the initial population size is fixed at 40. The GA needs a number of initials segmentations as the initial population to start with. The choice of the population size is very important. If the selected population size is too small, as shown in (Raghad 2010) [64], then the algorithm may result in premature convergence without finding an appropriate solution.

On the other hand, a large population size will lead to long computation time. The previous experiments show that premature convergence is likely to occur when the population size is smaller than 30. In this research, the population size is set to 40, which appears to be appropriate to avoid the problem of premature convergence.

4.3.3 Selection

The selection strategy addresses which of the chromosomes in the current generation will be used to reproduce offspring in hopes that next generation will have even higher fitness. The selection operator is carefully formulated to ensure that better members of the population (with higher fitness) have a greater probability of being selected for mating or mutate, but that worse members of the population still have a small probability of being selected.This is important to ensure that the search process is global and does not simply converge to the nearest local optimum.

Different selection strategies have different methods of calculating selection probability [35].The differing selection techniques all develop solutions based on the principle of survival of the fittest. Fitter solutions are more likely to reproduce and pass on their genetic material to the next generation in the form of their offspring. There are two major types of selection schemes will be discussed and experimented in our thesis; tournament selection, roulette wheel and rank-based roulette wheel. The subsequent section will describe the mechanism of each strategy.

a) Tournament Selection

Tournament selection is probably the most popular selection method in genetic algorithm due to its efficiency and simple implementation [65].

In tournament selection, *n* individuals are selected randomly from the larger population, and the selected individuals compete against each other. The individual with the highest fitness wins and will be included as one of the next generation population. The number of individuals competing in each tournament is referred to as tournament size, commonly set to 2 (also called binary tournament). Tournament selection also gives a chance to all individuals to be selected and thus it preserves diversity, although keeping diversity may degrade the convergence speed. Fig. (4.11) illustrates the mechanism of tournament selection , The tournament selection has several advantages which include efficient time complexity, especially if implemented in parallel, low susceptibility to takeover by dominant individuals, and no requirement for fitness scaling or sorting [65].

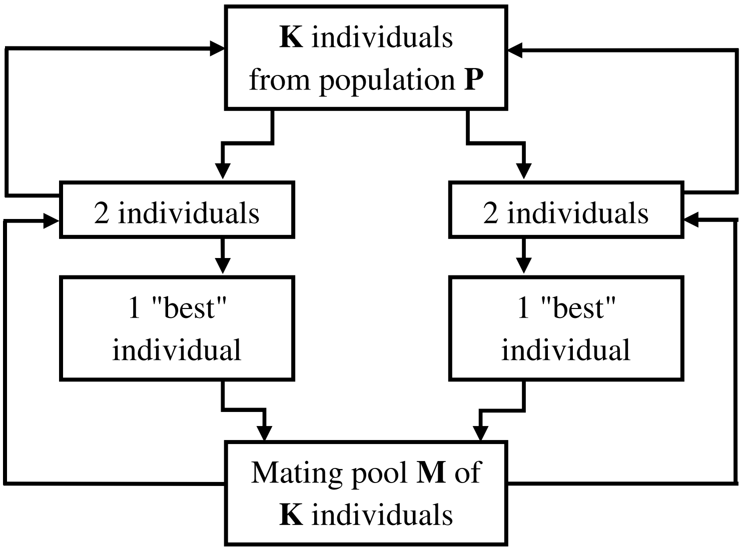


Figure (4.12) : Selection strategy with tournament mechanism.

In tournament selection, larger values of tournament size lead to higher expected loss of diversity [66, 67]. The larger tournament size means that a smaller portion of the population actually contributes to genetic diversity, making the search increasingly greedy in nature. There might be two factors that lead to the loss of diversity in regular tournament selection; some individuals might not get sampled to participate in a tournament at all while other individuals might not be selected for the intermediate population because they lost a tournament.

b) Proportional Roulette Wheel Selection

In proportional roulette wheel, individuals are selected with a probability that is directly proportional to their fitness values an individual's selection corresponds to a portion of a roulette wheel.

The probabilities of selecting a parent can be seen as spinning a roulette wheel with the size of the segment for each parent being proportional to its fitness. Obviously, those with the largest fitness (i.e. largest segment sizes) have more probability of being chosen. The fittest individual occupies the largest segment, whereas the least fit have correspondingly smaller segment within the roulette wheel. The circumference of the roulette wheel is the sum of all fitness values of the individuals. The proportional roulette wheel mechanism and the algorithm procedure *are* depicted in Fig. (4.12) and Fig (4.13)respectively. In Fig (4.12) when the wheel is spun, the wheel will finally stop and the pointer attached to it will point on one of the segment, most probably on one of the widest ones. However, all segments have a chance, with a probability that is proportional to its width. By repeating this each time an individual needs to be chosen, the better individuals will be chosen more often than the poorer ones, thus fulfilling the requirements of survival of the fittest. Let f_1 , f_2 , … , f_n be fitness values of individual 1, 2, … , n. Then the selection probability, P_i for individual i is define as,

$$\boldsymbol{P_i = \frac{f_i}{\sum_{j=1}^{n} f_j}} \tag{4.30}$$

The basic advantage of proportional roulette wheel selection is that it discards none of the individuals in the population and gives a chance to all of them to be selected. Therefore, diversity in the population is preserved. However, proportional roulette wheel selection has few major deficiencies. Outstanding individuals will introduce a bias in the beginning of the search that may cause a premature convergence and a loss of diversity.

For example, if an initial population contains one or two very fit but not the best individuals and the rest of the population are not good, then these fit individuals will quickly dominate the whole population and prevent the population from exploring other potentially better individuals. Such a strong domination causes a very high loss of genetic diversity which is definitely not advantageous for the optimization process.

On the other hand, if individuals in a population have very similar fitness values, it will be very difficult for the population to move towards a better one since selection probabilities for fit and unfit individuals are very similar.

Moreover, it is difficult to use this selection scheme on minimization problems whereby the fitness function for minimization must be converted to maximization function as in the case of TSP. Although to some degree this solves the selection problem, it introduces confusion into the problem. The best chromosome in the TSP problem, for instance, will continually be assigned a fitness value that is the maximum of all other fitness functions, and thus we are seeking the minimum tour but the fitness maximizes the fitness value.

As a consequence several other selection techniques with a probability not proportional to the individual's fitness values have been developed to encounter proportional selection problem. In general there are two types of such non-proportional selection operators: tournament based selection techniques which already been described in the previous section, and the rank-based selections that assign the probability value depending on the order of the individuals according to their fitness values, which will be discussed in the following section.

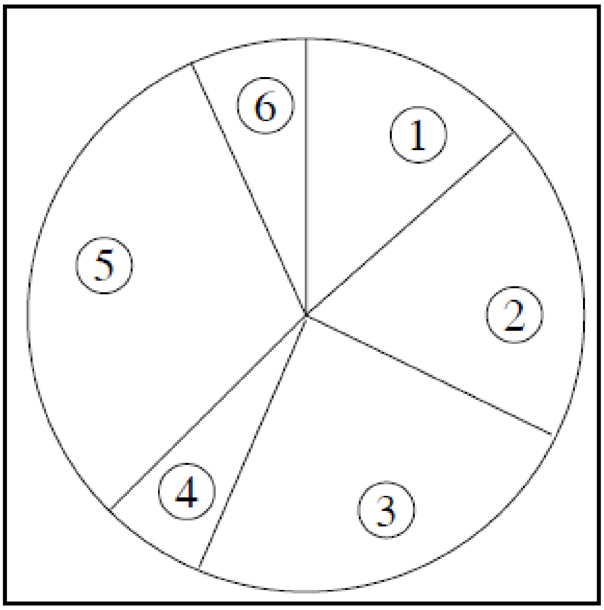


Figure (4.13) :Figure of the proportional roulette wheel.

```
Procedure: Roulette wheel selection
While population size <pop_size do
    Generate pop_size random number r
    Calculate cumulative fitness, total fitness (Pi) and
    sum of proportional fitness (sum)
    Spin the wheel pop_size times
    If sum < r then
        Select the first chromosome, otherwise, select $j^{th}$
    End If
End While
Return chromosome with fitness value proportional to the
size of selected wheel selection
End Procedure
```

Figure (4.14) :Procedure of the proportional roulette wheel [71].

We use the standard 2-tournament selection operator. In this selection procedure, two individuals are chosen randomly, and the element with the lowest makespan is selected. Afterwards, we determine randomly whether a or b represents the father F. The other parent represents the mother M. The crossover used in this work is the standard 2-point crossover operator which exploits the advantages of the codification chosen, randomly mating pairs of individuals of the population. The crossover operation is performed with a probability of P_{cross}. If the operator is not performed they remain unaltered for the next stage. P_{cross} is set to 0.8. the result is shown in section 5.3.

Selection and crossover

Both the selection and crossover of the real-coded GA have been used to insure a steady convergent behavior of the GA. The trade-off we had to make is the well-known trade-off between exploration and exploitation present in any search method including GA.

The convergent exploitation assured by selection and crossover should well-balance the wide exploration effect achieved by our mutation operator.

The selection method was chosen as a combination between binary tournament which has a constant and relatively high selection pressure [69], with a *K*–elitist scheme [68] that assures the preservation of the *K* best individuals in the population.

The crossover operation was chosen such that the correlation between the parents and the children would be high, again to assure an exploitative behaviour of the search algorithm.

4.3.3 Crossover unit

GA has two main types of operator which are used to reproduce new individuals in the next generations. These operators are: Crossover and Mutation.

Crossover is one of the main characteristics which distinguishes GA from other revolution techniques. It is a process of exchange of genes between two individual (chromosomes) to reproduce new individuals which inherent their parent's behavior.

Crossover is used ,firstly, to represent the search in the parameters space. Secondly, it is concerned in finding a way to keep the information stored by parents chromosomes because they are considered good chromosomes resulted from selecting process.

All crossover methods depend on encoding method and problem type. There are many common crossover strategies such as [50, 70]:Two-point crossover (2x).

Two-point crossover is different in its high probability for not tearing up the edge of chromosome. Instead, it has an exceptional ability in tearing genes of chromosomes since there are two crossover points. Two-point crossover(2x) has better performance than 1x or at least they are equivalent [71]. Two-point crossover(2x) is used widely in SSGA so that we used it in our thesis.

Crossover is accomplished by using crossover probability **Pc (0.6 < Pc < 0.9)** and selects random position $\mathbf{k_1, k_2}$ ($\mathbf{k_1, k_2 \in \{ 1, 2, ... , \mathit{l}\text{-}1\}, k_1 < k_2}$) where the genes between $\mathbf{k_1}$ and $\mathbf{k_2}$ are switched [71]. Figure (4.15) shows how 2x works.

Single point crossover (1x) still suffers from a shortage in diversity within the community, and it tears up the edge of one parents chromosome. To get over these problems, researchers suggest using an alternative method called Two-point crossover.

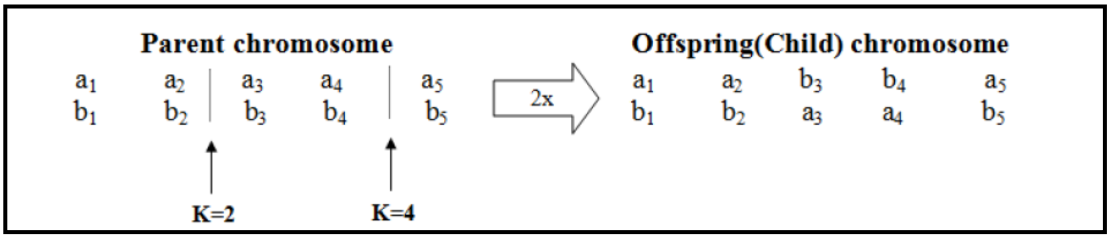


Figure (4.15) : 2X crossover

Crossover value is set to the default value 0.8, while testing our algorithm with other crossover values it gives long computation time and bad results. The result is shown in section 5.3.

4.3.4 Mutation unit

Mutation is a random changing of genes in chromosome. The process of changing genes is concerned with introducing certain diversity in the population. One of the strong points of mutation is producing new individuals different from the existing ones and to get more exploration in order to discover unknown situations in the search space. To apply mutation, compare the given value of mutation probability ($\mathbf{P_m}$) with a random number. If the first value is larger than the second one, perform mutation otherwise, do nothing. Repeat that for all chromosome gene's and for all chromosomes in generation. The way of performing mutation depends on the used encoding method. For example, in binary encoding, flip bits if random number is less than $\mathbf{P_m}$, otherwise, do nothing for all bits in the chromosome as shown below :

Before Mutation	**After Mutation**
11111	**00101**

In SGA the mutation probability (Pm) is low in order to reduce the impact of mutation on tearing chromosomes. While SSGA has higher mutation probability than SGA. The main idea is to keep community stable even if we use a high rate of mutation because we will replace a low number of individuals each time. As a result, this will not affect SSGA performance. In addition, using a high rate of mutation will increase the exploration effect for GA.

After performing evaluation, crossover and mutation on selected chromosomes, the next decision will be how we can add new chromosome to the community of chromosomes by using Replacement process.

In addition, there is an adaptive method for mutation where the value of probability for mutation ($\mathbf{P_m}$) will be increased or decreased according to the performance of problem solution and how close we are from solution.

The uniform mutation value in our thesis is set to the uniform mutation while the other values gives bad results. In the migration process the fraction value is set to 0.2 and the interval value is 20.

In our model, we use the insertion operator for the activity list and the standard flip bit for genes. The insertion operator works as follows: for each activity in the activity list AL, a new position is randomly chosen between the highest position of its predecessors and the lowest position of its successors. The activity is inserted into the new position with a probability of $P_{muta} = 0.05$. The genes could be altered with the same probability.

4.3.5 Replacement unit

Replacement is used as a deletion process performed on the worst individuals in order to be replaced by better new individuals. We used the Binary Tournament Replacement (BTR).

Binary Tournament Replacement (BTR)[71]**:** BTR is intended for binary sets of chromosomes to replace them by the worst chromosome from previous generations which have been selected randomly. The following equation explains BTR:

$$\mathbf{Replace}_{\ n} = \begin{cases} \mathbf{indi} & \mathbf{if\,F(indi) < F(indj)} \\ \mathbf{indj} & \mathbf{otherwise} \end{cases} \tag{4.31}$$

$$For\ n = \{1, 2\}, random\ number\ i, j \in \{1, 2, \dots \dots \dots, Npop\}, i \neq j$$

$Where$:

$\mathbf{replace_n}$: $individual\ n\ that\ will\ be\ replaced,$

$\mathbf{F(ind_i)}$: $fitness\ of\ indivual\ i,$

$\mathbf{F(ind_j)}$: $fitness\ of\ indivual\ j.$

BTR sustains better individuals by performing replacement always with better individuals [71]. Furthermore, the best individual will never be replaced. To enhance the probability and to sustain the best individuals, in our thesis we used the Binary Tournament Replacement (BTR).

4.3.7 Stopping condition unit

This unit uses various stopping conditions, the number of generation has been used 100, time and fitness have been used the default values.

The stall generation has been used the default value 50, the function tolerance has been used the default values1 $\times 10^{-6}$, and the nonlinear constraint tolerance has been used same values 1×10^{-6}. Figure (4.15) the modification that has been done on the SSGA.

Step 1 :

Initialize t = 0

P (t) // P (t) = Population

Step 2 :

Assume a source image ***f(i,j)*** is given that contains **M** by **N** and a reconstructed image F(i,j) where F is reconstructed by decoding the encoded version of ***f(i,j)***.

Step 2.1: Calculate **MAE** as shown in equation (4.32):

Error metrics are computed on the luminance signal only so the pixel values ***f(i,j)*** range between black (0) and white (255). First the mean absolute error of the reconstructed image is computed (MAE) as follows:

$$\mathbf{MAE} = \frac{1}{MN}\sum \quad \sum(F(i,j) - f(i,j)) \qquad (4.32)$$

The summation is over all pixels. PSNR in decibels (dB)[4] is computed by using:

Step 2.2 : Calculate **PSNR** from equation (4.33), where:

$$\mathbf{PSNR} = \log_{10}(\frac{255^2}{M}) \qquad (4.33)$$

Step 3:

Calculate the new suggested fitness function as shown in equation (4.34):

$$\mathbf{fw(t)} = \frac{ft}{\sum_{i=1}^{n} ft} * (\frac{MAE}{n} - \frac{PSNR}{n}) \qquad (4.34)$$

Step 4 :

Perform SSGA perorations s

Step 4.1: Selection P(t+1) from P(t)

Stop 4.2 : Perform Crossover on P(t+1)

Step 4.3 : Perform Mutation on P (t+1)

Figure (4.16) :The modification that has been done on the SSGA.

4.4 Phase three the testing phase

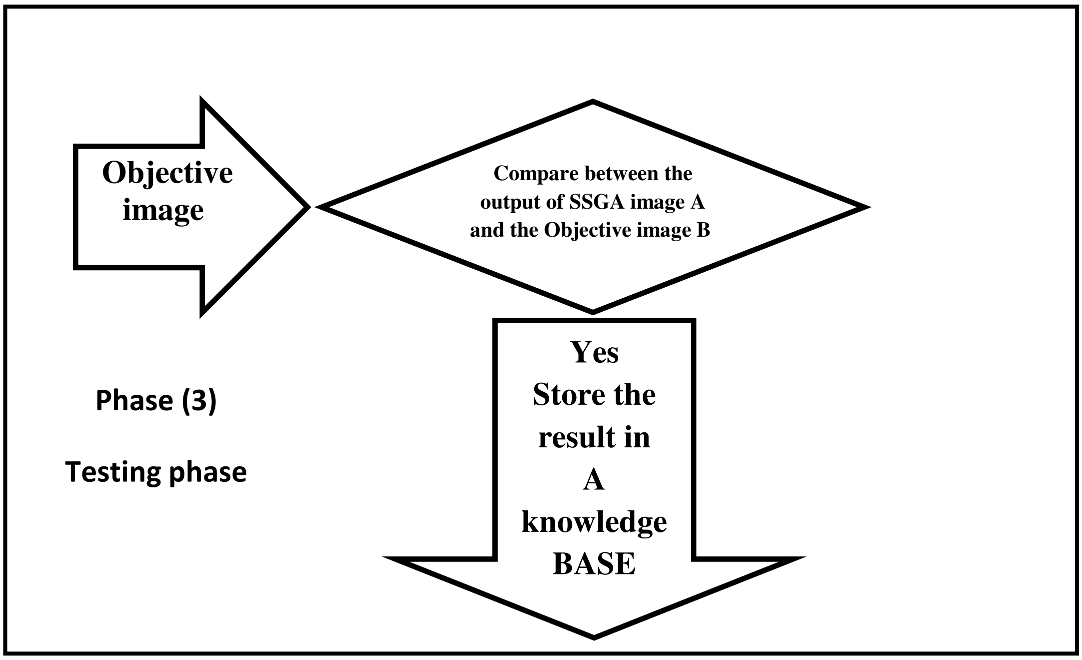


Figure (4.17) : Representation of testing phase.

After performing **SSGA** using modified or traditional fitness function**,** on the data from phase (3) we ensure that image should satisfy the conditions of segmentation and then we compare the SSGA result with objective image.

We need to ensure that the image has good segmentation rate and less noise. If the result identifies the objective image then we will store the result in knowledge base, If it doesn't identify we may repeat the **SSGA** with different type of parameters, to get better performance, There are three basic approaches for evaluating the effectiveness of a segmentation method:

i. **Subjective evaluation**: in which a human visually compares the image segmentation results for separate segmentation algorithms.

ii. **Supervised evaluation**: in which a segmented image is compared against a manually-segmented or pre-processed reference image.

iii. **Unsupervised evaluation**: enables the objective comparison of both different segmentation methods and different parameterizations of a single method, without requiring human visual comparisons or comparison with a manually-segmented or pre-processed reference image.

We will use the supervised evaluation in our proposed model. Also, we will use the **Dice Similarity Coefficient (DSC**) and the **partial Hausdorff distance** (**H**) for evaluating the performance of our algorithm.

The **Dice Similarity Coefficients DSC** [73] provides a measure of the degree of overlap between two segmentations of the **result image A** and the **objective image B** as:

$$\boldsymbol{DSC(A,B)} = \frac{2\|A \cap B\|}{(\|B\| + \|A\|)} \tag{4.35}$$

Where $\|\quad\|$ is the Norm.

A DSC of 1 indicates *a perfect match* and 0 indicates *no match.*

The **partial Hausdorff** [72] distance is derived between the boundary points of two contours. If $\boldsymbol{A} = \{a_1, \dots, a_p\}$ and $\boldsymbol{B} = \{b_1, \dots, b_q\}$ be finite sets of points on two images then the partial Hausdorff distance between them.

$$\boldsymbol{H(A,B)} = \max\left(h(\boldsymbol{A},\boldsymbol{B}), h(\boldsymbol{B},\boldsymbol{A})\right) \tag{4.36}$$

Where : $h(\boldsymbol{A},\boldsymbol{B}) \;=\; \max_{a \in \boldsymbol{A}} \min_{b \in \boldsymbol{B}} \|a - b\|$

The function $h(\boldsymbol{A},\boldsymbol{B})$ takes each point in $\boldsymbol{A}$ and finds the closest point in $\boldsymbol{B}$ from that point. It then ranks the points in $\boldsymbol{A}$ based on the distance values and finds the point with the greatest "mismatch". Thus, the partial Hausdorff distance is a measure of the distance of the two images.

Note in testing phase we will make comparison between **SGA** and **SSGA**, and compare the performance time of each method to check the efficiency of our model. Also to evaluate the performance of our SSGA model we will use the statistical properties of image. Therefore the image is divided into possible number of non-overlapping 50 x 50 pixel blocks.

4.5 Qualitative attributes of an image

1) **PSNR** (peak signal-to-noise ratio) :- Ratio between the maximum possible poser of a signal and the power of corrupting noise that affects the fidelity of its representation.
    - Measure of quality of reconstruction.
    - Signal in this case is the original data, and the noise is the error.
2) **MSE** (Mean Square Error) :- The MSE is the cumulative squared error between the compressed and the original image, whereas PSNR is a measure of the peak error.

$$PSNR = 20\, log_{10}\left(\frac{255}{\sqrt{MSE}}\right) \tag{4.37}$$

    - A lower value of MSE means lesser error, and as seen from the inverse relation between the MSE and PSNR, this translates to a high value of PSNR. Logically, a higher value of PSNR is good because it means that the ratio of Signal to Noise is higher. Here, the 'signal' is the original image, and the 'noise' is the error in reconstruction. So, having a lower MSE (and a high PSNR), is a better one.
3) **RMSE** (Root-Mean-Square Error) :- To get a measure of how similar two images are, you can calculate the root-mean-square (RMS) value of the difference between the images. If the images are exactly identical, this value is zero. The following function uses the difference function, and then calculates the RMS value from the histogram of resulting image.
4) **LMSE** :- Producing the least mean squares of the error signal (difference between the desired and the actual signal). "Least mean square" means that you :-
    - Calculate the difference between the data value and the model prediction at several different places (this is called the error).

- Square the error to make all values positive (square).
- Calculate the average (mean square).
- Find the model alternative that gives the smallest error (least mean square).

5) **Normalized Cross Correlation** :- The Cross-Correlation function can be described as:

$$CrossCorr(s,t) = \sum_x \sum_y R(x,y) I(x-s, y-t) \tag{4.37}$$

Where,

I : input image intensity , R : reference image intensity and the summation is taken over the region (s , t) where R and I overlap. For any value of (s , t) inside R(x , y) the Cross Corr(s , t) indicates the position where I(x , y) best matches R(x , y).

$$NCC = \frac{1}{var(Y)} \sum_b \frac{num\ Y(b)}{num\ TotY} varY(b) \tag{4.38}$$

The correlation ratio ranges from 0 for very image to 1 for very bad image. Based Upon these parameters, image can be judged either it's a good or bad image.

Chapter Five 5

Results of the Enhancement

5.1 Overview

Chapter 5 includes the results that have been done on the images, with various methods such as histogram equalization, the brightness, Contrast Modification, SVLM method and DCT method.

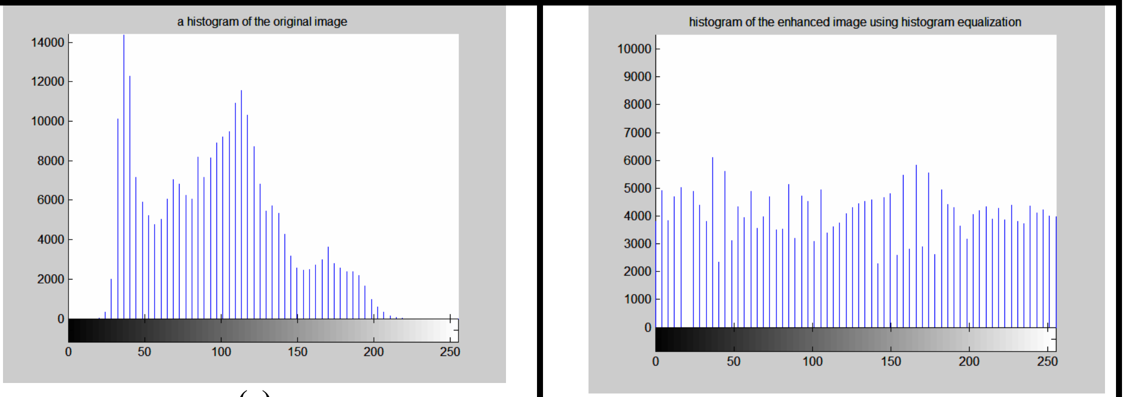
5.2 Results related to SSGA colored enhancement method

Figure (5.1) : The colored image enhancement

The image shown in Fig.(5.1) (a), is used for testing our algorithm, this image had a poor contrast. The resulted image after executing our proposed algorithm (SSGA) is shown in Fig.(5.1) (b). We can observe from the resultant image, that it has more contrast than the input image. This shows that our algorithm enhancing the image in contrast. The following figure show Comparison between the input image and after the contrast enhancement using the histogram equalization.

(a)
Original image

(b)
contrast enhancement using histogram equalization



(c)
Original image histogram

(d)
Histogram after the contrast enhancement

Figure (5.2) : Comparison between the input image and after the contrast enhancement.

We apply our algorithm, SSGA enhancement method, to the famous image Luna and try to enhance it by the histogram equalization as illustrated in Fig. (5.2) (a) and (b), where the first image (a) is an original image and the second one (b) is the result of the histogram equalization. This result shows the high performance of the histogram equalization in enhancing the contrast of an image as a consequence of the dynamic range expansion, which can be easily understood by comparing the respective histograms of those images shown in Fig. (5.2) (c) and (d). The original image has the high contrast, while the enhancement result of histogram equalization has the highest brightness.

Figure (5.3) : Results on Luna image. (a) Original Image (b) proposed method (SSGA) (c) S-type enhancement with n = 2 and m = 1.5, (d) histogram equalization (e) Yang et al.'s method in LHS system, and (f) Weeks et al.'s method.

Figs. (5.3) provide results of applying our proposed algorithm SSGA , Yang et al. [76] and Weeks et al.'s [75] methods on Luna. Note that the effect of clipping is not distinctly visible in these images. Our proposed algorithm, SSGA, preserves the order of occurrence of intensity. It may also be stated that, visually, edges are not deleted in the enhanced versions of the artificial image, using the proposed histogram equalization method and the S-type function based scheme. Weeks et al. have applied normalization to bring back the out of bounds values to within the bounds. Effect of it can be seen that the image (d) in Fig. (5.3) is not as bright as the other images in the respective figures. Equalization of saturation sometimes degrades the quality of the image since it leads to very large saturation values that are not present in the natural scenes [74]. Sometimes, increase in both luminance and saturation cause unnatural color. This can be observed in the case of Luna image [Fig. 5(d)]. The feathers in the hat of Luna look different from the original. In the original these have low luminance, thus look black. After the enhancement, with the increase in saturation as well as luminance, the colors of these pixels have been changed. On the other hand, the proposed enhancement scheme does not distort the image. The output obtained indicates that the proposed scheme provides acceptable enhancement with Luna image.

5.2 Based on following, results calculate :-

- A lower value for MSE means smaller error, and as seen from the inverse relation between the MSE and PSNR, this translates to a high value of PSNR. Logically, a higher value of PSNR is good because it means that the ratio of Signal to Noise is higher. Here, the 'signal' is the original image, and the 'noise' is the error in reconstruction. So our results having smaller MSE and a higher PSNR, it is a better one. High PSNR means less noise in image and Low value of RMSE indicates good contrast.
- If RMSE approaches zero means we have good contrast.
- The correlation ratio, CR, ranges from 0 to 1, if it's close to one mean we have bad image, otherwise we have good image .

No.	Enhancement Method	PSNR	MSE	RMSE	UIQI	MAE
1.	proposed method	18.3769	952.34	30.8510	0.3474	6.3129
2.	S-type enhancement	17.9354	1054.24	32.4691	0.3367	6.3672
3.	histogram equalization	18.3615	955.71	30.9146	0.2549	6.3462
4.	Yang et al.’s method	18.6289	898.65	29.9775	0.2213	6.3907
5.	Weeks et al.’s method	17.3326	1211.21	34.8024	0.2460	6.4125

Table (6.1) : For Luna image.

In table 6.1 we compare between PSNR, MSE and RMSE for various image enhancement methods. The mean squared error (MSE) or the peak signal to noise ratio (PSNR) are commonly used. MSE and PSNR are used because they are simple to calculate and there is no measure that is widely used in the image processing. Both MSE and PSNR rely on pixel intensities and therefore fail to take into account the human visual system. In addition, the MSE and PSNR measures do not correlate well with perceived visual quality measurement[73]. Despite their drawbacks, MSE and PSNR are commonly used.

Yang et al. has high PSNR value and less value of MSE, i.e., low noise in image. Value of RMSE is also very less than all others, i.e., image is good in contrast. Value of NCC is also good, which indicates good image after enhancement with Yang et al.'s method. Our proposed algorithm has high PSNR value and less value of MSE, value of RMSE is also smaller than all the others, i.e., Luna image has good contrast.

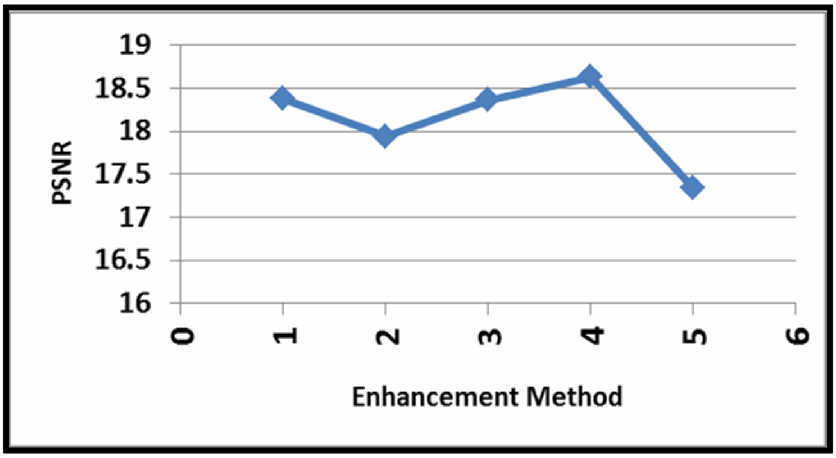


Figure (5.4) : Graph showing PSNR for Luna image using different methods of enhancement.

Fig. (5.4) shows PSNR for five different methods of image enhancement. Five different points shows different techniques. In this PSNR is high for our proposed algorithm (SSGA) for Luna image in comparison with the other methods.

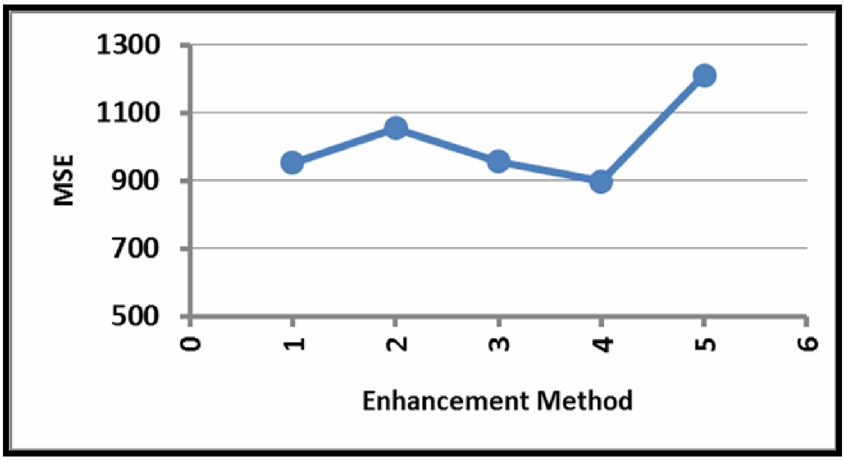


Figure (5.5) : Graph showing MSE for Luna image using different methods of enhancement .

Fig. (5.5) shows MSE for five different methods of image enhancement. Five different points shows different techniques. In this MSE is low for our proposed algorithm ,SSGA, for Luna image in comparison with the other methods.

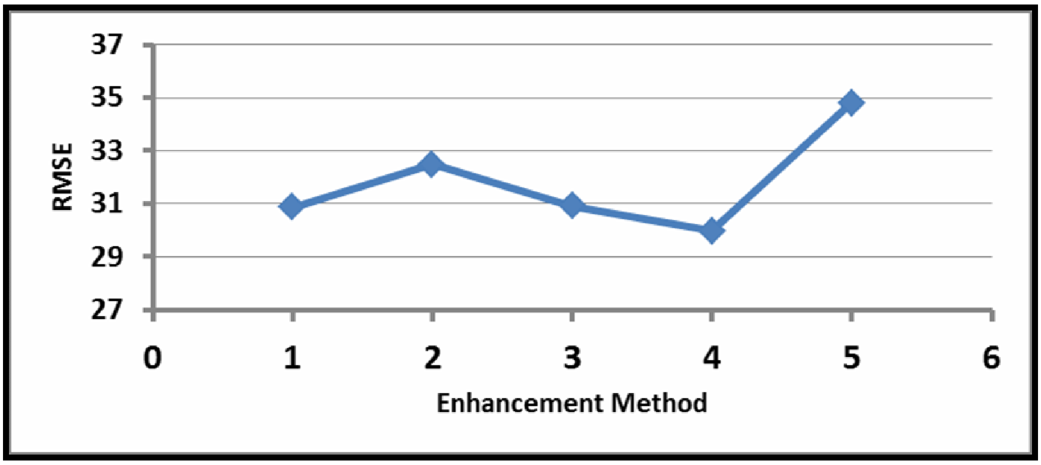


Figure (5.6) : Graph showing RMSE for Luna image using different methods of enhancement .

Fig. (5.6) shows RMSE for five different methods of image enhancement. Five different points shows different techniques. In this RMSE is low for our proposed method (SSGA) for Luna image in comparison with the other methods.

5.3 Comparison Of Performance Of SGA and SSGA for “Luna” Image

In our model, the SSGA, the population size is 30, (default crossover probability) is 0.8, (default mutation probability) is 0.01, predetermined number of generations is 40. Natural evolution of the population continues until the predetermined number of generations is reached or the optimal threshold of each generation remains same for 10 generations.

We introduce 4 measures: average computational time (Time), average optimal threshold (Threshold), average number of generations to obtain global optimal threshold (Generations), and the number of runs for which the GA gets stuck at a local optimum (Stuck), i.e., fail to locate the global optimal threshold. The images in the experiments are 256 color-level with the size of 256×256.

(a) (b) (c)

Figure (5.7) : Color-level image of “Luna” : (a) original image; (b) SGA (average threshold = 122.06); (c) SSGA (average threshold = 124.2)

	Time	Threshold	Generations	Stuck
SGA	0.06549	122.06	10.15	15
SSGA	0.0655	124.2	10.42	1

Table (5.2) Comparison Of Performance Of SGA and SSGA for “Luna” Image

We measured the performance of the SSGA segmentation relative to that of SGA. SGA produced the optimal threshold in 10~16% of the experimental runs while SSGA determined the optimal threshold in only 0~2% of the experimental runs using the same data.

Once an image segmentation criterion is chosen, the optimal threshold can be determined accurately by it. The task for any optimization algorithm is to converge to this threshold as rapidly as possible.

To "converge rapidly to global optimum" and "sustain the global convergence capacity" are two twin goals in any optimization algorithm, but unfortunately they are considered incompatible. When it comes to GA, the diversity of individuals in the population may be disrupted when GA tries to "converge rapidly to global optimum", hence cause "premature convergence". On the opposite, convergence speed may not be assured if GA tries to "sustain the global convergence capacity". A good algorithm is supposed to strike a balance between the two incompatible goals.

SGA employs static crossover probability P_c and mutation probability $\mathrm{P_m}$, which is one of the reasons for that SGA fail to promise convergence speed or global convergence in some cases. The SSGA takes both "converge rapidly to global optimum" and "sustain the global convergence capacity" into account. P_c and P_m are increased when the SSGA tends to converge to a local optimum and decreased when a population scatters in the solution space. On the other hand, the adaptation to P_c and P_m is imposed on the entire population so as to enable the population to head for the global optimum in harmony.

In SSGA, the settings of P_c and $\mathrm{P_m}$ are adjusted automatically depending on the evaluation. The SSGA is applied to color images. Experiments are conducted to evaluate the performance of SSGA and their results show that the SSGA yield better enhancement than the SGA.

5.4 Saturation Enhancement in Luna Image

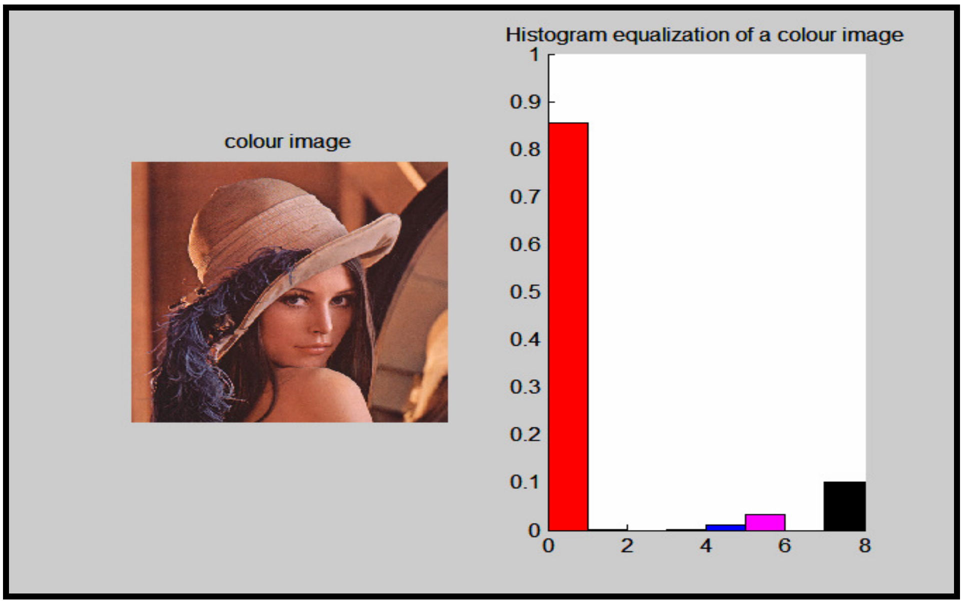


Figure (5.8) : Histogram figure for the color image enhancement

We use HSV colour model to obtain the histogram equalization of an image. HSV (Hue, Saturation, Value)-Defines a type of colour space, It is similar to the modern RGB and CMYK models. The HSV Colour space has three components: Hue, Saturation and Value. 'Value' is sometimes substituted with 'brightness' and then it is known as HSB. The height of each rectangle can be equalent to the number of pixels. The total area of the histogram is the same in the direction of on number of data. This is known as histogram equalization.

Color images, i.e. Luna image, have been processed using the two-step procedure proposed in this thesis. The experimental results demonstrate that the proposed approach can enhance the colors of Luna image more vividly.

(a) **(b)** **(c)**

(d) **(e)**

Figure (5.9) : Saturation enhancement of Luna image **(a)** Original image. **(b)** Pei's method [20] applied to (a). **(c)**, **(d)** and **(e)** Application of the proposed method, SSGA, to (a) The saturation transfer function *f(r)* as Fig. (4.7) with empirical parameters as shown in table (5.3).

Image	The saturation transfer function *f(r)* empirical parameters				The saturation ratio ***(r)***
	r_1	r_2	r_1'	r_2'	
c	0.3	0.4	0.3	0.6	0.2
d	0.3	0.4	0.3	0.7	0.4
e	0.2	0.4	0.2	0.7	0.7

Table (5.3) The saturation transfer function *f(r)* empirical parameters and the saturation ratio for the proposed method, SSGA, for Luna image in Fig. (5.9)

Luna image has been processed using the two step procedure proposed in this study. The experimental results demonstrate that the proposed approach, SSGA, can enhance the colors of Luna more vividly.

Fig. (5.9) (b) shows the image obtained by applying Pei's saturation enhancement [20] to the original image, Figs. (5.9) (c), (d) and (e) show the images obtained by using the proposed method, SSGA, with different empirical parameters listed in the captions. The empirical threshold r_1 is chosen to be in [0.2, 0.3], and the color with saturation less than r_1 is considered with low saturation. To fix the saturation of colors with low saturation, r_1' equals r_1. The effect of magnifying the color contrast of middle saturation is determined by the difference between r_2 and r_2'. Hence, at least they must differ from each other by 0.2; otherwise, the contrast enhancement could be unnoticeable. However, that difference cannot be too large to make the resultant image over saturated or to let the contrast between colors of high saturation diminish. That is, r_2' could not be too close to one. Hence, with the above constraints, r_2 and r_2' are suggested to be numbers in [0.4, 0.5] and in [0.6, 0.7], respectively. Despite the saturation of Fig. (5.9) (b) being enhanced globally, the saturation contrast of Fig. (5.9) (b) is not enhanced. Instead, the proposed method, SSGA, adjustment improves the contrast between unpainted and painted regions. The proposed saturation enhancement retains the background achromatic and enhances the saturation of objects. The hues of objects, for example, the feathers in the hat of Luna in Figs. (5.9) (c), (d) and (e) are more easily recognized than those in Fig. (5.9) (b). For fig. (5.9) (c), (d) and (e) we calculate PSNR, MSE and RMSE for each image as shown in table (5.4)

Image	The saturation ratio *(r)*	PSNR	MSE	RMSE
c	0.2	18.3615	955.71	30.9146
d	0.4	18.3769	952.34	30.8510
e	0.7	18.6289	898.65	29.9775

Table (5.4) PSNR, MSE and RMSE for images (c), (d) and (d) in fig. (5.9)

We notice from table (5.4) as the saturation ration (r) increases the PSNR for the three images will increase. In this PSNR is high for high saturation ration (r) for Luna image in comparison with the other two images. Also, we notice that as the slope of transfer function *f(r)* increases, the saturation ratio (r) increase; this means we can adjust the saturation ration (r) by controlling the transfer function *f(r)*to obtain the best ratio for saturation enhancement. The MSE decreases as the saturation ration (r) increases. The mean squared error (MSE) for our practical purposes allows us to compare the “true” pixel values of our original image to our degraded image. The MSE represents the average of the squares of the "errors" between our actual image and our noisy image. The error is the amount by which the values of the original image differ from the degraded image. The proposal is that the higher the PSNR, the better degraded image has been reconstructed to match the original image and the better the reconstructive algorithm. This would occur because we wish to minimize the MSE between images with respect the maximum signal value of the image.

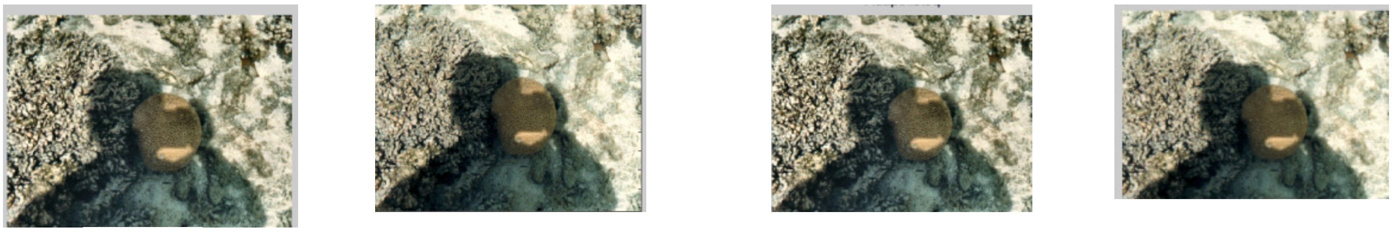
5.5 Enhancement in other Images

This research enhanced the greyscale image as seen in figure5.10, the original image A has low contrast , B & C have better contrast while D is result which gives better saturation enhancement .

(A) (B) (C) (D)

As seen in image D in figure 5.11 the brightness increased as the sharpess decreased, as well as the noise decreased.

In this thesis we enhanced the shadow image to enhance the brightness as in B & C & D the shadow will appear more visually using the proposed algorithm.



In this part we try to remove noise from the original image as shown in figure 5.12 (A) by applying the HSV enhancement on the image to get more visual image and less noise as shown in figure B.

(A) (B)

Figure (5-12) the HSV enhancement method

The given enhancement has a small drawback that it increases the component to be enhanced which doesn’t effect the total processing .

Chapter Six 6

Conclusion& Future Work

We have developed a Steady State Genetic Algorithm (SSGA). This thesis combined three enhancements which made it special; it enhanced the Contrast, Saturation and Luminance Enhancement**.** We have converted the RGB images to HSI, then the HSV will be enhanced separately and then recombined and transformed to RGB again.

The proposed method is tested on large color images; it has presented a contrast enhancement method by use of the saturation value of a pixel to determine if the Hue or the Intensity of the pixel is more close to human perception of color that pixel represents. Gaussian Smoothing Filter gave more smooth images; Space Variant Luminance Map SVLM applied the performance intensity (luminance).The input RGB color image is converted to an intensity image.

In this research we proposed a new approach to automatic image enhancement using SSGA. Results obtained indicate that our method outperforms the classical point operations (Linear contrast stretching and histogram equalization),which are also automatic methods, in terms of high effectiveness on a large category of images. The method applies SSGA with significant modifications in order to attain better explorative behavior. To profit from this behavior the SSGA uses high pressure selection scheme and a more exploitative scheme of recombination, that balance the exploratory effect of the mutation used.

The search is therefore well-balanced, and robust (the same good results are achieved when experiments are repeated). Automatic behavior was achieved by specifying a suitable fitness function proportional to the number and intensity of edges in the image and to the entropic measure of the image. The fitness function is fully objective, no human subjective term being required.

The SSGA evolves the parameters of a local enhancement method that better adapts to the local features in the image, in comparison to linear contrast stretching and histogram equalization that treat the image globally.

Summarizing, our method applies a local enhancement technique driven by SSGA evolution, to achieve both automatic behavior, i.e. method doesn't require user interaction, and robustness, i.e. applicability to a large category of images, a combined goal that is not attained by other existent enhancement methods.

The proposed saturation enhancement method makes colors more vivid and bright, and also improves the image contrast.

To obtain satisfactory enhancement results and processing speed, future works should focus on the following:

1. Fine tuning of the SSGA parameters in order to reduce the population size and maximum number of generations required.
2. A more substantial extension is to be researched, in which the chromosome will code local parameters of the method that applies to each neighborhoods.
3. Apply our proposal algorithm to particular consumer applications.
4. Minimize the parameters of preprocessing phase to increase the efficiency and minimize the complexity function.

Also, the trade-off between efficiency and computational cost will be investigated We have studied some of the important properties of the HSV color space and have developed a framework for extracting features that can be used both for image segmentation and color histogram generation two important approaches to content based image retrieval. While it is well established that color itself cannot retain semantic information beyond a certain degree, we have shown that retrieval results can be consider.

However, we found that the performance of the colored image enhancement method depends upon the correlation of color components. Evaluation results with natural and synthetic images confirm our theoretical analysis.

We introduced the combining of colored component to give more accurate results.To give more accurate image we merged the Saturation, Contrast and Luminance (V) Enhancement.

To give more robustness and less dependnce on the human, we designed the GA algorithm, to enhance the GA we used the SSGA with modified fitness function to give more accurancy in term of MAE and SNR as shown in chapter four and five.

References

1. Akram,A. B., Moustafa S. A. &Alqadi, Z. A.(2009) : Reconstructed Color Image Segmentation. ***Proceedings of the World Congress on Engineering and Computer Science***, 2(10), 20-27.

2. Ameur,H.B.,Chavent,G.G.&Weis,P.P.(2011) : Image segmentation with multidimensional refinement indicators.***World Academy of Science Engineering and Technology,***9(73),2022-2044.

3. Dutta,S.S.,Bidyut, D.D.&Chaudhuri, B.B.(2009) : Homogenous region based color image segmentation. ***Proceedings of the World Congress on Engineering and Computer Science,***2(9),2023-2044.

4. El-Sayed,A.B.,Aldahshan, B.C., Abdel badeeh,M.S.&Younis,T.F.(2011) : A hybrid technique for automatic MRI brain images classification.***Canadian Journal on Image Processing and Computer Vision***, 2(24),126-137

5. Ganesan, R.S. &Krishnan, S.S. (2010) : Segmentation of computed tomography brain images using genetic algorithm**.** ***Journal Of Computing,***2(12), 2151-9617.

6. Han,J.H., Yang, S.S.&Lee,B.U. (2011) : A Novel 3-D Color Histogram Equalization Method With Uniform 1-D Gray Scale Histogram.***IEEE transaction on image processing***,20(2),2245-2265.

7. Hanmandlu,M.&Jha, D.(2006) : An Optimal Fuzzy System for Color Image Enhancement. ***IEEE transactions on image processing***, 15(10),2956-2966.

8. Indira,D.F.&Ramesh,H.J.(2011) : Image Segmentation Using Artificial Neural Network and Genetic Algorithm. ***Computer Aided Soft Computing Techniques for Imaging and Biomedical Applications, CASCT***,3(14),2033-2054.

9. Jabarouti,M.N., Addam,S.M. &Zadeh,H.S.(2011) : Medical image segmentation using artificial neural networks. ***JJMIE***,3(4), 246 – 251.

10. Kaur,N.D.&Banga,V. K.(2011) : Color image segmentation using soft computing.***Sensors,***11(2),6480-6492.

11. Lee, S., Kwon, H., Han,H., Lee, G.&Kang,B.(2010) : A Space-Variant Luminance Map based Color Image Enhancement. ***IEEE Transactions on Consumer Electronics***,56(4),2636-2643.

12. Liu,L.L.&Liu,Y.K.(2009) : An Adaptive Algorithm Based on Image Segmentation.***IEEE Journal of selected topic in signal processing,***3(1),2020-2030.

13. Mohan,B.K. &Ladha, S. N. (2009) : Comparison of object based and pixel based classification of high resolution satellite images using artificial neural network. ***ProQuest Dissertations and Theses.***

14. Mukherjee, J.&Mitra, S. K. (2008) : Enhancement of Color Images by Scaling the DCT Coefficients.***IEEE transaction on image processing***,17(10),1783-1752.

15. Larson, G. W. and Rushmeier, H. (1997) : A visibility matching tone reproduction operator for high dynamic range scenes. IEEE Trans. Visualization and Computer Graphics, 3(4), 165-188.

16. Arich, T. and Dikbas, S. (2009) : A Histogram Modification Framework and Its Application for Image Contrast Enhancement. **IEEE Trans. Image Processing**, 18(9), 1921-1933..

17. Shahade, M. R., Saklecha, I. I., Shukla, J., Raut, A. V.& Desai, P. B. (2010) : Enhancement and Manipulation of Color Images by Scaling the DCT Coefficients. ***International Journal of Computer Applications***, 1(18), 79-85

18. Naik, S.P.& Murthy, C. A. (2009): Hue preserving color image enhancement without gamut problem. ***IEEE transaction on image processing***, 12(12),6455-6470.

19. Ocarlose,C.S.(2011) : Image segmentation with kohenen neural network self-organization map. ***International Conference on Machine Learning and Computing IPCSIT,***3(14),231-243.

20. Pei, S. C., Zeng, P.P. & Chang, C.C.(2009) : Virtual restoration of ancient Chinese paintings using color contrast enhancement and lacuna texture synthesis. ***IEEE transaction on image processing,*** 13(3),416-429.

21. Pei,S. C.& Chiu, Y.M.(2006) : Background Adjustment and Saturation Enhancement in Ancient ChinesePaintings. ***IEEE transaction on image*** p***rocessing***,15(10),3230-2234.

22. Rabin,J.J.,Delon,J.D. &Gousseau, D.P.(2011) : Removing artefacts from color and contrast modifications.***IEEE transaction on image processing***, 20(11),3073-3086.

23. Rajendran, P.M. &Madheswaran, M.N. (2010) : Hybrid medical image classification using association rule mining with decision tree algorithm.***International Journal of Grid and Distributed computing,***2(12),1038-1055.

24. RenLina, K.C., Yangb,M.S.,Liuc, H.S.,Lirngd,H.F.&Wangc,P.N.(2011) : Generalized kohonen's competitive learning algorithms for ophthalmological MR image segmentation.***International Journal of Soft Computing and Engineering,***2(11),202-220.

25. Sarkar, A.(2008) : Method for color and contrast enhancement in image**.MS Thesis** by AbhijitSarkar on Color Processing in Still Image and Video May

2008, MCSL, RIT, Rochester, NY, USA

26. Sezgin,M.M.(2010) : Survey over image thresholding techniques and quantitative performance evaluation.***Current Opinion in Neurobiology,***10(20), 1–14.

27. Song, M.D., Tao, D.T., Chen,C.C. &Xuelong, L.L.(2010) : Color to gray: visual cue preservation. ***IEEE transaction on image processing***,32(9),1233-1255.

28. Talebi,M.M.,Ayatollahi,A.A. &Kermani,A.S.(2009) : Medical ultrasound image segmentation using genetic active contour. ***IEEE transaction on medical imaging***,17(3),2022-2045.

29. Tang,B.D., Sapiro, G. D. &Caselles, V. R.(2010) : Color Image Enhancement via Chromaticity Diffusion. ***IEEE transaction on image processing***,10(5),701-708.

30. Tsai,C. M.&Yeh,Z. M.(2009) : Contrast enhancement by automatic and parameter-free piecewise linear transformation for color images. ***IEEE transaction on image processing***,24(11), 213-219.

31. Tsai, D.Y.,Lee,Y.Y.,Sekiya, M.M. &Niigata,M.O.(2010) : Medical image classification using genetic based fuzzy logic approach.***World Academy of Science Engineering and Technology***,69(10),3012-3022.

32. Wei, B.C. &Rajeswari, M.N.(2010) : Multiobjective optimization approaches in image segmentation. ***Soft Comput. Appl***.,2(1),243-256.

33. Xu,Z.G.,Ren, H.W. &Yu,X.D. (2010) :**ColourImage Enhancement by Virtual Histogramm**.*IEEE Transactions on Consumer Electronics*,56(2),2222-2266.

34. Munteanu, C. &Rosa, A.(2010) : Towards Automatic Image Enhancement Using Genetic Algorithms.**Conference Publication**. 2, 1535 – 1542.

35. Razali, N.M.&Geraghty,J.(2011) :Genetic Algorithm Performance with Different Selection Strategies in Solving TSP. *Proceedings of the World Congress on Engineering*(***WCE***),2, (Online).

36. Lin,D.F.,Su,F.H.,Huang,H.S. & Fan,F.G.(2011) : Colour image segmentation using relative values of RGB in Various illumination circumstances.**Proceedings of the 9th WSEAS International Conference on APPLICATIONS of COMPUTER ENGINEERING**, 46-51

37. Pan, Q., Zhang, L., Dai, G. & Zhang, Hon. (1999): Two Denoising Methods by Wavelet Transform. **IEEE TRANSACTIONS ON SIGNAL PROCESSING,** 47(12), 3401-3406.

38. Xu, Z. D., Weng, H.B, & Yu, X.X. (2010) : Colour Image Enhancement by Virtual Histogram Approach. **IEEE Transactions on Consumer Electronics**, 56(2), 704 - 712.

39. Julien, R.R.,Delon, J.J. &Gousseau, Y. (2011): Removing Artefacts From Color andContrast Modifications. **IEEE TRANSACTIONS ON IMAGE PROCESSING**, 20(11), 3073-3085.

40. Xu, Z. ,Wu, H. R. , Yu, X. & Qiu, B. (2010) : Colour Image Enhancement by Virtual Histogram Approach.**Transactions on Consumer Electronics**, 56(2), 704-712.

41. Dutta, S.S.,Bidyut, B. R. & Chaudhuri, S.H. (2009) : Homogenous Region based Color Image Segmentation. Proceedings of the World Congress on Engineering and Computer Science 2009 Vol II (**WCECS)** 2009, October 20-22, 2009, San Francisco, USA

42. Kanungo, p., Nanda, P. K. &Ghosh, A. (2010) : Parallel genetic algorithm based adaptive thresholding for image segmentation under uneven lighting conditions. **Systems Man and Cybernetics (SMC), 2010 IEEE International Conference,** 1904-1911.

43. Lin, C.C., Su, C.H., Huang, H.S.&Fan, K.C. (2011) : Colour Image Segmentation Using RelativeValues of RGB in Various Illumination Circumstances. **International Journal Of Computers**, 2(5), 179-184.

44. Almuhairi, H. (2010) : Objective Methods of Evaluating Colour Image Segmentation. **A thesis submitted for the degree of Doctor of Philosophy** School of Computer Science and Electronic Engineering University of Essex Date of submission: July 2010

45. Jung, S. H., Mitra, S. K. and Mukherjee, D. (1996) : Subband DCT : Definition, analysis and applications. **IEEE Trans. Circuits Syst. Video Technol.**, 6(3), 273–286.

46. Jiang, J. and Feng, G. (2002) : The spatial relationships of DCT coefficients between a block and its sub-blocks. **IEEE Trans. Signal Process.**, 50(5), 1160–1169.

47. Martucci, S. A. (1994) : Symmetric convolution and the discrete sine and cosine transforms. **IEEE Trans. Signal Process.**, 42(5), 1038–1051.

48. Awad, M.M. (2010) : An Unsupervised Artificial Neural Network Method for Satellite Image Segmentation. **The International Arab Journal of Information Technology**, 7(2), 199-205.

49. Lee, S. (2007) : An efficient content-based image enhancement in the compressed domain using retinex theory. **IEEE Trans. Circuits Syst. Video Technol.**, 17(2), 199–213.

50. Mitchell, M. (1996): An introduction to Genetic Algorithms. The MIT press.

51. Tsai, C.M., Yeh, Z. M. & Wang, Y. F. (2009) : Decision tree-based contrast enhancement for various color images. **Machine Vision and Applications,** published online.

52. Tsai, D.M.: A fast thresholding selection procedure for multimodeand unimodel histograms. **Pattern Recognit. Lett. 16**, 653–666.

53. Tsai, C.M. &Lee, H.J. (2002) : Binarization of color document images vialuminance and saturation color features. **IEEE Trans. Image Process.**,11(4), 434–451.

54. TSAI, C. M., YEH, Z. M. & WANG, Y. F. (2008) : Contrast Compensation for Back-Lit and Front-Lit Color Face Images Via Fuzzy Logic Classification and Image Illumination Analysis. **Proceedings of the Seventh International Conference on Machine Learning and Cybernetics, Kunming**, 3563-3568.

55. Mallat, S. (1999) : A Wavelet Tour of Signal Processing. 2nd ed. New York: Academic.

56. Sullivan, G. J. and Baker, R. L. (1994) : Efficient quadtree coding of images and video. **IEEE Trans. Image Process.**, 3 (3), 327–331.

57. Ha, J., Lee, S., Kim, T., Choi, W. & Kang, B. (2007) : A New Approach to Color Adjustment for Mobile Application Display with a Skin Protection Algorithm on a CIE1931 Diagram. **IEEE Trans. Consumer Electronics**, 53(1), 191-196.

58. Gonzales, R. and Winter, P. (1987) : Digital Image Processing. Addison Wesley.

59. Zimmerman, J. B., Pizer, S. M., Staab, E. V., Perry, J. R., McCartney, W. &Brenton, B. C. (1988) : An Evaluation of the Effectiveness of Adaptive Histogram Equalization for Contrast Enhancement. **IEEE Transactions of Medical Imaging**, 7(4), 304-312.

60. Saitoh, F. (1999) : Image Contrast Enhancement Using Genetic Algorithm. **Proceedings of IEEE SMC'99**, Tokyo, Japan, 899-904.

61. DaPonte, J. S. & Fox, M. D. (1988) : Enhancement of Chest Radiographs with Gradient Operators. **IEEE Transactions on Medical Imaging**, 7(2), 109-117.

62. Rosin, P. L. (1997) : Edges: saliency measures and automatic thresholding. Machine Vision and Applications, Springer Verlag, 9, 139 – 159.

63. Jain, A. K. (1991) : Fundamentals of Digital Image Processing. Prentice Hall.

64. Raghad, J. A. (2010) : Genetic-Based Multi Resolution Noisy Color Image Segmentation. World Academy of Science, Engineering and Technology, 69, 573-579.

65. Goldberg, D.E. & Deb, K. (1991) : A comparative analysis of selection schemes used in genetic algorithms, in: G.J.E. Rawlins (Ed.), Foundations of Genetic Algorithms, Morgan Kaufmann, Los Altos, 69–93.

66. Blickle, T. & Thiele, L. (1995) : A Comparison of Selection Schemes used in Genetic Algorithms. TIK-Report, Zurich.

67. Whitley, D. (1989) : The genitor algorithm and selection pressure: Why rank-based allocation of reproductive trials is the best. In Proceeding of the 3rd International Conference on Genetic Algorithms.

68. Bäck, T. and Hoffmeister, F. (1991) : Extended Selection Mechanisms in Genetic Algorithms. Proceedings of Fourth International Conference on Genetic Algorithms, San Mateo: CA, Morgan Kaufmann, 92-99.

69. Miller, B. L. and Goldberg, D. E. (1996) : Genetic Algorithms, Tournament Selection and the Effects of Noise. Complex Systems 9, 193 - 212.

70. Schmidit, M. and Stidsen, T. (1997) : Intelligent Hybrid Systems: Fuzzy Logic, Neural Networks, and Genetic Algorithms. Kluwer Academic Publisher.

71. Al-Sharafat, W. S. (2009) : Development of Genetic-Based Machine Learning Algorithm for Network Intrusion Detection (GBML-NID). A Thesis Submitted to Arab Academy for Banking and Financial Science, in Partial Fulfillment of the Requirements for the Degree of Doctorate of Philosophy in Computer Information Systems.

72. Huttenlocher, D., Klanderman, G. &Rucklidge, W. (1993) : Comparing images using the hausdorff distance. IEEE Trans Patt Analysis and Mach Intell, 15, 850–863.

73. Van Rijsbergen, C. J. (2004) : The Geometry of Information Retrieval. Cambridge University Press, Cambridge, UK.

74. Pitas, I. and Kinikilis, P. (1996) : Multichannel techniques in color image enhancement and modeling. **IEEE Trans. Image Processing** , 5(1), 168–171.

75. Weeks, A. R., Hague, G. E. and Myler, H. R. (1995) : Histogram specification of 24-bit color images in the color difference (C-Y) color space. **J. Electron. Imag.**, 4(1), 15–22, 1995.

76. Yang et al., (1996) : Saturation clipping in the LHS and YIQ color spaces. In Proc. IS&T/SPIE Int. Symp. Electronic Imaging: Science & Technology –Color Imaging: Device-Independent Color, Color Hard Copy, and Graphic Arts, San Jose, CA.

77. Sezgin, M. and Sankur, B. (2004) : Survey over image thresholding techniques and quantitative performance evaluation. Journal of Electronic Imaging, 13(1), 146–165.

Electronic References

1. http://web-us.com/brain/neur_hopfield.html**, Viewed at 24 December 2011.**

2. http://fbim.fh-regensburg.de/~saj39122/jfroehl/diplom/e-12-text.html, V**iewed at 15 December 2011.**

3. http://en.wikipedia.org/wiki/RGB_color_model**,Viewed at 24 November2011.**

4. http://www.sketchpad.net/basics4.htm,**Viewed at 25 October 2011**.

5. http://www5.informatik.tuenchen.de/lehre/vorlesungen/graphik/info/csc/COL_24.html,**Viewed at 25 September 2011.**

6. http://subsimple.com/genealgo.asp**, Viewed at 15 October 2011**.

7. http://www.ro.feri.unib.si/predmeti/int_reg/Predavanja/Eng/3.Genetic%20algorithm/_18.html, **Viewed at 9 September 2011**.

8. http://www.calresco.org/lucas/fitness.htm, **Viewed at 15 September 2011**.

9. http://aicoder.blogspot.com/2010/12/stochastic-universal samplingselection.html, **Viewed at 21 September 2011.**

10. http://www.obitko.com/tutorials/genetic-algorithms/encoding.php,**Viewed at 3 September 2011**.

11. http://www.sc.chula.ac.th/courseware/2309507/Lecture/remote18.html**, Viewed at 1 September 2011**.

12. http://www.doc.ic.ac.uk/~nd/surprise_96/journal/vol4/tcw2/report.html**,Viewed at 24 October 2011.**

13. http://www.obitko.com/tutorials/genetic-algorithms/ga-basic-description.php, **Viewed at 18 November 2011.**

14. http://web-us.com/brain/neur_hopfield.html, **Viewed at 24 December 2011.**

15. http://fbim.fh-regensburg.de/~saj39122/jfroehl/diplom/e-12-text.html, **Viewed at 15 December 2011.**

16. http://en.wikipedia.org/wiki/RGB_color_model**, Viewed at 24 November2011.**

17. ttp://www.sketchpad.net/basics4.htm, **Viewed at 25 October 2011**.

18. http://www5.informatik.tuenchen.de/lehre/vorlesungen/graphik/info/csc/COL_24.html, **Viewed at 25 September 2011.**

19. ttp://subsimple.com/genealgo.asp**, Viewed at 15 October 2011**.

20. http://www.ro.feri.unib.si/predmeti/int_reg/Predavanja/Eng/3.Genetic%20algorithm/_18.html, **Viewed at 9 September 2011**.

21. http://www.calresco.org/lucas/fitness.htm, **Viewed at 15 September 2011**.

22. http://aicoder.blogspot.com/2010/12/stochastic-universal samplingselection.html, **Viewed at 21 September 2011.**

23. http://www.obitko.com/tutorials/genetic-algorithms/encoding.php,**Viewed at 3 September 2011**.

24. http://www.sc.chula.ac.th/courseware/2309507/Lecture/remote18.html**, Viewed at 1 September 2011**.

25. http://www.doc.ic.ac.uk/~nd/surprise_96/journal/vol4/tcw2/report.html, **Viewed at 24 October 2011.**

26. http://www.obitko.com/tutorials/genetic-algorithms/ga-basic-description.php, **Viewed at 18 November 2011.**

27. http://www.eng.uah.edu/~hitedw/E100/Chapter11/EE100CH11.pdf, **Viewed at 22 December 2011.**

Appendix

```
x = imread('lina.bmp')
J = imadjust(x,stretchlim(x),[]);
Imshow(x), title ('Original Image');
%figure, imshow(J), title('contrast stretch image');
figure, imshow(J) ,title('Enhance contrast using histogram equalization');
I = RGB2GRAY(x);
J = histeq(I);
figure, imshow(I)
figure, imshow(J),title('Enhance contrast using histogram equalization')
figure; imhist(I,64),title('a histogram of the original image')
figure; imhist(J,64),title('histogram of the enhanced image using histogram equalization')
```

```
clear all;
% Reading image
y=imread('test.jpg');
x=double(y);
a=size(x);
w(:,:)=(255*ones(a(1),a(2)));
% Normalising R,G,B values
for i=1:1:a(1);
   for j=1:1:a(2);
Y(i,j,1)=x(i,j,1)/w(i,j);
Y(i,j,2)=x(i,j,2)/w(i,j);
Y(i,j,3)=x(i,j,3)/w(i,j);
   end;
end;
Y1=Y;
for i=1:1:a(1);
   for j=1:1:a(2);
   r=Y(i,j,1);
   g=Y(i,j,2);
   b=Y(i,j,3);
   l=(r+g+b);
   % Defining s-type enhancement function
   if l<=(.25) && l>=(0)
```

```
fl=.25*(l/.25)^2;
elseif l>(.25) && l<=(3)
fl=3-(3-.25)*(((3-l)/(3-.25))^2);
    end;
    % Enhancing the color levels linearly
    alpha=fl/l;
    if alpha<=1
        Y(i,j,1)=alpha*r;
        Y(i,j,2)=alpha*g;
        Y(i,j,3)=alpha*b;
    else
        nr=1-r;
ng=1-g;
nb=1-b;
nl=3-l;
gl=3-fl;
nalpha=gl/nl;
        Y(i,j,1)=1-nalpha*nr;
        Y(i,j,2)=1-nalpha*ng;
        Y(i,j,3)=1-nalpha*nb;
    end;
end;
end;
for i=1:1:a(1);
    for j=1:1:a(2);
Y2(i,j,1)=Y(i,j,1)*w(i,j);
Y2(i,j,2)=Y(i,j,2)*w(i,j);
Y2(i,j,3)=Y(i,j,3)*w(i,j);
Y1(i,j,1)=Y1(i,j,1)*w(i,j);
Y1(i,j,2)=Y1(i,j,2)*w(i,j);
Y1(i,j,3)=Y1(i,j,3)*w(i,j);
 end;
end;

figure(1);imshow(uint8(Y1));

figure(2);imshow(uint8(Y2));


'DC Adjustment'

clc;
close all;
```

```
% clear all;
inImg = imread('lina.bmp');
figure;imshow(inImg);title('Input Image');
s_inImg = size(inImg);
outImg = zeros(s_inImg);
ycbcrOutImg = zeros(s_inImg);
%DCT Parameters
blkSize = 8;

ycbcrInImg = rgb2ycbcr(inImg);
y_inImg = ycbcrInImg(:,:,1);
cb_inImg = ycbcrInImg(:,:,2);
cr_inImg = ycbcrInImg(:,:,3);

I_max = max(max(y_inImg));

%Block-wise Splitting
y_blocks = Mat_dec(y_inImg, blkSize);

s = size(y_blocks);
dctBlks = zeros(s);

for i = 1 : s(3)
   for j = 1 : s(4)
localBlk = y_blocks(:,:,i,j);
localdctBlk = dct2(localBlk);
localdctBlk = localdctBlk ./ 8;

orig_dc = localdctBlk(1,1);

       %Adjustment of Local Background Illumination
       x = localdctBlk(1,1) / double(I_max);
mapped_dc = x * (2 - x) * double(I_max);

       %Preservation of Local Contrast
       k = mapped_dc / orig_dc;

localdctBlk(1,1) = k * localdctBlk(1,1);

dctBlks(:,:,i,j) = localdctBlk;
   end
end
```

```
dctImg = merge_blocks(dctBlks);
dctImg = dctImg .* 8;
y_outImg = blkproc(dctImg, [8 8], 'idct2(x)');

ycbcrOutImg(:,:,1) = y_outImg;
ycbcrOutImg(:,:,2) = cb_inImg;
ycbcrOutImg(:,:,3) = cr_inImg;

ycbcrOutImg = uint8(ycbcrOutImg);
rgbOutImg = ycbcr2rgb(ycbcrOutImg);
figure;imshow(rgbOutImg);title('DC Adjustment');



%%

clear all; clc;

%% report format characters

newlineInAscii1 = [13 10];

spaceInInAscii = 32;

% for printing, newline causes much confusion in matlab and is provided

here as an alternative

newline = char(newlineInAscii1);

spaceChar = char(spaceInInAscii);



%% plot parameters

plotIndex = 1;

plotRowSize = 1;

plotColSize = 2;
```

```
%% read the image

targetFolder = 'images';



IMG = '6.jpg';   % IMG : originalImage

IMG = strcat(targetFolder, '\', IMG);

IMG = imread(IMG);

IMG = rgb2gray(IMG);

IMG = double(IMG);



%% noise parameters
sigma = 0.05;
offset = 0.01;

erosionFilterSize = 2;
dilationFilterSize = 2;
mean = 0;

noiseTypeModes = {
    'gaussian',        % [1]
    'salt & pepper',   % [2]
    'localvar',        % [3]
    'speckle',         % [4] (multiplicative noise)
    'poisson',         % [5]
    'motion blur',     % [6]
    'erosion',         % [7]
    'dilation',        % [8]
    % 'jpg compression blocking effect'   % [9]
    % [10] Interpolation/ resizing noise <to do>
    };

noiseChosen = 2;
```

```
noiseTypeChosen = char(noiseTypeModes(noiseChosen));

originalImage = uint8(IMG);

%% plot original
titleStr = 'Original';

imagePlot( originalImage, plotRowSize, plotColSize, ...
plotIndex, titleStr );
plotIndex = plotIndex + 1;

%%
for i = 1:(plotRowSize*plotColSize)-1

IMG_aforeUpdated = double(IMG);    % backup the previous state just in
case it gets updated.

% returns the noise param updates for further corruption
% IMG may be updated as the noisy image for the next round
[IMG, noisyImage, titleStr, sigma, dilationFilterSize, erosionFilterSize] =
...
noisyImageGeneration(IMG, mean, sigma, offset, dilationFilterSize,
erosionFilterSize, noiseTypeChosen);

imageQualityIndex_Value = imageQualityIndex(double(originalImage),
double(noisyImage));

titleStr = [titleStr ',' newline 'IQI: ' num2str(imageQualityIndex_Value)];

imagePlot( noisyImage, plotRowSize, plotColSize, ...
plotIndex, titleStr );
plotIndex = plotIndex + 1;

end

if (~strcmp(char(class(noisyImage)), 'uint8'))
disp('noisyImage is NOT type: uint8');
end

%% PSNR
psnr_Value = PSNR(originalImage, noisyImage);
fprintf('PSNR = +%5.5f dB \n', psnr_Value);
```

```
%% RMSE
[mse, rmse] = RMSE2(double(originalImage), double(noisyImage));
fprintf('MSE = %5.5f \n', mse);
fprintf('RMSE = %5.5f \n', rmse);
%% Universal Quality Index
imageQualityIndex_Value = imageQualityIndex(double(originalImage),
double(noisyImage));
fprintf('Universal Image Quality Index = %5.5f \n',
imageQualityIndex_Value);
%% Enhancement : measure of enhance- ment, or measure of improvement
[M M] = size(originalImage);
L = 8;
EME_original = eme(double(originalImage),M,L);
EME_noisyImage = eme(double(noisyImage),M,L);
fprintf('EME (original image) = %5.5f \n', EME_original);
fprintf('EME (noisy image) = %5.5f \n', EME_noisyImage);
%% PearsonCorrelationCoefficient
pcc = compute_PearsonCorrelationCoefficient (double(originalImage),
double(noisyImage));
fprintf('PearsonCorrelationCoefficient (originalImagevsnoisyImage) =
%5.5f \n', pcc);
pcc = compute_PearsonCorrelationCoefficient (double(originalImage),
double(originalImage));
fprintf('PearsonCorrelationCoefficient (originalImagevsoriginalImage) =
%5.5f \n', pcc);

%% Signal to signal noise ratio, SNR
noise = double(noisyImage) - double(originalImage); % assume additive
noise

% check noise
noisyImageReconstructed = double(originalImage) + noise;
residue = noisyImageReconstructed - double(noisyImage);

if (sum(residue(:) ~= 0))
disp('The noise is NOT relevant.');
end

snr_power = SNR(originalImage, noise);
fprintf('SNR = %5.5f dB \n', snr_power);

%% Mean absolute error, MAE
```

```
mae = meanAbsoluteError(double(originalImage), double(noisyImage));
fprintf('MAE = %5.5f \n', mae);

function snr_power = SNR(signal, noise)
% SNR (Signal to noise ratio)

[signalRowSizesignalColSize] = size(signal);
[noiseRowSizenoiseColSize] = size(noise);

signalAmp = signal(:);
noiseAmp = noise(:);

signalPower = sum(signalAmp.^2)/(signalRowSize*signalColSize);
noisePower = sum(noiseAmp.^2)/(noiseRowSize*noiseColSize);

% snr_amp = 10*log10((signalAmp./noiseAmp)^2);
snr_power = 10*log10(signalPower/noisePower);

end
```