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# An Evolutionary Approach to CT Image Reconstruction<sup>†</sup>

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**Abstract** There is presented an evolutionary approach to the problem of CT image reconstruction: a genetic algorithm is used to reconstruct a CT image from a limited number of projection data, where conventional methods (e.g. Algebraic Reconstruction Techniques ART) solution tends to be unsatisfactory. We use traditional as well as adapted genetic operators in our evolutionary approach to the CT image reconstruction problem. The genetic algorithm yielded good results that challenge the conventional ART.

## 1. Introduction

There are many fields nowadays where applications of the problem of digitally reconstructing an image from projections exist. One important field is computed tomography (CT) in the medical field. The CT image is a digitized view of the cross-section of the body. A CT image production begins with a *scanning phase*, where the data with which the image is eventually reconstructed is obtained by measuring the transmission of multiple x-ray beams projected through the image plane, from several different directions.

The second phase of image production is known as *image reconstruction*. This is performed by the digital computer which is part of the CT system. Image reconstruction is usually a mathematical procedure that combines projections and converts them into a computed digital image. Algebraic reconstruction techniques (ART)[1, 2] are well known techniques in the field. ART methods have merits over many other known reconstruction techniques due to the possibility of providing a reasonable solution even in case of a limited number of angular projections. With further limitation of projection directions, however, ART approximation is not always satisfactory[2, 4].

Here, we are presenting an evolutionary approach to CT image reconstruction problem from a limited number of projection data (*four* directions). In the following sections, we present the genetic operators, show experiments results, then comparative evaluation of the new approach as well as of the conventional ART are given, followed by comments and future work.

## 2. The genetic algorithm

In order to apply a genetic algorithm, we need to encode an image in a genetic chromosome. This is simply done by representing each pixel in the plane of the image by one allele in a genetic chromosome (Figure 1). A *float-bit* representation [0.0, 1.0] for a string allele values is used.

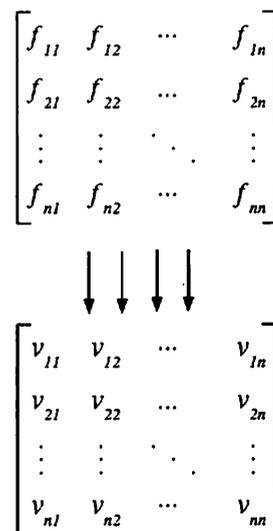


Figure 1: Mapping an image array into a chromosome array

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## 2.1 Fitness measure

A formula that compares the original image projection data to those of the reconstructed image is used to return a chromosome fitness. A Laplacian constraint term, that penalizes non-smooth images, is included in the fitness function ( $F$ ) which comes below.

$$F = \frac{1}{1 + \lambda \times (E + \kappa \times Lap^2)}$$

where

$$Lap = \nabla^2 f(i, j) = [f(i+1, j) + f(i-1, j) + f(i, j+1) + f(i, j-1) - 4 \times f(i, j)]$$

$$E = \frac{1}{c} \sum_{\theta=1}^c \frac{1}{width} \sum_r^{width} [P(\theta, r) - R(\theta, r)]^2$$

and

- $C$ : number of projection directions
- $\theta$ : index of projection angle
- $P(\theta, r)$ : projection of original image
- $R(\theta, r)$ : projection of reconstructed image
- width: width of the image
- $r$ : index of projection subdata
- $f(i, j)$ : value of pixel  $(i, j)$
- $\lambda$ : an integer scaling factor
- $\kappa$ : a real scaling factor

In the fitness function  $F$ ,  $E$  measures the mean square error between the given projection and the calculated projection of the reconstructed image, and  $Lap$  is the Laplacian operator.

One remark need to be made here with respect to the fitness function used in this work. Though the mean square error ( $E$ ) may tend to 0, the Laplacian term would never be zero. But once a zero-mean square error is encountered, the Laplacian term is neglected and the fitness value is set to 1.

## 2.2 Genetic operations

Chromosomes of an initial population are generated *randomly*: for each allele, its value is selected randomly from the unit interval  $[0.0, 1.0]$ .

### 2.2.1 Selection

In the reproduction operation of a new generation, an *elitist* selection scheme is used for selection of parents, where strings with high fitness are exempted undertaking genetic operations and given chance to survive to the next generation.

### 2.2.2 Crossover

A *uniform* crossover operation is applied to

parents to produce offspring for the next generation. The uniform crossover generates *an offspring* from two randomly-selected parents (Figure 2).

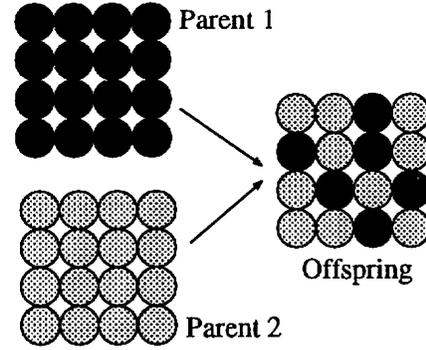


Figure 2: Uniform crossover

### 2.2.3 Mutation

Two mutation operators are applied: *probabilistic uniform* mutation and a *median* mutation. The *probabilistic* mutation uses the Boltzmann probability to guide its performance. The probability ( $P_i$ ) has the form

$$P_i = \frac{1}{1 + \exp(-\Delta F_i/T)}$$

where

$\Delta F_i$ : Difference between a chromosome fitness before and after a pixel is being mutated.

$T$ : constant

The *median* mutation changes the pixel value ( $v_i$ ) to the mean value ( $v^m$ ), among the neighborhood pixels (Figure 3).

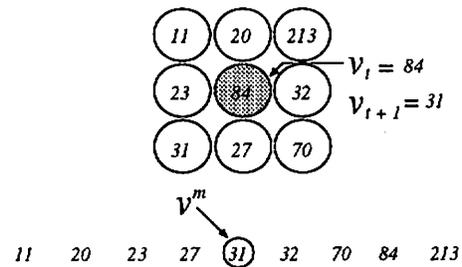


Figure 3: Median mutation

## 2.3 Variable-length chromosomes

The genetic algorithm starts with a small size chromosomes ( $8 \times 8$ ), and then increases the size exponentially (when certain conditions are satisfied)

over generations till the actual size of the image is reached (Figure 4). The expansion takes place at occasions when the fitness of the best chromosome remains the same for a certain number of successive generations.

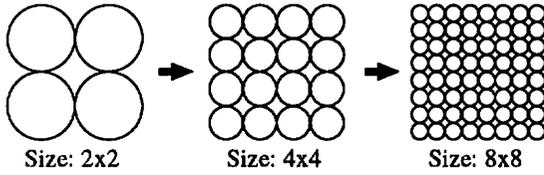


Figure 4: Expansion of chromosome size

Since the size of projection data corresponds to the original size of the unknown image, preprocessing of the given projection data (projections resizing) is necessary in order to match the current size of the reconstructed image (Figure 5).

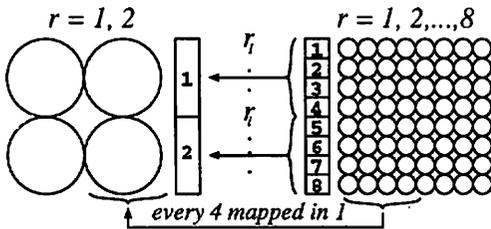


Figure 5: Projections resizing

The whole process of the genetic algorithm is shown in the following algorithm.

```

Begin
  t = 0
  chromosome_size = 8 × 8
  Initialize P(t)
  Evaluate P(t)
  While (Not termination_condition) Do
    Select P̂(t) from P(t)
    Select P̃(t) from P(t)
    Crossover P̂(t)
    Mutate P̃(t)
    Evaluate P̃(t)
    P(t + 1) = P̂(t) ∪ P̃(t)
    t = t + 1
    If expand_condition Then
      Expand chromosome_size
    End
  End
End

```

In this algorithm,  $P(t)$  denotes a population of  $\mu$  individuals at generation  $t$ ,  $\hat{P}(t)$  is a special set of  $\lambda$  ( $\lambda < \mu$ ) elite individuals, and  $\check{P}(t)$  is a population of  $(\mu - \lambda)$  randomly selected individuals from among  $P(t)$ .

### 3. Digital simulation<sup>1</sup>

Tables 1,2 below show parameters and environment for experiments.

Angles of projections	0°, 45°, 90°, 135°
Image size	32 x 32

Population size	100
Elite selection rate	0.2
Probabilistic mutation rate	0.01
Median mutation rate	0.01
Scaling factor ( $\lambda$ ), in the fitness function	10
Penalty term scaling factor ( $\kappa$ )	10
Factor $T$ , in $P_i$ formula	0.1

Figure 6 shows reconstruction results for two images by the GA as well as by ART.

As a base for a quantitative comparison between the conventional ART and the proposed GA, a pixel error estimator ( $\delta_e$ ) is used to estimate an over all error in the reconstructed image.

$$\delta_e = \sqrt{\frac{\sum_{x=1}^{Width} \sum_{y=1}^{Width} (f_{org}(x,y) - f_{rec}(x,y))^2}{\sum_{x=1}^{Width} \sum_{y=1}^{Width} f_{org}(x,y)^2}} \times 100.0$$

where

$f_{org}(x,y)$  : value of pixel(x,y) in the original image

$f_{rec}(x,y)$  : value of pixel(x,y) in the reconstructed image

### 4. Comments and future work

In this paper, an evolutionary approach to the CT image problem is presented. A genetic algorithm GA is used to reconstruct CT images from four projection data. The GA works on a population of artificial chromosomes each of which represents an estimation of the original unknown image.

<sup>1</sup>IBM(Pentium) machines with GNAT(Ada95) compiler were used.

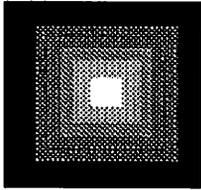
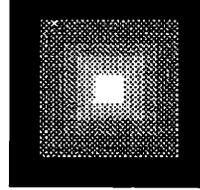
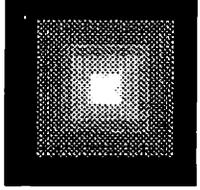
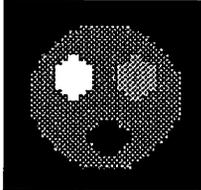
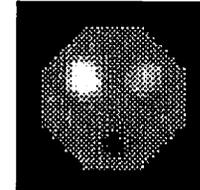
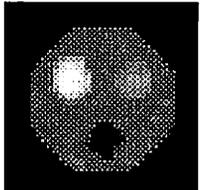
Original Image	ART Image	GA Image
		
$\delta_e$	6.33	5.32
		
$\delta_e$	18.21	17.00

Figure 6: Results of reconstruction by ART & GA for two images

The fitness of each chromosome is measured by a refined function that makes use of the given original image projection data as well as some *a priori* assumption about the smoothness of the unknown image.

Good estimations of the reconstructed images are obtained by the genetic algorithm, and the quality of reconstruction is superior to that of the conventional ART.

A merit of the genetic algorithm is the ease of incorporation of constraints or *a priori* information about the original image in the reconstruction process, and that is an advantage over the conventional ART.

The system suffers from high time complexity; the algorithm takes long computational time before the program converges to a satisfactory solution, and that necessitates parallelization of the algorithm.

At present we are working on some new adaptive genetic operators and methods for better quality and speed up of reconstruction. Application of the algorithm to real CT images of larger size is also being considered in order to be able to declare general conclusion and consolidate the effectiveness of the proposed method.

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