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INDIRECT ENCODING OF THE GENES OF A CLOSED CURVE FOR INTERACTIVELY CREATE INNOVATIVE CAR SILHOUETTES

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1. Introduction

Design is an engineering activity for creating new and innovative structures and shapes. Finding a new shape and style for an object can be seen as a profound human and sometimes artistic refinement process. Indeed, starting from an initial idea, the style designers continuously refine it through multiple sketches and drawings using their intuition and perception of their own production in a reflexive manner. Is it possible to help such style designers in their refinement process? Such an aiding tool should help him or her to explore more easily and systematically a large space of possible styles or shapes, and also to converge towards an ideal shape the designers could have more or less represented in their mind.

In the field of implementing this creative design process, Evolutionary Computation (EC) has become one of the primary approaches. A method in EC uses basically genetic algorithms (GA) [Bentley *et al*; Renner *et al* 2003], which were originally used to find solutions for complex optimisation problems. Taking the evolution in nature as paradigm, the GAs work on the basis of a population of individuals, where each individual represents a possible solution for the initial problem. The structure and the qualities of each individual are encoded in their genomes. Through recombination of these genomes the individuals can reproduce themselves and produce new individuals (solutions), while by a sort of natural selection the individuals who are not adapted to the environment (what is expected of their properties) are not selected for procreation. In this way, the individuals display better and better qualities over the generations. Interactive Genetic Algorithms (IGA, see [Kim *et al* 2000; Yanagisawa *et al* 2005]) represent a special class of GAs where a human (here, the style designer) is a key player embedded within the task of selection of individuals of a generation. IGAs are then particularly adapted to situations where it is impossible to explicitely express a preference function (the *fitness* function) on individuals or even when it is hard to qualify expected properties. This is typically the case with style designers.

A major difficulty when using GAs in automatic design systems is the *encoding* of the genome (see [Nicaise *et al* 2007]), which means the way of coding the phenotype (physical structure) of the individual into the genotype (genome). Most systems use a direct encoding where geometrical dimensions and structures of the design object are directly represented in the genome. When designing a bottle for example [Ang *et al* 2006] or finding a design for cylinder shapes [Yanagisawa *et al* 2005] the phenotype is represented in the genome by a sequence of geometrical parameters like radii, lengths and part locations. Consequently, the encoding is context dependent. Other works use tree structures [Liu *et al* 2002] or shape grammars [Osborn *et al* 2006] to encode the genome. Kim and Cho [Kim *et al* 2000] have used a set of predefined parts of clothes to find new designs in fashion by recombining

these parts. As the combinatorial dimension of the space of possible solutions is limited, the utility of such an automated exploration is questionable.
In addition, all these systems are conceived for a given design domain. Implementing these methods in new fields of design is a difficult and time consuming process. However, a good design method should be applicable, as much as possible, on a large spectrum of situations.
In this paper, we first propose a method of encoding a 2D-closed-curve which is supposed to meet a desired style. This method can be applied to all possible objects represented by their 2D-silhouettes. For instance a car silhouette or profile is a primordial style feature of a car since it has been proved that the aesthetic aspects of a car amounts for 70% of purchase intents for customers [Cheutet 2007] and the car silhouette in itself has been proved to have a strong determining influence on the car perception while embedding perceptual attributes such as: sportiveness, aggressivity or peacefulness, etc [Cheutet 2007]. Next, an Interactive GA (IGA) has been developed in defining a crossing-over operation between genes. The interactivity consists in letting a style designer qualitatively assessing individuals at each generation. In this manner, new innovative designs are expected to emerge by a balanced collaboration between an automatic process of design space exploration and the interaction of a designer. Finally, we provide measures for proving that innovation and surprise may emerge from this process. Indeed, we show that the initial population of individuals contains a sufficient richness of genes so as to be able to quickly converge towards a desired silhouette which is not an individual of this initial population.
The paper explains the principles of the Fourier decomposition of a closed curve and the encoding principle in section 2. Section 3 presents the process of the interactive genetic algorithm with the different operations required for generating an initial population and the principle of the crossover operator for combining the genomes. In section 3, a test of convergence toward a reference silhouette is carried out to show that it is possible to quickly converge toward a silhouette which was not present within the initial population. This test is based on a similarity index which is also presented before concluding on some forthcoming perspectives.

2. The genome

Usual methods for coding the phenotype of an object (i.e., its structure) are to parameterise the major dimensions of several parts of it [Ang *et al* 2006; Yanagisawa *et al* 2005], like its total length, the position of the tires and their radii for a car, for example. Another method is to use shape grammars [Osborn *et al* 2006].
Concerning the encoding of a 2D-closed-curve, McGarva [McGarva *et al* 1993] has proposed its development into a Fourier series as a method for coding its phenotype. We have personally already used this theory in [Vasiliu *et al* 2001] for encoding a 2D-closed-curves into the five first Fourier harmonics of this decomposition. In that way, we have been able to build an Artificial Neural Network for synthesizing four-bar linkage mechanisms following targeted trajectories. This approach is not as rigid as the approach of parameterisation for multiple reasons:

- this encoding is supposed to embrace a much vaster space of possible 2D-closed-curves – or 2D-silhouettes – than by a parameterisation approach;
- all kind of shapes may be represented even with small details, that can be of the highest importance for provoking feelings and emotions;
- the encoding may be performed through a constant length of genome, which simplifies a lot crucial GA stages such as the cross-over operation between parent individuals;
- finally, the genes in our solution have proved to be narrowly associated to apparent characteristics which is primordial to converge after several generations to the ideal 2D shapes.

The Mac Garva's theory of Fourier decomposition of a closed curve considers that the position of each point belonging to this curve can be expressed by a complex function in the complex plane:

$$z(t) = x(t) + i\,y(t) \tag{1}$$

As $z(t)$ is a closed curve, its function is periodic. The period is normalised with: $z(t+1) = z(t)$. This function $z(t)$ can be developed into a Fourier series:

$$z(t) = \sum_{m=-\infty}^{\infty} a_m \exp(2\pi i m t) \tag{2}$$

where the complex Fourier coefficients can be calculated by this formula:

$$a_m = \int_0^1 z(t) \exp(-2\pi i m t)\, dt \tag{3}$$

Coefficient a_0 is called fundamental, a_1 and a_{-1} represent the first harmonic, a_2 and a_{-2} the second harmonic, etc.
As we will see later, the function $z(t)$ is not known as an explicit function from the beginning. Instead, we assume that the curve has been initially defined by a set of successive points z_k ($k=0,..,N$) which belong to the curve. So, in order to calculate the a_m coefficients (3) we need a numeric approximation. We obtain this approximation by dividing the curve into N segments connecting each point with its successor. We call t_k the length of the curve between the first point z_0 and the point z_k. Under these conditions the integral can be calculated by the trapezium formula:

$$a_m = \sum_{k=0}^{N} \left(\frac{t_{k+1} - t_k}{2}\right) \left(z_{k+1} \exp(-2\pi i m t_{k+1}) + z_k \exp(-2\pi i m t_k)\right) \tag{4}$$

while z is a periodic function, ($z_{N+1} = z_0$).
The value of t_k is the ratio of the length of the curve to the point k and the total length of the curve.

$$t_k = \frac{L_k}{L}\ ,\ L = \sum_{i=0}^{N} \sqrt{(x_i - x_{i+1})^2 + (y_i - y_{i+1})^2} \text{ and } L = \sum_{i=0}^{N} \sqrt{(x_i - x_{i+1})^2 + (y_i - y_{i+1})^2} \tag{5}$$

where the total length L is the sum of the lengths of all segments, L_k is length from the origin to the current point, $x_{N+1} = x_0$ and $y_{N+1} = y_0$.
To construct the genome of an object, we develop its silhouette into a Fourier series and define the fundamental (the coefficient a_0) as gene number zero . The first harmonic (a_1, a_{-1}) will be called the first gene, the second harmonic the second gene, etc.

On the basis of the genome, the original shape of the individual can be reconstructed. Every point P_k with the coordinates (x_k, y_k) on the curve z^* which approximates the silhouette of the car, can be calculated by formula (6).

$$z^*(t_k) = x_k + i y_k = \sum_{m=-p}^{p} a_m \exp(2\pi i m t_k) \tag{6}$$

where t_k ($0 \le t_k \le 1$) is the position on the curve and p fixes the number of harmonics used for the decoding. When p equals 1 for example, we use one harmonic to reconstruct the silhouette of the car. The more harmonics used for the decoding the more precise will be the approximation to the original curve (as seen in figure 1). We call p the "precision" of decoding.

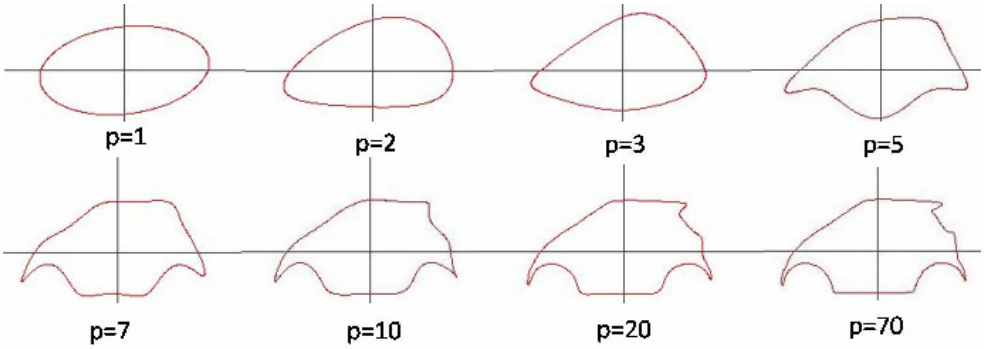

Figure 1. Decoding of a genome of a Smart car with different precisions

It can be easily proved that the first harmonic (the sole complex coefficient a_0) represents the coordinates of the centre of gravity of the curve in a complex plane. The second gene (a_1 and a_{-1}) contains the information defining an ellipse. The influence of the other genes cannot be illustrated easily. But we can say that the first genes influence the very basic structure and shape of the silhouette while the higher genes bring in the details of the shape.

3. The process of the interactive genetic algorithm

The process of finding new design solutions can be divided into two phases (see Figure 2). During Phase 1 an initial population of individuals is created. Phase 2 consists of a loop where the user evaluates the current population and a genetic algorithm evolves the population respecting the evaluation of the user.

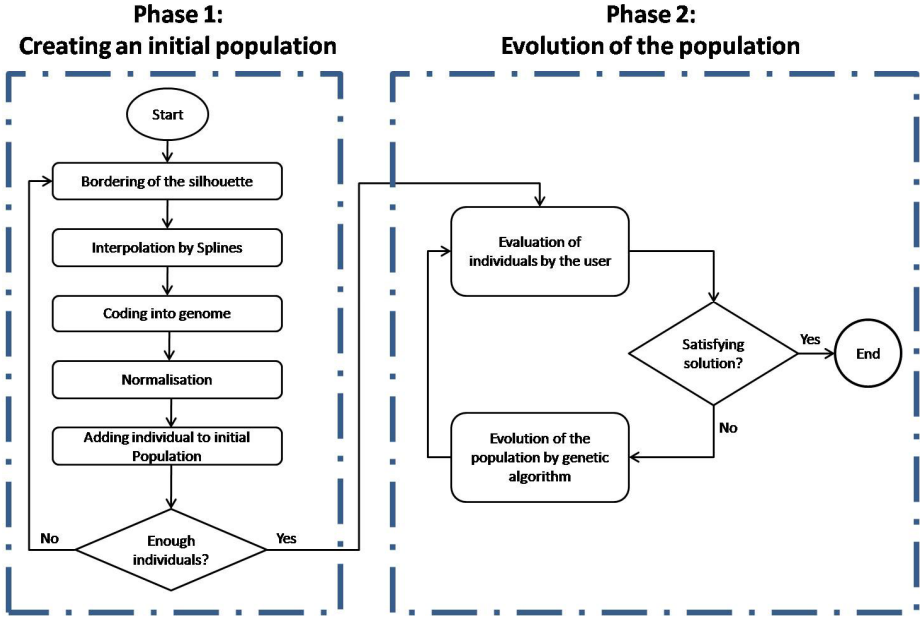

Figure 2. Diagrammatic plan of the IGA process

3.1 Phase 1: Creating an initial population

The genetic algorithm needs an initial population of individuals and their genetic code to start working. This initial population consists of silhouettes of 30 already existing car bodies. In order to easily sketch these silhouettes we programmed an interface in Java which allows to draw curves on a plain and code them into a genome. To border a silhouette we display the image of an existing car in the background of the screen and draw a contour-chart around the car on the image by clicking on the screen. The result is a closed curve representing the silhouette of an existing car-body (see figure 3). During bordering, a sufficient amount of points should be used to represent as many details as possible. When using a number *M* of 60 to 80 points per silhouette the result is satisfactory.

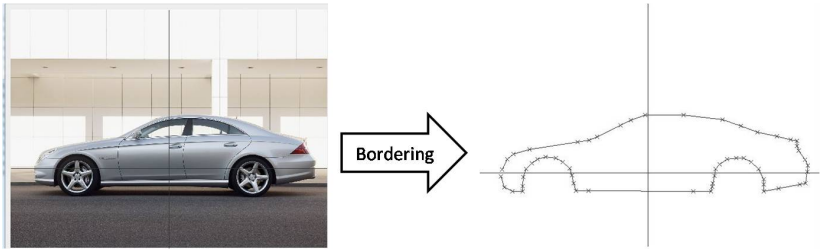

Figure 3. After bordering we obtain a closed curve representing the car silhouette of an existing car

However this amount *M* of 60 to 80 points is not sufficient to calculate a genome which is precise enough to allow a highly detailed decoding into the phenotype. Consequently we need to augment the number of points on the curve by smooth interpolations. The curve produced by interpolation should be very close to the original curve and should be continuously derivable in each point. If the curve is not continuously derivable, the decoding from the genotype into the phenotype produces high-frequency oscillations and is therefore useless. We chose to solve this problem with bicubic splines linking three successive points (see figure 4), because this method provides a curve which is very close to the original curve without producing oscillations (as it is the case when using polynomial interpolations like Lagrange's interpolation formula). Within each spline, a given number of points are interpolated, leading to a total number of *N* points with *N*>*M*.

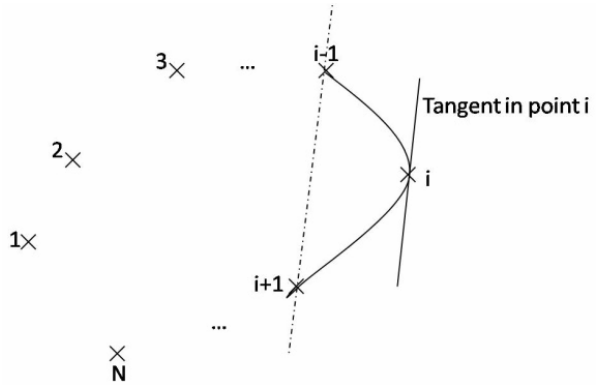

Figure 4. The tangent of the spline at point *i* is parallel to the line passing by points *i-1* and *i+1*

Taking care of the quality of the encoding amounts to find a satisfactory balance between the number *N* of points on the curve used for coding and the number *p* of harmonics used when decoding the genome into a curve. The number *p* of harmonics used for decoding has an influence on the production of details. The more harmonics used for the decoding the more precise will be the approximation to

the original curve. The number N of points on the curve used for coding the genome has an influence on the precision of the Fourier coefficients. This is due to the fact that we use the trapezium formula in (4) to approximate the integral during the calculation of the coefficients. We achieved numerous trials of (1) bordering a silhouette, (2) interpolating with N Points, (3) encoding with p harmonics, (4) decoding, for finally comparing the initial and the resulting silhouettes (see Figure 5). A qualitative design of experiments has been carried out (see Figure 6) with p varying from 80 to 2000 and N varying from 5 to 200. We clearly noticed that the if p is too low, the coding-deconding sequence – visually - fails to accurately represent the initial silhouette. In addition, for a given number p, there is a minimal number of points N beyond which the reconstructed curve displays strong oscillations (see such oscillations in Figure 5). In definitive, we found out that a satisfactory choice was achieved with a genome size of 71 and a number N of approximately 1500 points for the interpolation since both initial and resulting silhouettes were visually identitical.

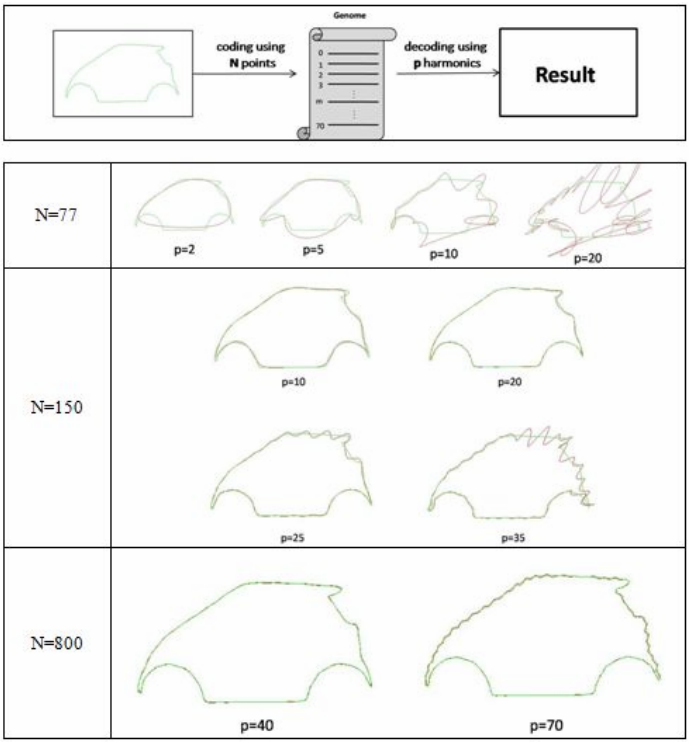

Figure 5. Comparison of silhouettes after interpolation with *N* points, encoding with *p* harmonics and decoding

A last operation of normalization is necessary to the genomes so that the phenotypes – silhouettes – be independent of a particular location, size or rotation but be compared uniquely in terms of their shape. The coefficient a_0 is simply set to 0 to fix the centre of gravity of all individuals at the origin of the representation plane. The invariance by rotation is useless because car silhouettes of the initial population are sketched horizontally and the next generations turn out to stay horizontal. Mc Garva [McGarva *et al* 1993] proposes to normalize the size of the curve in setting to 1 the small axis of the ellipse defined by harmonics 2. It would amount in our case to fix to a constant height the car silhouettes which is not fair for short cars. We prefer to have a surface area invariance instead. The

calculus is then a bit more sophisticated but simply consists in dividing all coefficients am by a value function of $|a_1|$ and $|a_{-1}|$ (formula not detailed here).

p\N	80	100	200	500	700	1000	1200	1500	2000
5	I	I	I	I	I	I	I	I	I
7	I	I	I	I	I	I	I	I	I
10	SO	I	I	I	I	I	I	I	I
15	SO	I	I	I	I	I	I	I	I
20	SO	O	G	G	G	G	G	G	G
30	SO	O	G	G	G	G	G	G	G
40	SO	SO	O	O	GG	GG	GG	GG	GG
50	SO	SO	O	O	GG	GG	GG	GG	GG
55	SO	SO	SO	O	O	GG	GG	GG	GG
60	SO	SO	SO	SO	O	O	GG	GG	GG
70	SO	SO	SO	SO	O	O	O	**GGG**	GG
80	SO	SO	SO	SO	O	O	O	GG	GG
90	SO	SO	SO	SO	SO	O	O	O	GG
100	SO	SO	SO	SO	SO	O	O	O	GG
120	SO	SO	SO	SO	SO	O	O	O	GG
140	SO	SO	SO	SO	SO	O	O	O	GG
170								O	GG
200								O	GG

Figure 6. The design of experiments carried out for finding an ideal (*p*, *N*). Initial and reconstructed silhouettes are visually compared to result in subjective assessments: I – inaccurate, O – oscillations, SO – strong oscillations, G – Good result, GG – very good result

3.2 Phase 2: Evolution of the population

We use an interactive genetic algorithm to evolve the population and create innovation. The individuals can reproduce among themselves and produce in this way new solutions. In our case the genetic algorithm handles a population of individuals where each individual represents a possible design for a car body silhouette. A fitness value is assigned to each individual by the user. Consequently the fitness value f is a number between 0 and 6 according to the grade given by the user via an interface. The interface developed (see figure 7) displays six individuals at a time and the user can browse through all the individuals of a population. The user is supposed to evaluate all the individuals of a population on a scale from 0 to 6, where 0 is the worst and six the best evaluation. This fitness decides if an individual has a good chance to reproduce and create children. Furthermore it influences the chance of an individual to survive and to live on in the next generation. This development is reached by applying the following genetic operators to the population:

- **Selection**: decides which individuals will reproduce and create children.
- **Crossover:** builds a child's genome from two parent genomes.
- **Mutation:** changes in a random way a genome after the crossover.
- **Killing:** decides which individuals from the parents' population will survive and live on in the new generation.

We decided to adopt some conventional choices in term of *selection* and *killing* operators and to propose an original crossover operator. First, apart the initial population of 30 individuals, we have fixed the number of individuals to 100 at each generation. We chose a turnover rate of 0.7, meaning that, for a coming generation, 30 individuals are kept from the previous one and 70 children are generated. In this way we do not lose potential good design solutions. The probability for an individual to be selected to be a parent is proportional to its fitness value (between 0 and 6). After choosing two individuals from the parents' population, their genomes are combined into the genome

of a child by applying the crossover and the mutation operators. Afterwards the two individuals are re-put into the parents' population. Indeed, an individual can be selected more than once by the selection operator.

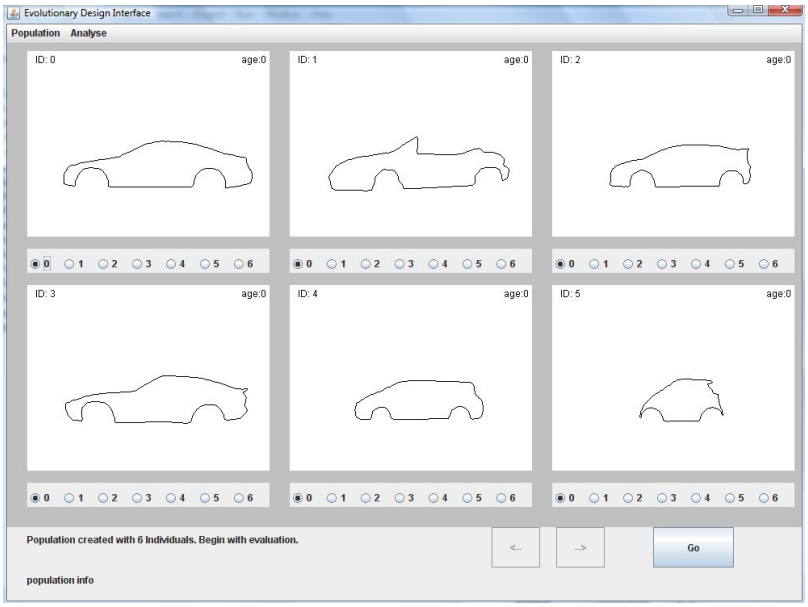

Figure 7. The User Interface for the designer evaluation showing 6 individuals of a larger population of 100. The designer can browse the individuals by clicking on the arrow buttons

We envisaged several possibilities to crossover the two genomes of parents into the one of the child. For instance, we envisaged a "Two-Part-Crossover"-method which seemed promising at the beginning. It consisted in choosing randomly a crossover point X, where X is a number between 2 and 69. The child's genome was built by the first X genes from the genome of parent A and the last (70-X) genes from the genome of parent B. This method produced innovative designs for car silhouettes and few useless forms. However the method didn't produce stable results over the generations. This means that after some generations the car silhouettes were useless because they lost the tires or began to oscillate.

The good idea is to operate a weighted mean between the gene values of the two parents to build the genome of the child. A crossover weight W is chosen randomly between 0 and 100. A new gene g^* is formed by calculating the weighted mean of the genes $g_{m,1}$ and $g_{m,2}$ of the parents after formula (7).

$$g_m^* = \frac{W g_{m,2} + (100 - W) g_{m,1}}{100} \tag{7}$$

In function of the weight W we obtain different new design solutions which continuously interpolate a silhouette between the two parents' silhouettes (see figure 8). The advantage of this method is the fact that a child resembles a lot to its parents and that it produces almost no useless car solutions (the tires keep their rounded shapes). The disadvantage is the relatively small explored space of possible solutions. In consequence, the population of design solutions has a tendency to converge rapidly. To enlarge the space of possible solutions we must apply a mutation operator (not detailed here).

The killing operator is applied to the original population and kills at first all the individuals who have a fitness of 0. These individuals are considered totally useless or totally non-satisfactory and shall no more contribute to the evolution of the population. All the other individuals have a chance to survive.

The individuals to be killed are chosen by an inverse roulette wheel method. That means that the probability pk_i for an individual to be killed can be expressed by formula (8).

$$pk_i = \frac{(7-f_i)}{\sum_{i=1}^{N^*}(7-f_i)} \tag{8}$$

where f_i is the fitness of individual i and $N^*$is the number of individuals in the population who have not been evaluated with a fitness of 0.

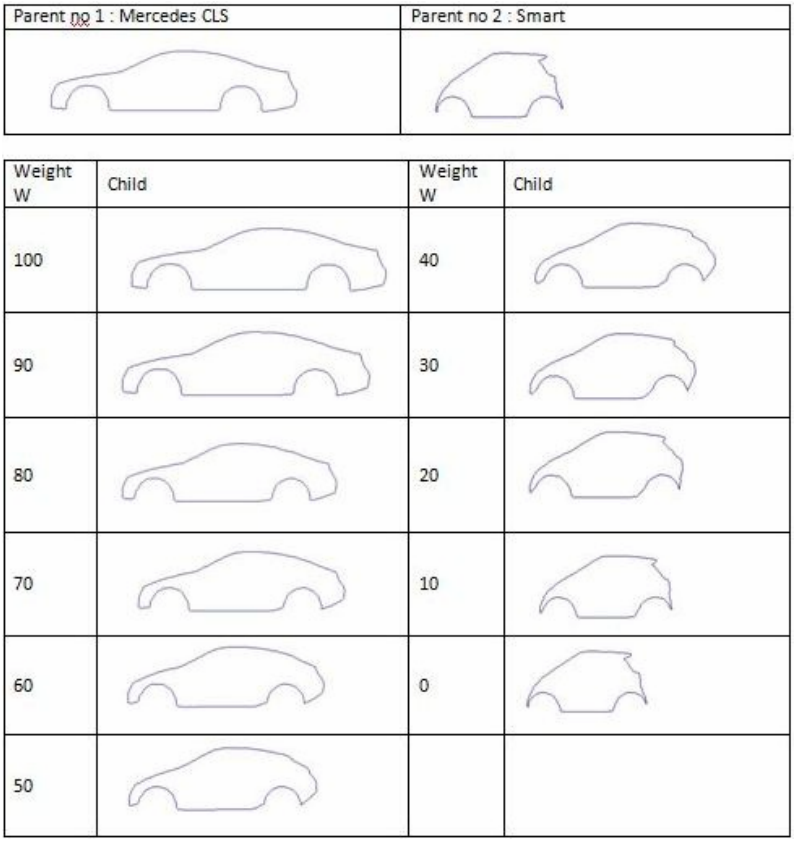

Figure 8. Results of a weighted mean crossover using different weights W

4. Test of convergence

Is our system really capable to produce innovation and novelty? Is it possible for a human being to design with the help of our system a new car body silhouette which was not part of the initial population? This question also implicates the question if the space of possible solutions which can be reached by our system is large enough to result in a car body which is really new and innovative?
To answer this question we can execute a simple test. A designer draws on a sheet of paper a car body silhouette which comes spontaneously to his mind and which is not part of the initial population. This car body silhouette is taken as “reference individual”. By working with our system he should try to obtain in the end the silhouette he had drawn before on the paper. To cope with this, he is supposed to evaluate the car solutions which look close to the reference individual with higher grades and those

who look different with lower grades. By counting the number of generations he needs to reach the reference individual, we can estimate the quality of our design system.
Alternatively the target car silhouette may be an individual of the initial population that is removed from this initial population.

We have preferred to make abstraction of the designer subjectivity in automating the ability of the system to converge towards an ideal car silhouette, so as to measure the sole quality of the method. The role of the designer is played by an algorithm, which automatically evaluates the individuals of a generation in terms of their similarity to the target individual. For that purpose, we defined a *similarity index* between two individuals.

4.1 The similarity index

The difference between two genomes G_k and G_l is given by $D(k,l)$ in formulas (9).

$$D(k,l) = \sum_{m=1}^{70} \alpha(m) \parallel g_{k,m} - g_{l,m} \parallel^2 \text{ with} \tag{9}$$

$$\parallel g_{k,m} - g_{l,m} \parallel^2 = (u_{k,m} - u_{l,m})^2 + (u_{k,-m} - u_{l,-m})^2 + (v_{k,m} - v_{l,m})^2 + (v_{k,-m} - v_{l,-m})^2$$

with $a_m = u_m + i\, v_m$, and $\alpha(m)$ a weight factor which should give more importance to the first genes than to the last genes because it is more easy to perceive. A series of user tests have been carried out to identify $\alpha(m)$ for several values of m. We found out that $\alpha(m)$ is exponential and we approximated it with:

$$\alpha(m) = 1.08\, e^{-0.08m} \tag{10}$$

Finally we define the *similarity index* between two genomes k and l as:

$$SimInd(k,l) = \frac{100}{1+\frac{1}{N}\cdot D(k,l)}\,\% \tag{11}$$

where N is a normalisation factor.

4.2 The results

For the test we used the car in figure 9.a as reference individual. The parameters for the genetic algorithm were the following: population of 100 individuals, turnover rate of 0.7 and mutation probability of 0.3. The mutation could change a gene in a range of ±(50%-200%). After 10 generations our system reached the car body silhouette in figure 9.b which has a similarity index of 92%, which can be considered as a much satisfactory result.

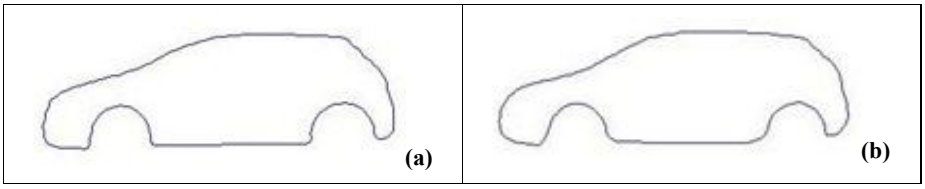

Figure 9. Comparison between the reference silhouette (a) and the final resulting silhouette (b)

The average fitness of the population converges over the generations to a high value (see figure 10), whereas the value of the best similarity index in the population (the fitness of the fittest individual) raises rapidly from relative low 44% to 92%.

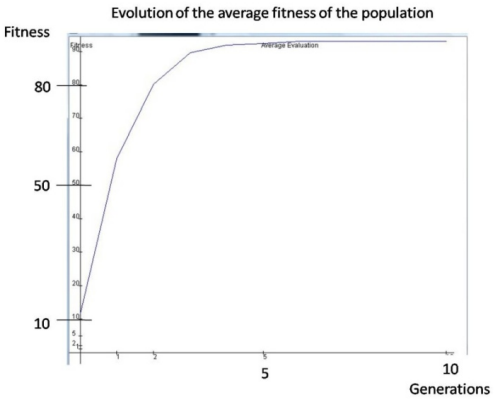

Figure 10. The average fitness of all individuals in the population over the generations

5. Concluding remarks

We have presented an encoding method which works on the basis of development of the design object's silhouette into Fourier series. This method is very flexible and applicable to many design objects. The quality of coding and decoding has been subjectively assessed and tuned to be satisfactory. Furthermore we have used this encoding method to conceive an automatic design system working with an interactive genetic algorithm to evolve the design and create novelty. A crossover method for this new concept of genomes has been defined and evaluated. Finally, a formula has been identified to express a *similarity index* between two genomes in terms of the perceived difference of the phenotypes. In less than 10 generations, it has been showed that our system is able to automatically converge with a good quality toward a reference silhouette individual which is not present within the initial population. In consequence, our system should allow style designers to converge towards intuitive ideas and to make emerging surprise in exploring large spaces of potential silhouettes.

This concept seems to be a promising way to create future automatic design systems. Several perspectives of extensions are:

- Allowing a step of "direct modification by the designer" within an intermediairy generation, i.e. modifying some details of a silhouette curve or even adding new individuals to the population. We must acknowledge here that all our 30 initial silhouettes are silhouettes of existing commercial cars. Then, the experiment in this paper has just consisted in morphing between known solutions. For really creating surprise and innovating, we must also test our system in a more creative way.
- Combining several series of closed curves to better define the important lines of a car (see [Cheutet 2007]).
- Making more complex the interactive assessment of individuals by the style designer through multicriteria assessments under several perceptual attributes like "Dynamic" or "Comfortable" (see [Dagher *et al* 2007]).

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