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EFFICIENCY ASSESSMENT OF AN EVOLUTIVE DESIGN SYSTEM OF CAR CONTOURS

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ABSTRACT

So as to create innovative car silhouettes, we propose in this paper a model based on an Interactive Genetic Algorithm using an encoding of a design solution by a Fourier analysis approach. This model permits the designer to browse through generations of car profiles from an initial population of existing silhouettes. By qualitatively assessing each individual, the user converges towards solutions complying with his/her requirements and thus potentially creates novelty. We describe here tests for assessing the efficiency of this innovative design platform. These tests are based on a similarity matrix, a similarity measure being the perceived distance between two cars silhouettes. The results show a highly satisfactory behavior of the model and open perspectives thanks to its flexible and extensible aspects.

Keywords: Interactive Genetic Algorithm, Evolutionary Design, user tests, similarity index, subjective evaluation.

1 INTRODUCTION

Novelty emergence is a priority for the style designer. Thus CAD tools that permit to help them in a creative way are really precious. However most of those existing tools often offer wide possibilities, but they are not really compatible with the human and sometimes artistic refinement process that leads to 2D sketches. In this field of study, the theory of Evolutionary Design (ED) seems to be very promising, and particularly Genetic Algorithms (GA) that were originally used for complex optimization problems [1] [2].

GAs work as an analogy to the theory of Evolution. The structure and the apparent qualities of each design solution, called *phenotype*, are encoded in a *genome*. From an initial population of such individuals, a GA permits to create generations of individuals that are combinations of individuals of the previous generation. This operation is called *crossing over*. By assessing each individual the algorithm displays better and better design solutions thanks to a selection operator that links assessment and probability for an individual to be used in the creation of the next generation.

The principle of an Interactive Genetic Algorithm (IGA) is similar, but the assessment is performed at each generation by the user himself [3]. Thus an IGA is particularly adapted to the situation that we described above, when human decisions and aesthetics are essential.

So we propose in this paper a model based on such an algorithm to design car silhouettes, or more generally 2D product profiles. Different ways to encode the silhouette individuals exist, but they often have the disadvantage to be conceived for a given domain. Our encoding method is based on a Fourier analysis approach and can be applied to all possible objects represented by a 2D-closed-curve. We have chosen to work on car silhouettes because it is often meaningful for everyone.

In this way, innovative and new concepts are expected from the collaboration between a car designer and the IGA.

As the human aspects are really essential in this process, we need a way to validate the model by taking the user perception into account. We propose to use a similarity index, that is described in this paper, and which permits to automatically measure the perceived distance between two car profiles. Automatic and user tests have then been performed to characterize our model of shape emergence. They show a satisfactory behavior in terms of convergence, diversity of satisfactory solutions and often interesting perspectives about the user perception.

We present in section 2 our model by detailing the encoding system and the IGA. Then in section 3 we present the construction of the similarity index and the different versions that have been tested to obtain an efficient tool. Section 4 describes the automatic test and the four user tests performed with this index to validate the model. Finally we conclude in section 5 with some remarks and perspectives.

2 MODEL DESCRIPTION

This part has been developed in more details in a previous paper (see [4]). However, the model description is necessary to understand the next parts of this paper.

2.1 Mathematic definition of the encoding of the silhouettes

The main difficulty when using genetic algorithms in automatic design is the encoding of the genome (see [5]). Different methods exist like direct encoding with geometrical dimensions [6; 7], tree structure [8] shape grammars [9; 10] or a set of predefined components [3]. But the main disadvantage of these methods is that they are dependent from the context, that means they are conceived for a given product design objective. In consequence, an expert and time consuming modeling process is necessary for each application.

We use here an encoding method for a 2D-closed-curve based on the works of McGarva [11], using development into Fourier series for coding the phenotype of the car silhouettes. We have personally already used this theory in [12] for encoding a 2D-closed-curve into the five first Fourier harmonics of this decomposition. Numerous advantages are associated with such a method:

- Almost all possible 2D-closed-curves may be generated
- Every detail may be represented (which is really important to stimulate emotions and create novelty)
- The genomes have a constant length (which is simpler for the crossing over operation)
- The Fourier harmonics are narrowly associated to apparent characteristics of the phenotype.

McGarva'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:

$$z(t) = x(t) + i\,y(t)\textbf{\textit{Erreur ! Signet non défini.}} \tag{1}$$

As $z(t)$ is a closed curve, its function is periodic. The period is normalized with: $z(t+1) = z(t)$. This function $z(t)$ can be developed into a Fourier series, according to formula (2):

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

where the complex Fourier coefficients can be calculated by formula (3):

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

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. In order to calculate the a_m coefficients (3) we need a numerical 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:

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

while z is a periodic function, ($z_{N+1} = z_0$). t_k is defined by:

$$t_k = \frac{L_k}{L} \tag{5}$$

where the total length L is the sum of the lengths of all segments, L_k is the length from the origin to the current point, with $x_{N+1} = x_0$ and $y_{N+1} = y_0$.

To construct the genome of an object, we develop its silhouette into 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).

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

where t_k ($0 \leq t_k \leq 1$) 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 the approximation to the original curve. We call p the "precision" of decoding.

2.2 Creation of the initial car silhouettes

We divide the IGA process into two main phases (see Figure 1): the creation of an initial population, and the evolution of the population.

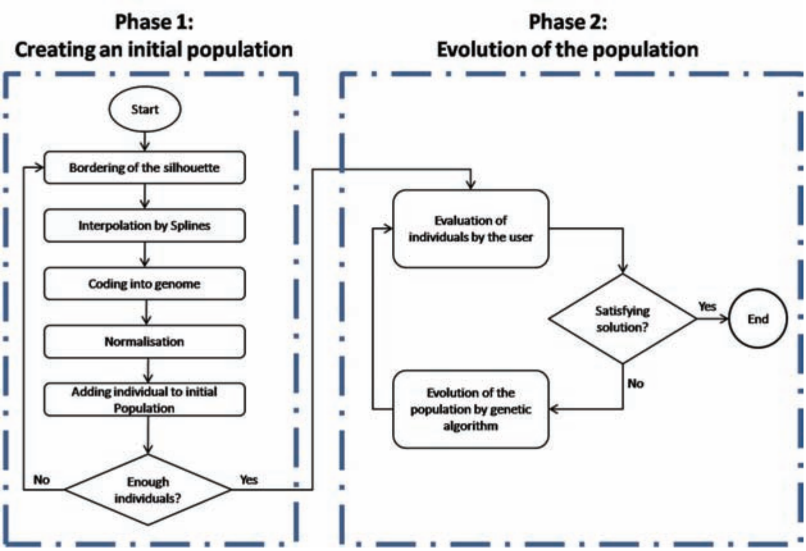

Figure 1. Diagrammatic plan of the IGA process.

The initial population consists of silhouettes of several already existing car bodies. We programmed an interface in Java to border a silhouette from a photograph by clicking on the screen and to encode it into Fourier harmonics. In order to obtain a good quality, a sufficient amount of points should be used to represent as many details as possible (a number M of 60 to 80 points are needed). However M is not sufficient.

Indeed to obtain a highly detailed phenotype (car silhouette after decoding), a high quality genome is needed, which is not the case with such values of M. Consequently we need to augment the number of points on the curve by smooth interpolations. We choose bicubic splines linking three successive points, because the result is very close to the original curve and few oscillations are noticed. We finally have a total number of N points with $N>M$. N has a strong influence on the precision of the Fourier coefficients.

The number p of harmonics used to decode the genome has a strong influence on the final result too. Thus it is necessary to determine a satisfactory balance between N and p. 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. A qualitative design of experiments has been carried out with p varying from 80 to 2000 and N varying from 5 to 200 (see [4]). 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 identical. Then a last operation of normalization is necessary in order to obtain car silhouettes that are independent of a particular location or size.

2.3 Evolution of the population

An initial population of silhouette individuals can evolve to create new generations of design solutions (Phase 2 on Figure 1). During an operation called crossing over, the car silhouettes reproduce themselves to create new individuals. A fitness value *f* between 0 and 6 (where 0 is the worst and 6 the best evaluation) is assigned to each individual, according to the grade given by the user-designer via an interface (see Figure 2). It is important to notice that the meaning of the scale is chosen by the user himself. No reason is stored, letting the user-designer freely behave. But it may sometimes have bad effects, because the user can change his/her own assessment scale and preferences during the evaluations.

On the interface of Figure 2 six individuals are displayed at a time and the user browses through all the individuals of a population. He/she is supposed to evaluate all the individuals of a population. In order to permit novelty emergence and to optimize creativity, four operators have been implemented: selection, crossover, mutation and killing.

After choosing two individuals from the parents' population thanks to the selection operator, 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.

- **Selection**: decides which individuals will reproduce and create children according to the fitness values. The probability for an individual to be selected to be a parent is proportional to its fitness value (between 0 and 6).
- **Crossover:** builds a child's genome from two selected genomes (called parents). 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):

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

  Varying weight W between 0 and 1, we can obtain different new design solutions which continuously interpolate a silhouette between the two parents' silhouettes. With this interpolating crossover operator, children inherit from visual characteristics of their two parents and no ill-car is produced. To enlarge the space of possible solutions and create more surprise and novelty for the designer, we further apply a mutation operator.
- **Mutation:** changes in a random way a genome after the crossover.
- **Killing:** decides which individuals from the parents' population survive and live on in the new generation. We chose a turnover rate of 0.7, in this way we do not lose potential good design solutions.

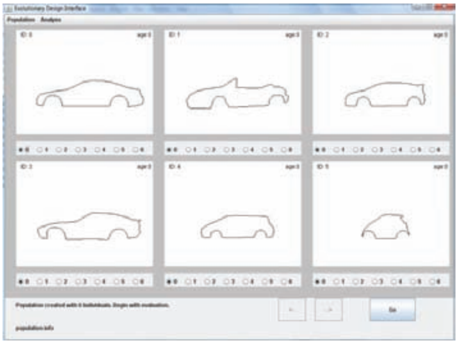

Figure 2. User Interface for the designer evaluation showing 6 individuals of a larger population. The designer can browse through the population by clicking on the arrow buttons.

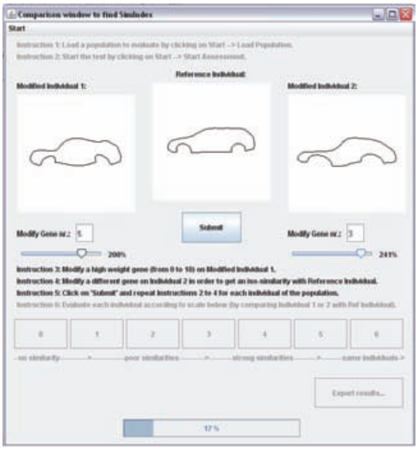

Figure 3. Java interface to calculate the parameters a *and* b

3 BUILDING OF THE SIMILARITY INDEX

Is our system really capable to produce innovation and novelty? Is it possible for a user to design with the help of our system a new car body silhouette which was not part of the initial population?

To answer these questions, it could be useful to have a tool that permits to automatically measure the perceived difference between two car silhouettes and to prove that two car silhouettes are really close or not. That is why we propose to create a similarity index. Based on user assessments, it would permit to easily measure the difference between two car profiles. It would be a helpful tool to realize tests and prove results.

We propose here a description of the process to get this similarity index. Two different ways have been tested. The first is based on an exponential formula, and the second uses weights associated to genes.

3.1 Mathematic definition

We first define *D(k,l)* the distance between two genomes G_k and G_l. As the modifications on the ten first genes only are visually significant (modifications on higher order genes produce small-scale perturbations), the sum only considers those ten genes. And *D(k,l)* is:

$$D(k,l) = \sum_{m=1}^{10} \alpha(m) \parallel g_{k,m} - g_{l,m} \parallel^2 \tag{8}$$

The factor $\alpha(m)$ is a weighting factor which should give more importance to some genes according to their participation in the modification of the silhouettes. Here $g_{k,m}$ is gene number m from genome k and $g_{l,m}$ is gene number m from genome l. One gene consists of two harmonics, called a_m and a_{-m}, which are complex numbers; they can be written as: $a_m = u_m + i.v_m$.

Then we define:

$$\parallel g_{k,m} - g_{l,m} \parallel^2 = \frac{(u_{k,m}-u_{l,m})^2}{(u_{max,m}-u_{min,m})^2} + \frac{(u_{k,-m}-u_{l,-m})^2}{(u_{max,-m}-u_{min,-m})^2} + \frac{(v_{k,m}-v_{l,m})^2}{(v_{max,m}-v_{min,m})^2} + \frac{(v_{k,-m}-v_{l,-m})^2}{(v_{max,-m}-v_{min,-m})^2} \tag{9}$$

where $u_{max,k}$ and $u_{min,k}$ (respectively $v_{max,k}$ and $v_{min,k}$) are the maximal and the minimal values of u_k and v_k on the whole initial population.

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

$$SimInd\,(k,l) = \frac{100}{1+D(k,l)}\,\% = \frac{100}{1+\sum_{m=1}^{10}\alpha(m)\parallel g_{k,m}-g_{l,m}\parallel^2}\,\% \tag{10}$$

As a result with this definition, the similarity index in included between 0 and 100%, where 100% means that the two individuals are identical.

We now have to define the factor series $\alpha(m)$.

3.2 Exponential form

In this section we assume that $\alpha(m)$ can be written as an exponential expression which gives more importance to the first genes than to higher order genes, because a modification of the first genes impacts more the car silhouette than a modification of the last ones. Thus $\alpha(m)$ is expressed as:

$$\alpha(m) = a\, e^{bm} \tag{11}$$

where *a* and *b* are two constant terms to estimate after user tests. So *D(k,l)* becomes:

$$D(k,l) = \sum_{m=1}^{10} a\, e^{bm} \parallel g_{k,m} - g_{l,m} \parallel^2 = a \times \sum_{m=1}^{10} e^{bm} \parallel g_{k,m} - g_{l,m} \parallel^2 \tag{12}$$

But now we need to find significant values of *a* and *b*.

We propose the following process to measure *b* (see also Figure 3):

1. Choose a genome, which is copied 3 times: *G0*, *G1*, *G2*.
2. Choose a gene *i* in *G1* (better with a low weight to be significant): $g1_i$.
3. Choose a gene *j* ($i \neq j$) in *G2* (better with a low weight to be significant): $g2_j$.
4. Modify the gene $g1_i$ of *G1* in an arbitrary way.
5. Modify the gene $g2_j$ of *G2* in such a way that there is an *iso-similarity* (defined below) between *G0* and *G1* on the one hand, and *G0* and *G2* on the other hand.

We define the *iso-similarity* in this way:

Two couples of car silhouettes are *iso-similar* if the perceived level of similarity is the same for the two couples. For example, it would mean here that the level of similarity is the same between *G0* and *G1*, and between *G0* and *G2*. Practically, it means that the user has to modify the gene $g2_j$ until the level of perceived similarity becomes the same between *G0* and *G1* as between *G0* and *G2*. In that way, *G2* and *G1* are not identical, but their level of similarity according to *G0* is the same.

Then we can write the following equality:

$$\alpha(i) \times \| g0_i - g1_i \|^2 = \alpha(j) \times \| g0_j - g2_j \|^2 \tag{13}$$

And *b* is:

$$b = \frac{1}{(j-i)} \times \ln \frac{\|g0_i - g1_i\|^2}{\|g0_j - g2_j\|^2} \tag{14}$$

By making *n* times this tests with different car profiles and different users, we get *n* different *b* values. The final value of *b* adopted is the average.

Table 1. Scale of similarity for user assessments

Level of similarity	Value of similarity index
0	5%
1	30%
2	50%
3	65%
4	80%
5	90%
6	100%

The next step consists in measuring *a*. We propose the following process: for each of the previous comparison (between *G0*, *G1* and *G2*), the user defines the level of similarity ("the similarity between G0 and G1 on the one hand and G0 and G2 on the other hand is 70%" for example). As it is very hard to express such a value, we propose to work with a 7 degrees scale; the user just chooses the level of similarity in the Table 1.

Then it is possible to write:

$$x\% = \frac{100}{1 + a \times \sum_{m=1}^{10} e^{bm} \|g0_m - g1_m\|^2} \tag{15}$$

where *b* is the average value of the previous tests. And *a* is:

$$a = \frac{1}{\sum_{m=1}^{10} e^{bm} \|g0_m - g1_m\|^2} \times \left(\frac{100}{x\%} - 1\right) \tag{16}$$

We also obtain 2*n* different *a* values. The average value is acceptable if the standard deviation is low. The calculation of the similarity index is now completed.

Practically, we use a Java interface (see Figure 3) that permits to follow the processes described above by loading a population.

3.2 Weighted form

In the previous section, we assumed that $\alpha(m)$ should give more importance to the first genes that to the last ones and can be written as an exponential expression. But some experiments showed us that this assessment could be wrong when using the ten first genes only: the importance of these genes is not necessarily relative to their rank. Each $\alpha(m)$ is now associated to a given weight p_m.

And *D(k,l)* becomes:

$$D(k,l) = \sum_{m=1}^{10} p_m \| g_{k,m} - g_{l,m} \|^2 \tag{17}$$

To obtain the weights values, we follow the same process as with the exponential form. And we finally obtain the following expression:

$$p_i = \frac{\|g0_j - g2_j\|^2}{\|g0_i - g1_i\|^2} \cdot p_j \tag{18}$$

By performing this test *n* times (*n>10*) with different values for *i* and *j* (to cover all the ten first genes), we have a system of *n* equations, that can easily be solved with the *logarithmic least square* method. The tests are performed with a modified version of the Java interface described in the previous section.

3.3 Performance comparison and choice of the index

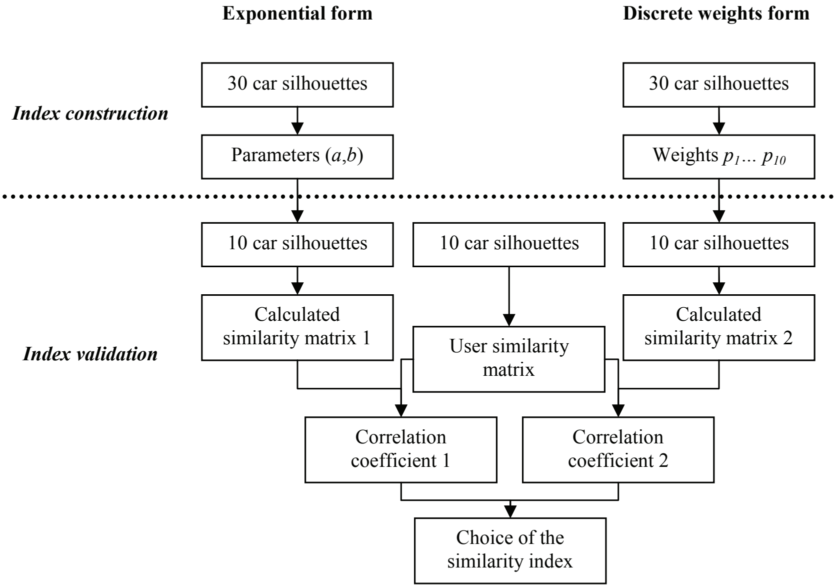

Figure 4. Choice of the similarity index type

To find out the best version of the similarity index, we perform the tests described in Figure 4. The same 30 car silhouettes are used to build the two similarity indexes. After that, the same 10 car silhouettes are used to validate it and permit to choose the best one. We obtain 2 similarity matrices, and we ask users to assess the same 10 profiles in a third matrix, according to the scale of the table. These three matrices permit to calculate two correlation coefficients.

We obtain with the exponential form of the index a correlation coefficient of 0.45, and the value is 0.7 with the discrete weights form. Thus we choose this second form for the similarity index. We can now perform user tests to validate our model thanks to this similarity index.

4 VALIDATION TESTS

To validate our model we first performed simple user tests without the similarity index, based on Kim works [3]. These tests are described in details in [13], so we just present here the important results that we obtained. The data were collected during a subjective evaluation workshop with 8 users and 2 semantic attributes (4 users worked with the word *friendly*, and 4 users with the word *sportive*). We asked the users to find out the best car silhouettes according to their semantic attribute, after 10 generations of 20 individuals and with non-hedonistic evaluations. Then we asked them to compare those best silhouettes with the best ones obtained in a basic way (profiles printed on paper, without genetic algorithm). Our conclusions are:

- The user satisfaction increases with the generations.
- The results are globally better with the IGA than without.
- However, some major differences can be noticed between the two semantic attributes. Indeed the user perception is really different from one user to another: *sportive* seems to be perceived in the same way by everyone, whereas each user has a different perception of *friendly*.

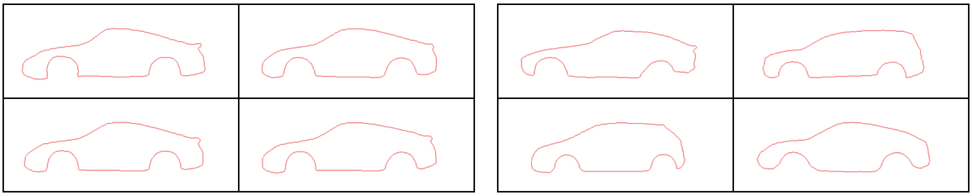

Figure 5. Examples of best sportive *(on the left) and* friendly *(on the right) car silhouettes (one from each user).*

So to confirm these observations we have proceeded to more sophisticated post-processing analysis, using the similarity index described in section 3.

We propose here five user tests that use the similarity index to process the same data (except the first one) as those used for the previous tests (see [12]).

4.1 Test of "novelty emergence"

4.1.1 Test construction

The goal of this test is to show that it is possible to reach a defined individual which is not part of the initial population.

A designer draws on a sheet of paper a car body silhouette which comes spontaneously to his/her 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 reckoning the number of generations he needs to reach the reference individual, one can estimate the quality of our design system.

But this method is highly linked to the designer subjectivity, which would probably influence the results. Our objective is just to estimate the convergence ability of the model. If no automatic convergence is observed, there will probably not be a convergence with any user test. That is why we have preferred to perform an automatic test. The target individual is a car silhouette that has been removed from the initial population. 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, using the similarity index.

4.1.2 Results analysis

For the test we used the car in Figure 6a 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 6b which has a similarity index of 92%, which can be considered as a much satisfactory result.

The average fitness of the population converges over the generations to a high value (more than 95%), 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%.

Thus our system is able to automatically and quickly (less than 10 generations) converge towards a given car silhouette that is not in the initial population. It means that the space of possible solutions which can be reached by our system is large enough. This is necessary to be able to produce innovation and novelty.

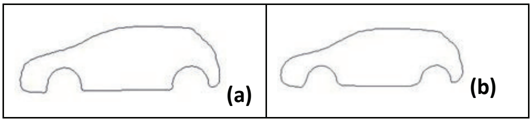

Figure 6. Example of comparison between the reference silhouette (a) and the final one (b).

4.2 Test of “diversity lowering”

4.2.1 Test construction

The aim of this test, called test of “*diversity lowering*” is to study:

- The evolution of the similarity index for each user along the ten generations.
- The similarities that could exist between the individuals of the last generation of each designer.

The idea consists simply to calculate the similarity index between all the individuals of all the users and for all the generations of the previous workshop (see [13]), and to group together the data to observe potential correlations.

A high value of similarity for the last generation would mean that the IGA converges towards a single individuals family, and so that there is a diversity lowering.

4.2.2 Results analysis

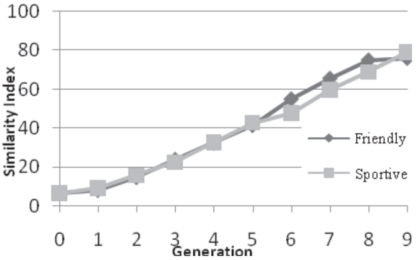

Figure 7. Evolution of similarity index along generations for the two semantic attributes.

These results concern the evolution of the similarity index of each user. The curves are shown on Figure 7 .The initial population has an average of 6.5% of similarity. In all the cases and for the two semantic attributes, the values increase quickly. At the 6th generation (Generation #5 on the graph), the averages of all the users are above 40% similarity, and at about 75% for the last generation. The averages of each user (in italic in tables 4 and 5) are all included between 60 and 90% of similarity, which correspond to a level of very strong similarities.

It shows that for each user, the model converges towards a single family of car silhouettes, which are very close in terms of visual aspect. But it means too that there is a real diversity lowering.

4.3 Test of “inter-designer convergence”

4.3.1 Test construction

The goal of this test, called test of “*inter-designer convergence*” is to study the similarities that could exist between the last generations of all the users.

As in the previous test, the idea consists simply to calculate the similarity index between all the individuals of all the users and for all the generations of the previous workshop (see [13]), and to group together the data to observe potential correlations.

4.3.2 Results analysis

The results are displayed on Tables 2 and 3. These matrices represent the averages of the similarity index for the two semantic attributes:

- Between all the users (in bold).
- For each user (in italic). These values are treated in the previous test.

The values are really consistent with the visual aspect of the individuals. For the semantic attribute *friendly*, the values inter-designer (in bold) are not high, and the total average is only 9.21% similarity, whereas this total average is 50.83% for the attribute *sportive*. It means that the similarity between the last population of the users with the attribute *sportive* is very strong, and that results obtained with the attribute *friendly* are strongly dissimilar.

These results confirm rigorously that the perception of the word *sportive* is well shared by all users (they all came to a similar type of profiles), whereas each user has its own perception and interpretation of the word *friendly* (they all have a different kind of car silhouettes at the end of the workshop). In fact, we will see further that everyone has been strongly influenced by the design of the *Porsche 911* which has been recognized by everyone as the most sportive car without any doubt.

Table 2. Similarity values between users for the semantic attribute friendly (in %).

	User 5	User 6	User 7	User 8
User 5	*79,07*	**6,91**	**4,02**	**2,89**
User 6		*89,65*	**20,65**	**8,81**
User 7			*61,02*	**11,97**
User 8				*74,16*
	Total average		**9,21**	

Table 3. Similarity values between users for the semantic attribute sportive (in %).

	User 1	User 2	User 3	User 4
User 1	*79,95*	**47,87**	**63,09**	**36,20**
User 2		*72,34*	**74,14**	**42,62**
User 3			*89,61*	**41,04**
User 4				*74,74*
	Total average		**50,83**	

4.4 Test of "superiority of the IGA model"

4.4.1 Test construction

This test is called test of "*superiority of the IGA model"*. Its goal is to show that our model obtains better results than without, in particular in terms of time and number of individuals.

It consists in comparing for each user the 3 best individuals of the IGA with the 3 best individuals obtained without the IGA (printed on paper, see [13]) with the similarity index.

4.4.2 Results analysis

The maxima of similarity are shown in Table 4. For 5 users out of 8, the maximum is above 70% of similarity. For 2 users, the maximum is included between 20 and 30%. For the last one, it is only 2.67% of similarity. These values mean that it is possible to obtain similar results with and without our model. 5 users have found with the IGA *at least* one individual that is common or very close to one of the paper individuals. 400 individuals were proposed on paper. It took about 45 minutes for the user to evaluate them. Less than 200 individuals were used with the IGA (10 generations of 20 individuals, minus those who survive from one generation to the next one), during about 20 minutes. Thus we can say that our system seems to be able to bring the same results as without the model, more quickly and with less individual assessments.

Table 4. maxima of similarity values between best individuals of the IGA and paper individuals (in %).

Sportive	User 1	84,49
	User 2	21,26
	User 3	80,92
	User 4	97,93
	Average	71,15
Friendly	User 5	2,67
	User 6	98,09
	User 7	71,32
	User 8	26,94
	Average	49,75
Total Average		60,45

4.5 Test of “attraction in the surroundings of initial individuals”

4.5.1 Test construction

The last test proposed in this paper is called test of “*attraction in the surroundings of initial individuals*”. It tries to answer the following question: is the user really able to design his/her own car silhouette, or are the final individuals influenced by the initial individuals and close to their genotypes? Our solution to this problem is to compare the best individuals of the IGA with the 20 car silhouettes of the initial population.

4.5.2 Results analysis

The results of this test are very interesting, but too sizeable to be displayed here. That is why only the case of user 2 is presented on Table 5.

Table 5. Example of similarity values for the comparison between the best individuals of the IGA and the initial population (in %).

		User 2		
		Best Individual 1	**Best Individual 2**	**Best Individual 3**
Initial Population	**Ind 0**	2,04	1,93	1,84
	Ind 1	2,95	2,77	2,65
	Ind 2	10,02	9,02	8,80
	Ind 3	0,91	0,88	0,90
	Ind 4	3,45	3,24	3,35
	Ind 5	2,04	1,94	1,91
	Ind 6	1,42	1,36	1,36
	Ind 7	1,78	1,74	1,52
	Ind 8	13,90	13,73	10,75
	Ind 9	6,62	6,17	6,53
	Ind 10	2,76	2,60	2,47
	Ind 11	3,28	3,41	2,91
	Ind 12	2,08	1,97	1,97
	Ind 13	69,65	69,89	53,21
	Ind 14	3,50	3,30	3,46
	Ind 15	7,15	7,23	10,83
	Ind 16	2,07	1,97	1,93
	Ind 17	3,05	2,88	2,87
	Ind 18	1,65	1,58	1,47
	Ind 19	1,99	1,93	1,69

This table shows that the best individuals of user 2 are very close to Individual #13 of the initial population (more than 50% of similarity). Individual #13 represents the silhouette of a Porsche 911. Two other minor influences can be noticed (with Individuals #2 and #8), but the values are below 20%, which is not significant. User 2 worked with the semantic attribute *sportive*, and it is important to notice that similar results are obtained with the 3 other users who worked with this attribute.

That means that they all came to a similar type of profile (see section 5.1.2) which is very close to a *Porsche 911*. In other words, all the users perceived a *sportive* car as a *Porsche 911*.

For the semantic attribute *friendly*, the results are totally different. No car that influences all the users can be identified. In 2 cases out of 4, no significant influence of an initial individual is noticed. In the two other cases, such a car can be identified, with the scores of 40% of similarity, but this car is different for the two users (*Porsche 911* for the one, *Chevrolet Corvette C4* for the other). It shows again that this attribute is differently perceived.

4.3 Synthesis

Those five tests based on the similarity index permit to prove rigorously some results. Indeed in all cases the system turns out to converge towards a uniformized population. For the semantic attribute *sportive*, this profile is similar for any of the four users and is close to a *Porsche 911*. It can be explained here by the fact that the user-designers that have performed these tests were intellectually too passive and in a concept-rating attitude than intellectually creative in a concept-pushing attitude.

For the semantic attribute *friendly*, no particular influence from the initial population is observed, and the final designs are specific to each user. In addition, the perception of the attributes is really different from one user to another. Moreover, our model converges quickly and with less individuals than without the model, which is highly satisfactory.

However, some remarks can be formulated:

- The model always converges towards one profile family. Is it not possible to converge towards at least two different families?
- What happens if the Porsche 911 or the other influencing cars are not in the initial population? Do the users even find them?
- Why are there so many differences in the perception of the semantic attributes? Some concepts of Emotional Design could be introduced to develop a more powerful model.

5 CONCLUDING REMARKS

From the user tests based on the similarity index that we have presented in this paper, we can say that our model is highly satisfactory. Indeed we obtain very promising results: the users are satisfied and the results are better with our model than without. It also potentially creates novelty and the results are potentially different from one user to another; in fact those two assessments depend on the chosen semantic attributes, and some further works have to be done to elucidate them.

The case study of car silhouettes is moderately realistic since other phenomena than side profiles must be considered to externally compare cars. But, our design platform has proved to be really flexible and extensible, because it is not confined to a product field. We believe that excellent results could be obtained with other case studies for which the profile embeds a major part of aesthetical assessment. The ideal shape might be a simple 2D-closed-curve from a solid of revolution, like stemmed glasses or vases. Finally, it could be really interesting to allow a step of direct modifications by the designer during the genetic algorithm process, which means to modify a selected individual with a graphic tool and to reinject it in the current population.

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