Simulation of Genetic Inheritance in the Generation of Virtual Characters

Roberto C. Cavalcante Vieira, Creto Augusto Vidal, Joaquim B. Cavalcante-Neto *{roberto, cvidal, joaquimb}@lia.ufc.br*

Department of Computing - Federal University of Ceará - Fortaleza - CE - Brazil

ABSTRACT

Nowadays, applications of virtual reality (VR) and computer games use human characters models with ever-increasing sophistication. Additional challenges are posed by applications, such as life-simulation computer games (The Sims, Spore, etc.), internet-based virtual worlds (Second Life) and animation movies, that require simulation of kinship and interaction between isolated populations with well defined ethnic characteristics. The main difficulty in those situations is to generate models automatically, which are physically similar to a given population or family. In this paper, human reproduction is mimicked to produce character models, which inherit genetic characteristics from their ancestors. Unlike morphing techniques, in our method, it is possible that a genetic characteristic from an ancestor be manifested only after a few generations.

KEYWORDS: Modeling of virtual characters · Genetic inheritance · Reproductive simulation.

1 INTRODUCTION

In many applications of virtual reality and computer games, it is necessary to populate the environments with virtual characters. The demand for realistic models that meet the current needs of new technologies and applications has become a major challenge.

Additional challenges are posed by applications, such as life-simulation computer games (The Sims - http://thesims.ea.com), internet-based virtual worlds (Second Life - http://secondlife.com) and 3D animation movies, which require simulation of kinship and interaction between isolated populations with well defined ethnic characteristics.

Sometimes, populating a virtual environment is a process, which occurs dynamically during the application run. When populations with distinct ethnic characteristics are put in contact, due to migration, for instance, it is reasonable to expect that, over time, the original populations will intermix and the resulting population of descendants presents mixed traits (genetically determined characteristics) from their ancestors.

The problem we address in this paper is the automatic transfer of traits through simulated human reproduction, for use in virtual reality systems (see Figure 1). In Section 2, we present some of the most relevant related works. In Section 3, we discuss concepts of anthropometry and some recent studies that relate the individuals' physical appearance to the action of genes. In Section 4, we summarize the important biological concepts of diploid reproduction. In Section 5, a case study illustrates the general process described in Section 4, focusing on face generation. In Section 6, we present some conclusions.

2 RELATED WORK

The most relevant related works presented in this section do not address directly the problem of transmission of traits across generations, but they do address the problem of variability in populations of virtual characters, which our technique can also address naturally. Our previous work [14] describes a model, based on simulated reproduction, which is focused on generating variability, from two parental models.

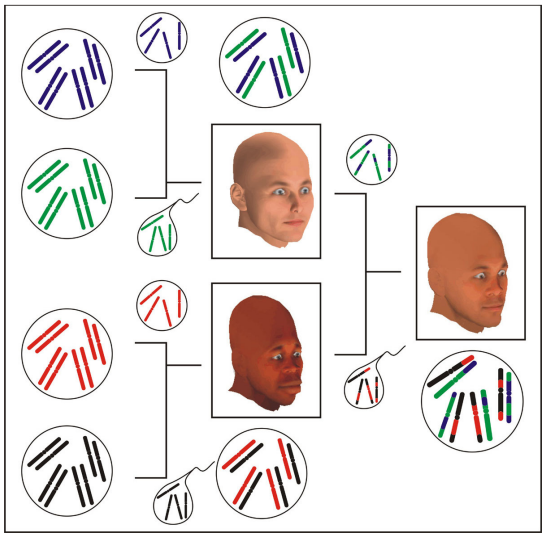

Figure 1. Transmission of traits to a descendant model.

In 1998, DeCarlo et al. [3] devised a system capable of generating facial models for virtual reality applications automatically. That work, which was one of the firsts to use anthropometric techniques [10] for face generation, inspired several other works [2, 6]. DeCarlo used B-Spline surfaces to construct a base model, which respected established anthropometric measures, and perturbed those measures randomly, within predefined ranges, in order to generate other models. Blanz and Vetter [2] treated faces as members of a vector space. Thus, starting from a database of faces, captured through scanning of real subjects, they used Principal Component Analysis (PCA) to determine a set of face basis vectors that could be linearly combined in order to generate new faces within that vector space. They were able to generate realistic models with a great deal of variability. Praun et al. [11] used parameterization techniques to combine features of two or more models with different topologies, generating interpolated models. Although their morphing technique showed interesting results, defining the parameters required considerable human effort. Kähler and his co-authors [5, 6] built a generic model with anatomical layers (skin, muscles and bones) associated with anthropometric landmarks and, based on anthropometric information of individuals at different ages, simulated facial changes in different stages of life. In 2003, Allen and his co-authors [1] extended Blanz and Vetter's work to generate the whole human body, combining models with different heights and weights. Seo and Thalmann [12] used Bezier patches to develop a base model that could be reshaped by manipulation of a set of parameters, whose values could be

determined by combining specific measures of scanned 3D models stored in a database. More recently, Golovinskiy and his co-authors [4] created a statistical technique to analyze and synthesize small 3D facial features such as wrinkles and pores. The goal was to provide greater visual realism to characters used in games and virtual reality. In our previous work [14], we proposed a biologically inspired technique for achieving diversity in the generation of virtual characters for virtual reality applications and games. In the implementation of that technique, different models are generated from simulated reproduction from two parental models. The facial model of the descendant was reconstructed from the information stored in his genome (a set of genetic characteristics), which contains a set of measures that control the facial Bezier patches. The genomic models were very limited, and could not handle sex distinction, eye and skin colors and did not simulate the transmission of characteristics through several generations. The results showed the potential of the technique, but did not achieve the desired realism. In this paper, we propose a new more robust structure, which overcomes those limitations, generating realistic models. We also demonstrate that, unlike the techniques reported in the literature, ours is able to transmit genetic traits that will be manifested only after several generations down the family line. Morphing techniques are not able to do that.

3 ANTHROPOMETRY

Anthropometry is the science that studies measures of the human body. To perform facial measurements it uses well-defined points of the face, called Landmarks (Figure 2) [7].

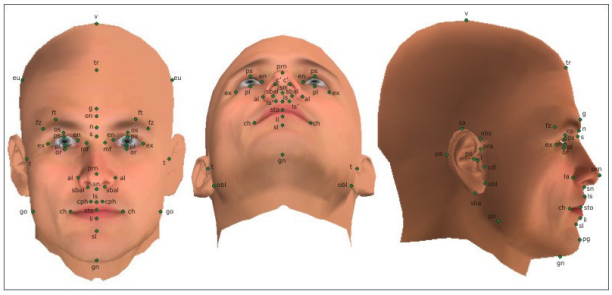

Figure 2. Facial landmarks.

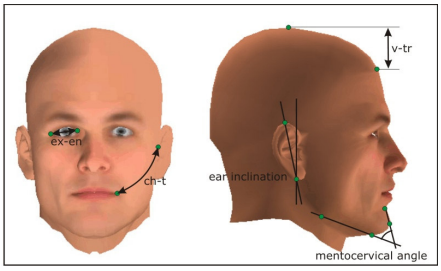

Figure 3. Landmark-based measures.

The five types of facial measurements (Figure 3) defined from the Landmarks shown in Figure 2 are [3,7]:

- Shortest distance between two landmarks. (e.g., ex-en);
- Axial distance between two landmarks (e.g., v-tr);
- Tangential distance between two landmarks (e.g., ch-t);
- Angle between landmarks and one of the coordinate axes (e.g., ear inclination); and
- Angle between points (e.g., mentocervical angle).

Measures of human faces from different places of the world have been collected over the past decades. The outstanding characteristics of individuals from different ethnicity, age and sex were stored in databases, which can be queried to simulate the possible variations in 3D facial models.

Little is known about the degree of influence of genetics and environment on the individual's physical appearance, such as the geometry of the human face. The mechanism by which the shape of a complex structure, such as the human skull (figures 4 and 5), results from the integration of morphogenetic rules (genetic rules that control the shape of an organ or parts of an individual), plastic responses and evolutionary forces are not well established [9]. Some genetic research on craniofacial anomalies has been conducted over several years, but little has been done to assess how genes and genetic ancestry influence the normal variation in human facial features [8]. The facial similarity between zygotic twins (twins originated from the same egg - cell resulting from the fecundation of one ovule by one spermatozoid) when compared with dizygotic twins (twins originated from two distinct eggs) indicates high heritability for those features.

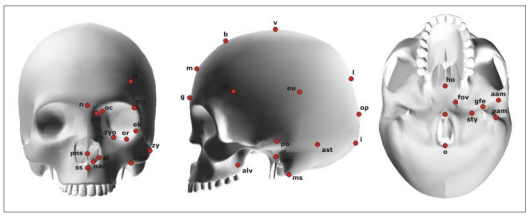

Figure 4. Craniofacial landmarks.

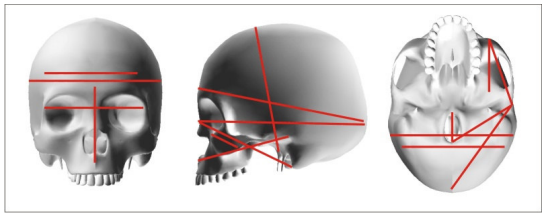

Figure 5. Craniofacial measures.

Traits that exhibit continuous or almost continuous variation and can be measured on a metric scale (quantitative traits), such as weight, stature, craniometrical measures and fitness, are assumed to be controlled by a large number of genes with small additive effects [8]. Some studies show that craniometric variations reflect the underlying patterns of population structure and history, despite the environmental influences. Thus, recently, quantitative traits such as craniometrical traits have been successfully incorporated into genetic population models in order to provide insight into the structure of human populations.

4 DIPLOID REPRODUCTION

Diploid reproduction is a type of reproduction that results in individuals whose cells have two copies of each chromosome, usually one from the mother and one from the father - see Figure 1. In this section, we summarize that biological process, which is described in more details in our previous work [14], for generating virtual characters.

4.1 Identification of genetic traits

Each genetic characteristic of a living creature is codified as a chemical string named a gene. A set of genes is stored in a rod-like structure called a chromosome. In diploid beings, each chromosome is paired with its homologous chromosome (a chromosome with the same set of genes). In humans, for instance, there are 23 pairs of chromosomes. Corresponding genes in the

homologous chromosomes (genes that occupy the same position in the chromosome) are called alleles.

The first step of our method is to choose the traits that will be used in the construction of a virtual character. Each of those traits – length of members, measures of the head, eyes, nose, mouth, ears, chin, and so on – can be seen as information that constructs part of the model and are represented as genes of diploid beings.

4.2 Storage of the genetic information

Once the total number, n, of genes has been defined in step 1, the next thing to define is the number m of chromosome pairs. Then, we distribute the n pairs of allele genes among the m chromosome pairs.

Let C be the set of pairs, c_i, of homologous chromosomes,

$$C = \{c_1, c_2, \cdots, c_m\}. \quad (1)$$

Eeach chromosome pair, c_i, consists of two homologous chromosomes: chromosome c_i^M originated from the male progenitor, and chromosome c_i^F coming from the female progenitor. Thus,

$$c_i = (c_i^M, c_i^F). \quad (2)$$

In our model, the number of genes per chromosome does not have to be the same for all chromosomes. Hence, denoting n_i the number of genes in chromosome i, the data structures for the homologous chromosomes in c_i are,

$$\begin{aligned} c_i^M &= \{g_{i1}^M, g_{i2}^M, \cdots, g_{in_i}^M\} \\ c_i^F &= \{g_{i1}^F, g_{i2}^F, \cdots, g_{in_i}^F\}. \end{aligned} \quad (3)$$

The total number of genes, n, is the sum of the number of genes in each chromosome

$$n = \sum_{i=1}^{m} n_i. \quad (4)$$

The choice of m has a direct influence on the variability of the descendants, since it contributes to the increase of combination possibilities during meiosis - a biological process of cellular division for the generation of gametes (see Section 4.3).

4.3 Generation of gametes

Specialized cells called germinative cells suffer a process of cellular division called meiosis that results in four gametes. In humans, for instance, the male germinative cells are transformed into four spermatozoids after meiosis, while the female germinative cells are transformed into four ovules. Simulating, several times, the meiosis of male and female germinative cells we construct one pool of spermatozoids and another pool of ovules.

For simulation purposes, the complete number of processes that constitute meiosis is reduced to only four processes (see Figure 6). First, there is a process of chromosome duplication (middle part of Figure 6 (A)). Second, within each duplicated pair of chromosomes, random exchanges of segments take place – the so-called crossover (upper part of Figure 6 (A)). Third, the duplicated pairs of chromosomes are randomly aligned on the cell's equator plane – this is the Metaphase I (Figure 6 (B)). Figure 6 (C) illustrates that the original cell is divided into two cells. Notice that the chromosome pairs, which were positioned above the equator plane, become part of a new cell, and the corresponding chromosome pairs, which were situated below the equator plane, stay together in the other cell. Fourth, in each of the two new cells, the chromosome pairs are, once again, randomly aligned in the cells' equator planes – Metaphase II (Figure 6 (D)), and the cells are divided into two. At the end of meiosis, four new haploid cells are generated – a haploid cell has half the number of chromosomes of a diploid cell (Figure 6 (E)).

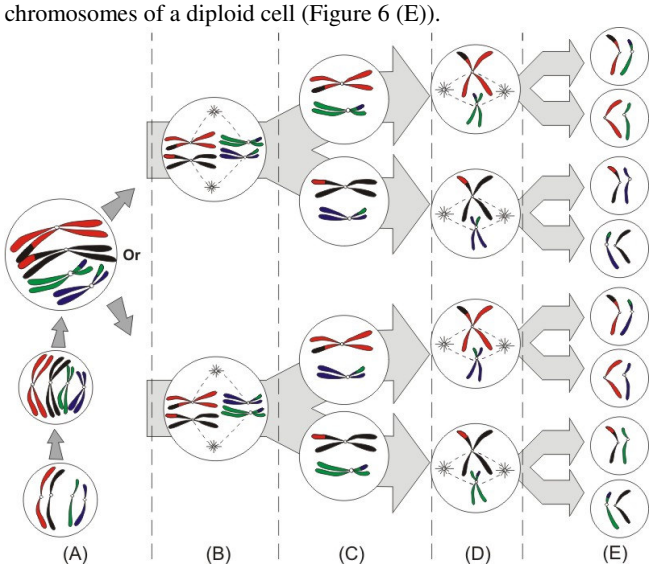

Figure 6. (A) Chromosome duplication and crossover, (B) simulation of metaphase I and (D) metaphase II.

Chromosome duplication. Each pair of homologous chromosomes is transformed into four chromosomes (two identical pairs – see equation (5)). The original chromosome and its replica – the so-called sister chromatid – are paired up with the original homologous chromosome and its sister chromatid

$$^d c_i(c_i^M c_i^M, c_i^F c_i^F). \quad (5)$$

Crossover. Figure 7 illustrates this process. In Figure 7 (a), the original chromosome pair (chromosome blue-red-yellow and chromosome green-brown-purple) is shown in its duplicated state – each chromosome has an identical sister chromatid – with black arrows indicating the pairing up of chromatids. In Figure 7 (b), the chromosomes which were paired up exchange pieces (chromosome blue-red-yellow exchange the blue segment with the green segment of chromosome green-brown-purple). After crossover, the four chromosomes that formed two identical pairs become distinct from one another.

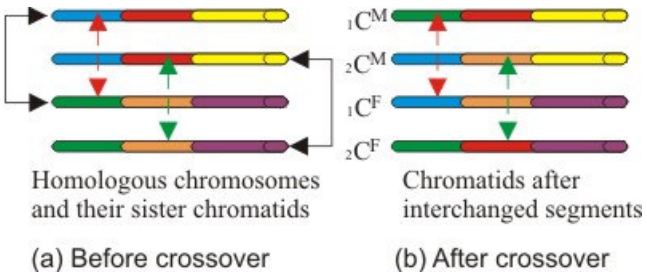

Figure 7. Crossover.

In the crossover simulation, each chromosome c_i^M in a pair of duplicated chromosomes $^d c_i(c_i^M c_i^M, c_i^F c_i^F)$ exchanges genes

with its homologous c_i^F. Thus, if the chromosomes of pair *i* have n_i genes, the number of possible exchanges are given by

$$\frac{1}{2}\sum_{k=0}^{n_i}\binom{n_i}{k} = 2^{n_i-1}. \quad (6)$$

Thus, after crossover, the structure of the duplicated chromosome is given by

$$^{d}c_i(_1c_i^M\ _2c_i^M, _1c_i^F\ _2c_i^F) \quad (7)$$

where the pairs $(_1c_i^M, _1c_i^F)$ and $(_2c_i^M, _2c_i^F)$ belong to the universe of 2^{n_i-1} possible pairs.

Metaphase I. For this simulation, it is convenient to rewrite equation (7) as

$$^{d}c_i(^{d}c_i^M, ^{d}c_i^F). \quad (8)$$

Consider the random distribution of pairs with respect to the basic alignment structure of the *m* pairs of chromosomes, where the *m* chromosomes $^{d}c_i^M$ are in one side and the *m* chromosomes $^{d}c_i^F$ are in the other side of the cell's equator plane. Thus, the two cells generated at the end of this process, belong to a universe of 2^{m-1} distinct pairs of cells.

Methaphase II. The two cells generated after Metaphase I are divided once again, generating four gametes. In each of the two cells generated before Metaphase I of meiosis, there is a set of *m* pairs of sister chromatids which were modified during crossover, that is, the *i*-th pair can be either $(_1c_i^M\ _2c_i^M)$ or $(_1c_i^F\ _2c_i^F)$. In Metaphase II, these *m* pairs will be lined up again in the equator of the cell, and then separated into two new cells. The simulation process is identical to the one of Metaphase I.

Again, the new pair of cells generated from the first cell belongs to a universe of 2^{m-1} distinct pairs. Also, the new pair of cells generated from the second cell, belongs to a different universe of 2^{m-1} distinct pairs. The four generated cells are gametes, that is, each cell has *m* chromosomes (haploid cells).

4.4 Fecundation

If only one meiosis simulation is run for each parent, the male pool of gametes would have four spermatozoids, and the female pool, four ovules. From those small pools, only sixteen distinct children would be generated after fecundation. Fecundation is the union of the two haploid cells – spermatozoid and ovule – to form a diploid cell structure of the descendant, which has *m* pairs of homologous chromosomes. However, the meiosis simulation can be run several times to increase the sizes of both pools, and the number of possible distinct children. The genetic characteristics of those children belong to a universe of probabilities that incorporates the random nature of the crossovers, and the random alignments of Metaphase I and Methaphase II. In human beings, this corresponds to a universe of 10^{600} [13]. After the combination, the new set of genetic information is used to construct the body of the child. This process is illustrated in the case study of Section 5.

5 Case Study: Generation of Face Meshes

The case study presented in this section illustrates the general process, described in Section 4, through the generation of faces resulting in genealogy trees of character families. The first simulation used characters from different ethnic groups (Figure 16), and the second simulation used caricature-like models resulting in the genealogy tree of Figure 17.

5.1 General considerations on face modeling

In the first simulation, the faces of the parent models were generated using Poser 6.0 (www.e-frontier.com), and imported to our system. The caricatured models were built by exaggerating the measures from a base model imported from Poser 6.0. It is important to mention, however, that the face meshes can be generated by any approach and imported into the system, as long as point-to-point association is maintained between the models. This association is similar to that proposed by Blanz and Vetter [2], so the technique could make use of databases obtained with 3D scanners.

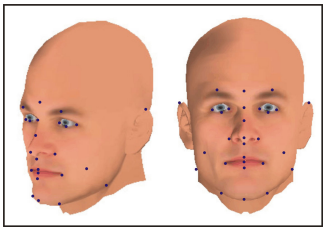

Figure 8. Landmarks used in the simulation.

The characteristics associated with genes and distributed among the chromosomes were the measures taken from the face landmarks defined by Anthropometry and shown in Figure 8.

A reference mesh with 2,076 vertices was adjusted to conform to the parents' models, and was also used to generate the offspring meshes automatically from the information stored in the genes.

The meshes associated with the parents' models can be constructed by manual fine-tuning or they can be selected from a database of previously generated meshes. The user can modify the models from the database, using scrollbars to alter their characteristics (nose silhouette, length of nose, etc.), thanks to spherical influence zones attributed to the landmarks used to define the measures (genes) (See figures 9 and 10).

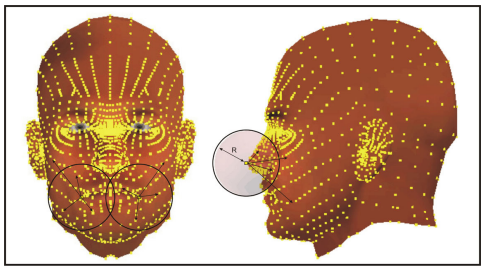

Figure 9. Genes' influence regions: mouth corners and nose tip.

```
for every vtx[j] do
begin
    dist = distance between vtx[j] and landmark
    if dist <= S_Radius then
    begin
        vtx[j].X:= vtx[j].X + v[0]*(S_Radius - dist)/S_Radius;
        vtx[j].Y:= vtx[j].Y + v[1]*(S_Radius - dist)/S_Radius;
        vtx[j].Z:= vtx[j].Z + v[2]*(S_Radius - dist)/S_Radius;
    end
end

* V = translation vector
* S_Radius = Sphere_Radius
* vtx = vertex
```

Figure 10. Perturbation within influence zone.

The influence zones adjust the neighborhood of a given landmark. Thus, perturbations to the landmark cause perturbations to a point that lies inside the sphere, which are inversely proportional to the distance from the point to the landmark.

After defining the traits, they were distributed in fictitious chromosomes (Fig. 12), which were used in the simulation of the reproductive process.

5.2 Chromosomes' definitions

In this study, twenty-three genes were defined (n = 23) and distributed over six chromosomes (m = 6 – this is a user's choice) (Figure 11). The genes comprise: eighteen measures (Figure 12) defined from the anthropometric landmarks; two genes to define the skin color; two genes for eye color; and one gene to define sex. In our model, we did not create sex chromosomes. Instead, a specific gene was defined to be the determinant of sex. A sex gene 'x' corresponds to female characteristics; a 'y' corresponds to male characteristics. Thus, an individual with 'xx' is female and an individual with 'xy' is male.

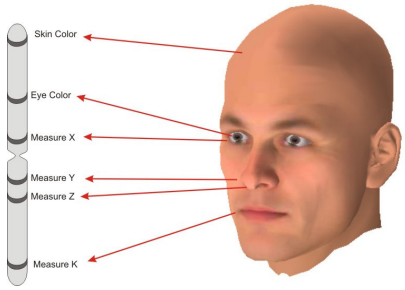

Figure 11. Distribution of characteristics in a chromosome.

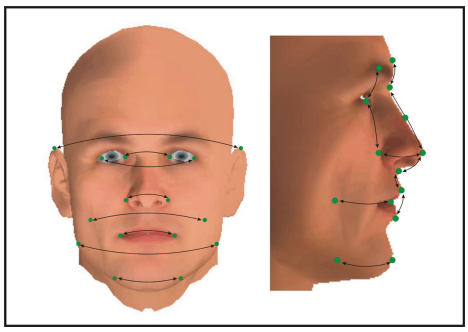

Figure 12. Genes based on measures.

5.3 Gamete generation

In the examples simulated in this case study; the 23 genes were distributed among six chromosomes, $C = \{c_1, c_2, c_3, c_4, c_5, c_6\}$. The first five chromosomes have four genes each and the sixth chromosome has three genes. The structure of each gene within the chromosomes is given in Equation 3.

In that structure, genes are associated with landmark measures, with influence zones and weights. To ensure high variety of gametes, crossover was allowed to happen between any genes in the chromosome (Figure 7). In other words, chromosome segments containing just one gene may be exchanged.

In this study, a meiosis process was executed on each parent chromosomic structure, C_{Male} and C_{Female} (Figure 13). Each time a meiosis run is performed on each parent, one of the four gametes from the father and one of the four, from the mother are selected for fecundation (Figure 18) – we did not generate all the possible children.

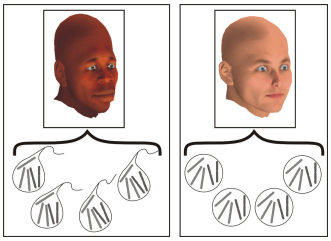

Figure 13. Meiosis applied to male and female models.

5.4 Generation of the offspring

The generation process consists of constructing a chromosome structure of a descendant by fertilization of a female gamete by a male gamete. The parent models, which are given as input to the first simulation, were defined as homozygous – the allele genes are identical. The subsequent generations become heterozygous, due to the combination of the parent genes. The descendant's chromosomic structure is used to generate its mesh (Figure 18) as follows:

- Definition of the skin color by combining inherited genes (Figure 14);

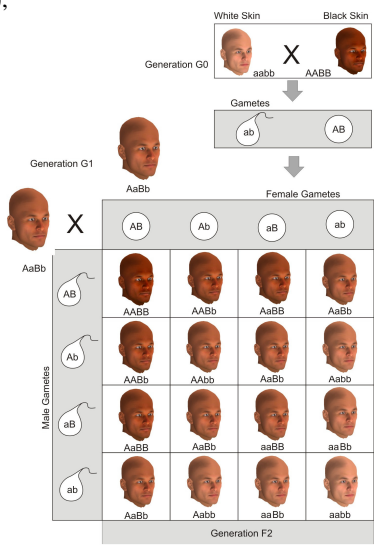

Figure 14. Determination of skin color.

- Definition of the eye color by combining inherited genes (Figure 15);

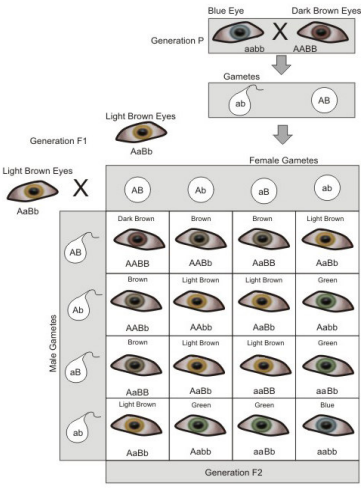

Figure 15. Determination of eye color.

- Definition of sex by combining "genes" ‘x’ and ‘y’, and processing the gender adaptation of figures 16 and 17;

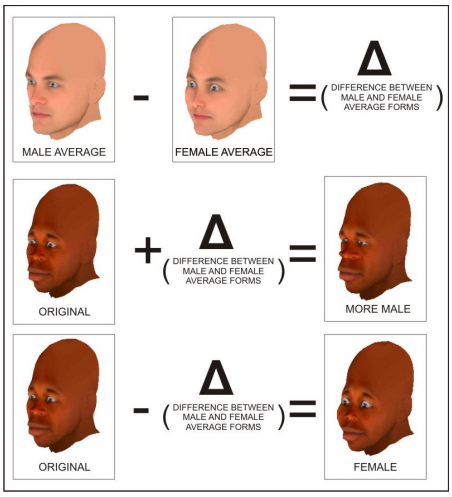

Figure 16. Model adaptation to gender.

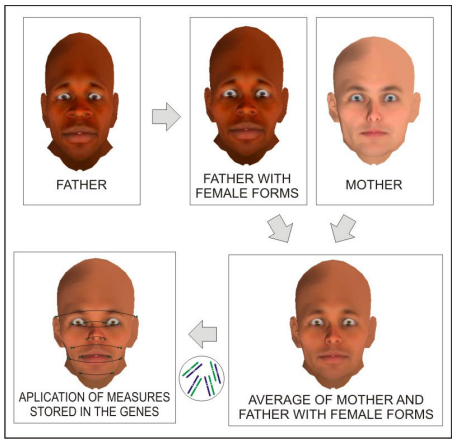

Figure 17. Process of descendant generation.

After fecundation, if the sex-determinant allele genes are ‘xx’, the descendant is a female. Therefore, the overall aspect of the geometry has to be within anthropometric bounds defined for a female. On the other hand, if the sex genes are ‘xy’, the descendant is a male, and the overall geometric aspect has to be within the anthropometric bounds determined for males. In order to generate the mesh of a female descendant, the characteristics originated from the father are transformed to female forms to combine with the mother’s measures stored in the other corresponding genes. On the other hand, if the descendant is male, the characteristics inherited from the mother are transformed to male forms to combine with the corresponding characteristics inherited from the father. These transformations are performed as described in Figure 16 and are based on Blanz and Vetter’s [2] work, with their 3D scanned database models.

In this work, the male and female average models were fictitious models – they do not represent true average obtained from values stored in databases. Models with male and female characteristics from this approach are illustrated in Figure 16.

- Set measure adjustments to the model (last step of figure 17), using the influence zones described in figures 9 and 10 for each gene, which may occur by complete or incomplete dominance.

The resulting characteristics of the measures are generated from the combination of pairs of genes (Figure 18). In the case studies, the first simulation used the concept of dominant and recessive measures. The dominance or recessivity of a given gene was assigned randomly. However, in the second simulation, incomplete dominance between alleles was adopted. Thus, weights are attributed to each gene, so that a trait in the descendant models is defined as a weighted average of the corresponding genes of the parents.

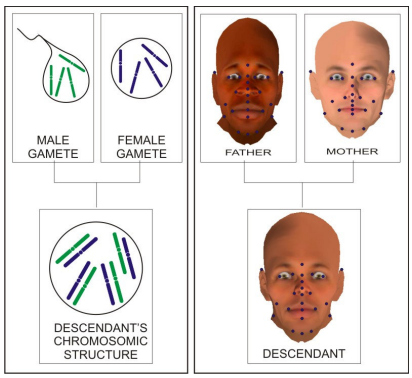

Figure 18. Fecundation process.

In this case study, we selected some couples in order to form families with descendants up to the great-grandchildren’s generation. Figure 19 shows a family tree originating from two couples of distinct ethnic groups. We introduced an outsider to marry a child of one of the couples. Figure 20 shows a second family tree with the same number of levels as the first tree, but using caricatured individuals with distinct facial features, skin colors and eye colors.

5.5 Analysis of results

Case study 1 (Figure 19):

The models of generation G0 (a, b, c, d) and the outsider model (e) are homozygous for the genes related to measures (see Figure 12). Models (a) and (b) have only recessive genes for the skin and eye colors, while models (c) and (d) have only dominant genes for skin and eye colors. The outsider model (e) has only one dominant gene for the skin color and only one recessive gene for eye color.

Generation G1: Excluding the model (e) that was not generated by the simulation, all the models have geometry very similar to their parents. This was due to the fact that their parents were homozygous, which reduced the possibility of combinations of traits, and belonged to the same ethnic group.

G2 Generation: The children of models (e) and (f) also did not have marked variability, because one of the parents, (e), is homozygous and the other was a child of ethnically similar parents. However, one can notice that the shapes of their heads were more similar to that of model (e). The children of models (g) and (h) presented more noticeable combinations of traits from both parents. One can see the combinations of nose, shape of the head and eyes. As an example, model (j) has the format of face more similar to those of models (c), (d) and (h), but has inherited the nose of the models (a), (b) and (g). All models have two recessive genes and two dominant genes for eye color and skin color. The recessive were inherited from model (g) and the dominant from model (h), therefore, all have the same skin color and the same eye color.

Generation G3: This generation presents a broad range of traits, because it is the result of gene combinations inherited from all five initial homozygous ancestors (a, b, c, d, e). It is possible to

identify some characteristics that were inherited from each homozygous ancestor. Model (l) has the head shape similar to that of model (e) and a thin nose, inherited from models (a) and (b). Models (m) and (n) have wider nose (despite the thin noses of their parents (i) and (j)), inheritance from their great-grandparents (c) and (d) that was hidden in (j). Model (o) inherited the thick lips from (c) and (d), and the high eyebrows from (g) and (p). Model (q) has the thin lips from (a) and (b) or (e), the form of the head from (c) and (d) and the eyes more similar to (e). The color of the eyes and skin varied considerably, since the eyes of (i) has two dominant and two recessive genes and its skin has only recessive genes while model (j) has two recessive and two dominant genes for the eye color, and two dominant and two recessive genes for the skin color.

Case study 2 (Figure 20):
The models of generation G0 (a, b, c, d) and the outsider model (e) are homozygous for the genes related to the measures (see Figure 12). Models (a), (b) and (e) have only recessive genes for skin color. Models (b) and (c) have only recessive genes for eye color as well. Model (a) has one of the genes associated to the eye color dominant. Models (c) and (d) have two recessive genes and two dominant genes for the skin color as well as for the eye color.
Generation G3: There are two interesting cases to be considered. One is concerned with models (m) and (n), which have more thick lips, despite the thin lips of their parents (i) and (j). It is possible to verify that this gene was inherited from models (c), (d) and (h) and was hidden in model (j). Another case concerns models (o), (p) and (q) that have wide chin. One can notice that only one of their relatives have wide chin. Their great-grandparents (a), (b) (c) and (d) all have thin chins. Their grandparents (f), (g) and (h) and their parents (i) and (j) alse have thin chins. Only their Grandfather, (e), has wide chin. Since (e) is homozygous in the measures, we can say that model (i) has this gene, and that, although it did not manifest, it was transmitted to its children (o), (p) and (q). Since the models in this case study have exaggerated measures, it was easier to identified the inherited characteristics.

6 CONCLUSION

In this paper, we proposed a new more robust structure for automatic transfer of traits through simulated diploid reproduction, to generate virtual families, which overcame the limitations of our previous work, and was able to generate realistic models. We also demonstrated that, different from the techniques reported in the literature, ours is able to transmit genetic traits that will be manifested only after several generations down the family line. Morphing techniques are not able to do that.

The proposed solution transmits characteristics from parent models through simulation of diploid reproduction, allowing for simulation of kinship relations and interaction between isolated populations with well-defined ethnic characteristics.

The process needs an underlying geometric description that is adapted according to genetic information stored in a diploid chromosomic structure. The adaptation of the model used points, which were defined by anthropometric landmarks whose subgroupings specified the characteristics that were stored as genes in the pairs of homologous chromosomes. Through the process of simulated meiosis, applied to the chromosomic structure of two parent models, gametes were generated and then used in simulated fecundation. The case study demonstrated the power of the technique. Although the examples were focused on face generation, the idea is general and can be applied to the complete model (head and body) of a virtual character. For that, one needs to make changes on the way the geometric characteristics of the various parts of the body should be controlled in the adaptation.

It is important to mention that, despite the analogies of biological reproduction, the method has clear differences from genetic algorithms and has different goals. Genetic algorithms are applied to the solution of optimization problems using the paradigm of the survival of the fittest, which removes unwanted solutions from the search space, relying on crossover and mutation.

It was also clearly demonstrated through the case study that the method is completely different from morphing techniques. In morphing methods, the user has much more control over the generated character, which can be interpreted roughly as a weighted sum of the participating models.

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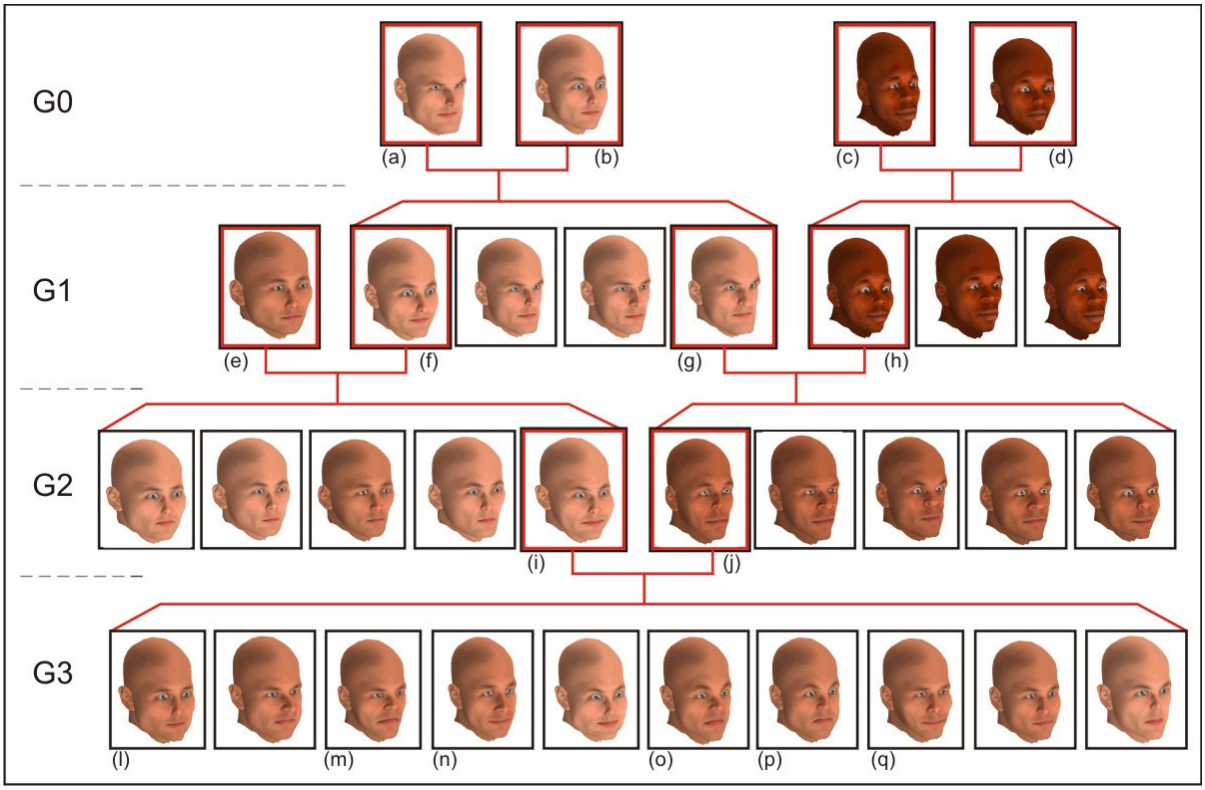

Figure 19. Genealogy tree of models ethnically different.

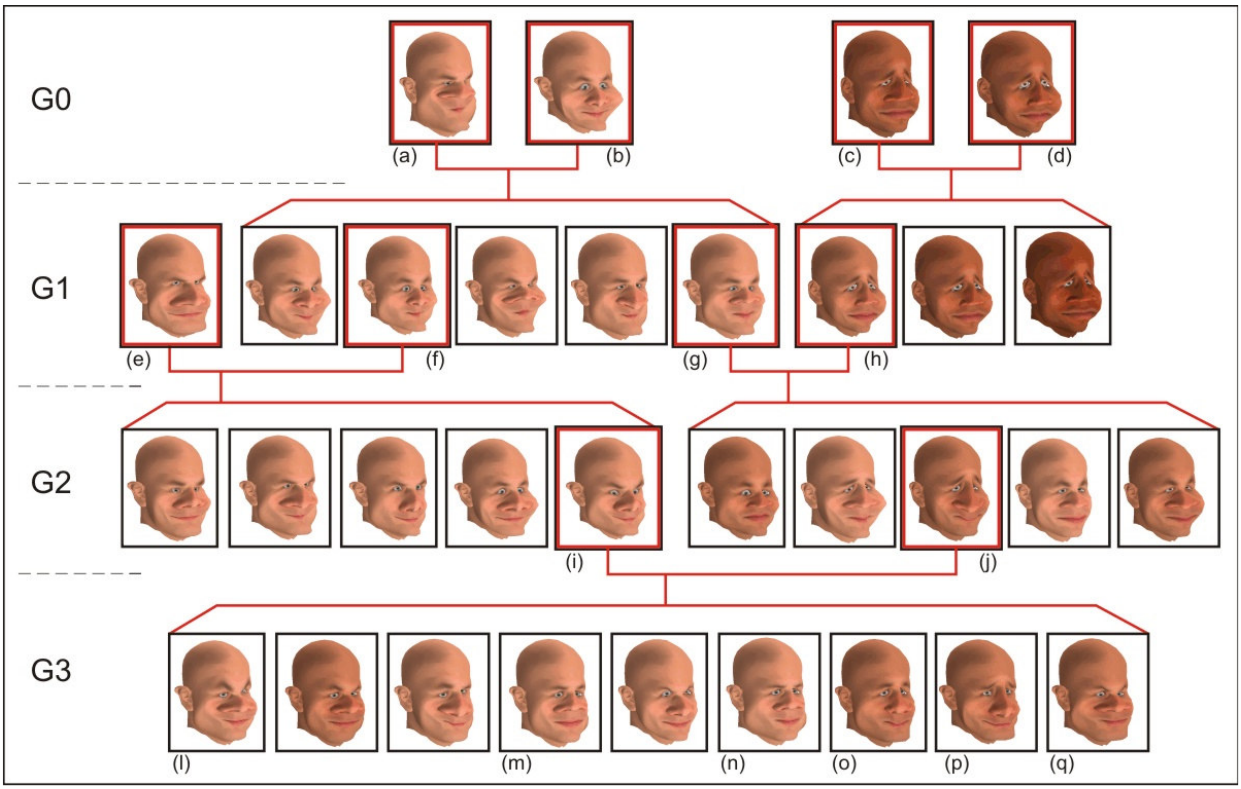

Figure 20. Genealogy tree of caricatured models.