Towards the Solution of the Missing Persons Problem by Simulated Reproduction of Virtual Characters

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***Abstract*—Virtual reality has applications in different fields of knowledge such as engineering, science, arts, entertainment and education. In this work, virtual reality is used to help solving the problem of missing persons. The proposed methodology uses simulated diploid reproduction of virtual characters carefully modeled taking into account the traits of the missing persons parents. The genetic characteristics of both parents are stored into their genomic data structure, which will be used to construct pools of male and female gametes to be used in a simulated fecundation. The descendants are generated with the same age of the missing person at the time of disappearance. Through an interactive process, a plausible model of the missing person is selected among the generated descendants and its genomic data structure is saved. The parents models and corresponding data structures are updated to reflect the age of the missing person at search time. Next, the genomic data structure of the missing person is updated with the information contained in the updated data structure of the parents, and an updated model of the missing person is generated. This updated model is a plausible model, upon which perturbations can be applied to generate several plausible variants. Case studies that demonstrate the potentials of the proposed methodology are presented.**

***Keywords*-age progression, missing person, aging**

I. Introduction

Virtual reality has applications in different fields of knowledge such as engineering, science, arts, entertainment and education. In this work, virtual reality is used to help solving the problem of missing persons. The proposed methodology uses simulated diploid reproduction of virtual characters carefully modeled taking into account the traits of the missing persons parents. One of the biggest difficulties of working with virtual characters is growing and aging simulation. This problem is also found in picture-based aging simulations, such as those used nowadays in the search for missing people, where, using old pictures of the person, attempts are made to recreate a plausible face after a certain number of years have passed. Aging simulation is a difficult problem because its process is influenced not only by genetic factors but also by environmental and life-style factors.

The proposed technique consists of nine steps: 1) Selection of pictures of the missing person and her parents with the approximate age of the missing person at the time of disappearance (reference age); 2) Construction of the 3D virtual models (father, mother and missing person), taking into account the information extracted from the selected photographs of Step 1; 3) Construction of genomic data structures for both parents, feeding traits extracted from the 3D models of Step 2; 4) Generation of two pools of gametes one for each parent through repeated meiosis simulation (meiosis is a cellular division process, responsible for gametes generation) applied to the genomic data structures constructed in Step 3; 5) Generation of offspring by simulating fertilization of ovules from the pool of female gametes with spermatozoids from the pool of male gametes; 6) Comparison of the 3D virtual models of the offspring with the 3D virtual model of the missing person the closest offspring model and its genomic data structure are saved; 7) Construction of the 3D virtual models of both parents at the target age (current age of the missing person); 8) Update of the genomic data structures of the parents to reflect the aging process that occurs during the elapsed time from the time of disappearance and the current time this update process is similar to steps 1 and 2 ; 9) Update of the genomic data structure selected in Step 7, using the updated genomic data structures of Step 8, and reconstruction of the updated 3D virtual model of the missing person. This updated model is a plausible model, upon which perturbations can be applied to generate several plausible variants. It is also desirable to apply accessories such as beard, moustache, hairstyles, hats, etc., to help with the investigation. Steps 3 to 5 are detailed in Vieira et al. [1], [2].

The remainder of this paper is organized as follows: in Section II, related works dealing with facial modeling and aging are presented; in Section III, the technique of creation of virtual characters through simulated reproduction is summarized; in Section IV, the proposed solution to the missing persons problem by simulated reproduction of virtual characters is described; in Section V, case studies demonstrate the power of the proposed methodology; in Section VI, conclusions about the work are presented.

II. Related Work

Several techniques of facial modeling have been proposed in the literature which, in one way or another, can be used in facial prediction. In this section, a selection of the most relevant work is briefly presented.

Blanz and Vetter [3] proposed the morphable model technique for generating facial models. That technique constructs a base facial 3D model as a result of the combination of various facial models, and, then, it is able to generate intermediate faces between the initial faces.

DeCarlo et al. [4] described a process where variational techniques are used for automatically generating the geometric models of human faces. The process takes a collection of anthropometric measures of a given facial model and applies random disturbances that do not violate the corresponding statistical bounds defined for a specific population.

Vieira et al. [1], [2] studied the automatic transfer of physical characteristics of parent models to their descendants, through simulation of human reproduction.

Lee et al. [5] dealt with the problem of automatic age progression. They proposed a method of cloning and simulation of the aging in a family. Initially father, mother, son and daughter of the same family are rebuilt, and their shapes and textures are combined to obtain virtual characters with some variation. Next, an automatic texture mapping is done, followed by a method of interpolation and morphing. Finally, wrinkles are generated in at certain facial points.

Ramanathan and Chellapa [6], [7] proposed a craniofacial growth model that is characterized by the variations related to the shape growth of observed human faces over the years of formation. The model takes into account anthropometric evidences collected from facial growth. Therefore, it agrees with the growth patterns observed in human faces over the years. The facial proportions of growth, measured by anthropometry, were translated into linear and nonlinear constraints of the facial growth parameters in an optimization problem, which was set up in order to adjust those parameters.

Scherbaum et al. [8] focused their work in the construction of aging trajectories with the purpose of identifying missing children. Until then, this type of work was the responsibility of forensic artists, which reconstructed the model of a missing person at the target age in a totally manual fashion. To simplify the process, Scherbaum and his co-workers proposed a new algorithm to calculate aging individual trajectories of certain faces, based on a nonlinear function that assigns to a vector the age of the face. The algorithm exploited the morphable model technique developed by Blanz. The model proposed is a learning method, from a data set of 3D children face images in different stages of growth. The aging trajectories exhibit nonlinear dependence of both the age and individual faces.

Suo and Zhu [9] proposed composition and dynamics model of facial aging. They adopt a hierarchical three-level And-Or graph representation to account for the rich information crucial for age perception and large diversity among faces in each age group. The aging process is modeled as a Markov chain to describe the evolution of parse graphs across age groups and to account for the intrinsic randomness of the aging process. The first level of the graph describes face and hair appearance, the facial components are refined at the second level, and wrinkles and skin marks are further redefined at the third level.

Scandrett et al. [10] proposed a statistically rigorous approach to human face aging, applied to the missing children issue. The technique is based upon a Principal Component Analysis (PCA) and involves the definition of an aging direction through the model space, using an age-weighted combination of model parameters.

Albert et al. [11] presented a synthesis of findings of adult age-related craniofacial morphological changes. They focus on the relevance of this information to forensic science research and applications, such as the development of computer facial age-progression and face recognition techniques and contributions to forensic sketch artistry.

Fu and Huang [12] developed a pattern classification framework for estimating human age, using quadratic regression on the discriminative aging manifolds of face images. They find a low-dimensional aging manifold subspace, which embodies the discriminative properties, by applying Conformal Embedding Analysis. Then, they fit the extracted low-dimensional feature with a learned regression model in order to estimate age or an age interval.

Hubball et al. [13] focused on the hypothesis that the patterns of age progression are related to the face concerned, as it implicitly embraces gender, age group and ethnic origin features, as well as the person-specific development patterns of the individual. They used a data-driven framework for automatic image-based facial transformation crossed up with a database of facial images. Also, they built a parameterized model for encoding age transformation in addition to the traditional model for face description, and used evolutionary computing to learn the relationships between the two models.

Lanitis [14] focused on an experimental evaluation of the face-aging algorithms, and aimed at assessing the applicability of human-based against typical machine-based performance evaluation methods. In his later work [15], he compared the performance of a method based on age prototypes, a method based on aging functions defined in a low-dimensional parametric model space, and two methods based on the distributions of samples belonging to different individuals and different age groups.

Gibson et al [16] proposed a computer-assisted method for altering the perceived age of a human face. The technique is based on calculating a trajectory or axis within a multidimensional space that captures the changes in large-scale facial structure, shading and complexion associated with aging.

Giraldi and Thomaz [17] have reviewed some approaches for age progression, in special statistical learning techniques. The active appearance model is based on the Principal Component Analysis theory. The method works in the PCA space by defining a set of model parameters that control

modes of shape and gray-level variation learned from a training set.

Recently, Ramanathan and Chellappa [18] presented a survey on computational methods for modeling facial aging. They group the contributions from two areas of research: human perception and psychophysics, and computer vision. The first group deals with the ability of humans to perceive age-related changes in facial appearances and their readiness in judging the relative age differences. The second group concentrates on the problems of age estimation and age progression.

III. Virtual Characters Creation for Simulated Reproduction

Simulated reproduction is an algorithmic process that includes the biological process responsible for the production of gametes (male or female germinative cells) and the process of fertilization. In this section, a summary of the biological processes required for the creation of virtual characters is presented (for details, see [1]).

A. Identification of genetic characteristics

Every genetic characteristic of an individual is encoded as a molecular sequence known as gene. A set of genes is stored into a more complex structure called chromosome. In diploid beings, every chromosome is matched with its homologous chromosome (a chromosome with the same set of genes). Human body cells have 23 chromosome pairs. Corresponding genes in the homologous chromosomes (genes that fill the same chromosome position) are called alleles.

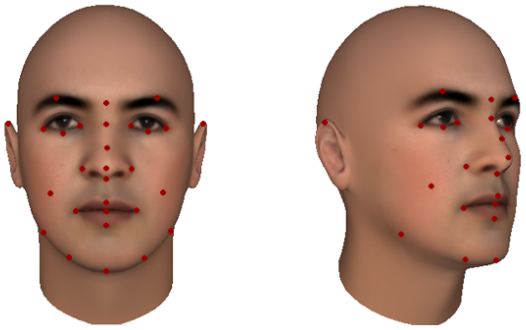

Figure 1. Facial Landmarks.

The first step in the process of virtual characters creation by simulated reproduction is to select the genetic features that are used for building those characters. These features limbs length, skull size, eye shape, nose type, mouth size, ears shapes, etc. can be seen as high-level control parameters that, together, define the models final appearance. Thus, they will play the role of genes in the simulation (figures 1 and 2) and need to be stored in a genomic structure of the model (Section III-B).

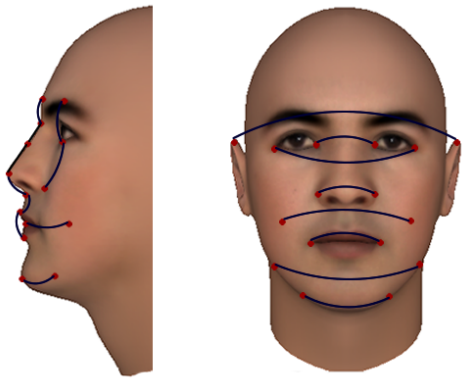

Figure 2. Landmark-based measures.

B. Storage of the genetic information

Assuming that the number of features, as described in Section III-A, is n, the genetic model has n genes. So, the next decision is to define the number, m, of chromosome pairs (homologous chromosomes) that will define the genomic structure of the model. Thus, the n allele genes will be distributed among those m chromosome pairs.

Let

$$C = \{c_1, c_2, ..., c_m\} \tag{1}$$

represent the set of m homologous chromosome pairs, c_i, which are defined as

$$c_i = \left(c_i^M, c_i^F\right) \tag{2}$$

with c_i^M being the i-th chromosome coming from the father's gamete, and c_i^F, its homologous chromosome, coming from the mother's gamete cell. Note that a chromosome pair c_i needs not to have the same number of allele genes as a chromosome pair c_j. Therefore, if n_i represents the number alleles within chromosome i, the data structures for the homologous chromosomes in c_i are

$$\begin{aligned} c_i^M &= \{g_{i_1}^M, g_{i_2}^M, ..., g_{in_i}^M, \} \\ c_i^F &= \{g_{i_1}^F, g_{i_2}^F, ..., g_{in_i}^F, \} \end{aligned} \tag{3}$$

and the total number of alle genes, n, is

$$n = \sum_{i=1}^{m} n_i \tag{4}$$

The choice of m influences the variability of the offspring that can be generated, since it affects the number of possible combinations during meiosis – the biological process of cell division for the generation of gametes– (Section III-C).

C. Generation of gametes

Specialized cells called germinative cells undergo a process of cell division (meiosis) that results in four gametes. In humans, for example, meiosis of a male germinative cell

results in four spermatozoids. Similarly, meiosis of a female germinative cell results in four ovules. Simulating meiosis of male and female germinative cells several times generates two pools of gametes: one with spermatozoids, and the other with ovules.

For simulation purposes, meiosis is assumed to comprise only four biological processes: Chromosome duplication, Segment exchanging (crossover), Chromosome alignment for the first cellular division (Metaphase I), Chromosome alignment for the second cellular division (Metaphase II). The last three processes are random processes, which are responsible for the large variety of gametes that can be generated from the same genomic structure of the germinative cell.

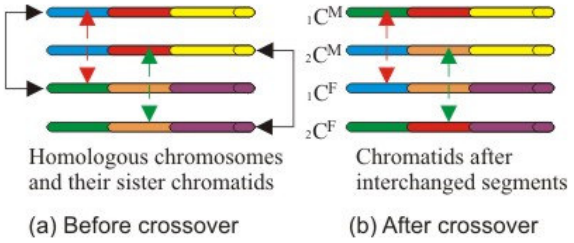

Figure 3. Recombination of homologous chromosomes.

Chromosome duplication prepares the genomic structure for the exchanging of segments between homologous chromosomes (see Figure 3). After those first two processes, the genomic structure of the germinative cell comprises m sets of four distinct chromosomes. The i-th set consists of chromosomes $\left({}_1c_i^M, {}_2c_i^M\right)$ and chromosomes $\left({}_1c_i^F, {}_2c_i^F\right)$. Notice that, before the exchange of segments, the two chromosomes in $\left({}_1c_i^M, {}_2c_i^M\right)$ were identical copies (called sister chromatides) of c_i^M. Similarly, $\left({}_1c_i^F, {}_2c_i^F\right)$ were identical copies of c_i^F.

Next, during Metaphase I, those m sets of four chromosomes are randomly aligned on the cells equator plane, in such a way that, in the i-th set, the pair $\left({}_1c_i^M, {}_2c_i^M\right)$ stays in one side of the plane and the pair $\left({}_1c_i^F, {}_2c_i^F\right)$ stays in the other side. After that alignment, the cell is split into two diploid cells, whose genome is distinct from the genome of the original germinative cell.

Finally, during Metaphase II, a new random alignment of chromosome pairs occurs in the equator planes of each of the two cells generated after Metaphase I. The i-th pair in one cell is $\left({}_1c_i^M, {}_2c_i^M\right)$ and the corresponding pair in the other cell is $\left({}_1c_i^F, {}_2c_i^F\right)$. Each of those two cells is, then, split into two, resulting in four new haploid cells (gametes). Thus, the i-th chromosome pair, $\left(c_i^M, c_i^F\right)$, of the germinative cell, contributes to the i-th chromosomes, ${}_1c_i^M, {}_2c_i^M, {}_1c_i^F, {}_2c_i^F$, in each of the four gametes. The gametes are haploid cells because they have only m chromosomes, instead of m chromosome pairs. The data structures associated with each one of the meiosis processes are shown on Table I.

D. Fertilization

As mentioned in Section III-C, running the meiosis simulation several times for the male and female germinative cells, results in two pools of gametes (one pool of spermatozoids and one of ovules). The offspring of a couple of virtual characters can be obtained by fertilization the fusion of a spermatozoid with an ovule, resulting in a diploid cell with the data structure described by equations 1 to 4. The

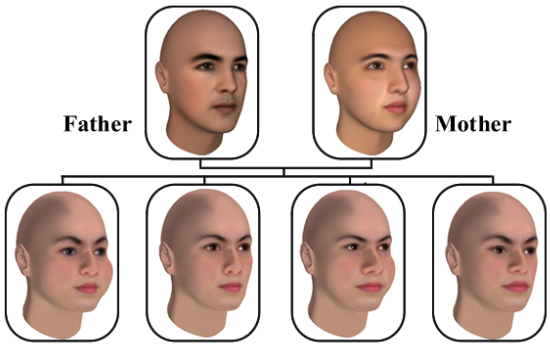

Figure 4. Four children of a virtual couple.

larger the pools of gametes are the larger the size of the offspring can be. However, there is a theoretical upper bound on the number of distinct children that depends on the total number of genes and on the number of chromosome pairs. For the human genome, that limit is about 10^{600} [19]. Figure 4 illustrates the generation of the offspring, showing just the faces of four descendants of a couple of virtual characters.

IV. Modeling the Missing Person at the Target Age

In this section, the proposed technique assumes that the genetic factors are determinant of the missing individuals appearance at the target age. In other words, age progression is assumed to depend upon genetic factors for simulation purposes. The epigenetic factors (diet, lifestyle, environment, etc) can be considered in the construction of plausible models around a base model obtained at the target age by taking into account only genetic factors. Furthermore, the base models characteristics are determined only from the chromosomal structure of the missing individual and those of his parents. The missing individuals model at the target age is obtained through the 9 steps described briefly in Section 1 and detailed next:

Step 1. Selection of photographs at disappearance age (reference age).

Identify the reference age of the missing person, and select three sets of frontal photographs: 1) photographs of the missing individual at an age as close as possible to the reference age; and 2) photographs of both parents also at an age as close as possible to the reference age.

Table I
DATA STRUCTURES IN THE MEIOSIS PROCESSES

Step	Input	Output	
Duplication	$c_i = \left(c_i^M, c_i^F\right)$	$c_i^d = \left(c_i^M, c_i^M, c_i^F, c_i^F\right)$	
Crossover	$c_i^d = \left(c_i^M, c_i^M, c_i^F, c_i^F\right)$	$c_i^d = \left({}_1c_i^M, {}_2c_i^M, {}_1c_i^F, {}_2c_i^F\right)$	
Metaphase I	$c_i^d = \left({}_1c_i^M, {}_2c_i^M, {}_1c_i^F, {}_2c_i^F\right)$	$c_i = \left({}_1c_i^M, {}_2c_i^M\right)$	
		$c_i = \left({}_1c_i^F, {}_2c_i^F\right)$	
Metaphase II	$c_i = \left({}_1c_i^M, {}_2c_i^M\right)$	${}_1c_i^M$	${}_2c_i^M$
	$c_i = \left({}_1c_i^F, {}_2c_i^F\right)$	${}_1c_i^F$	${}_2c_i^F$

The photographs are pre-processed in order to eliminate the background of the image and the hair or the person hair is a characteristic that strongly affects the perception on the model.

Step 2. Construction of virtual models at the reference age.

Use the three sets of photographs selected at Step 1 and construct three 3D virtual models: one for the missing individual; one for the mother and another for the father (Figure5).

Figure 5. Mothers 3D virtual model at reference.

Step 3. Definition of the genomic data structures.

Using the 3D virtual models constructed in Step 2, take the anthropometric measures that will play the role of genes and build the genomic data structures (equations 1 to 4) for both parents at reference age.

Step 4. Generation of the pools of gametes.

Use the genomic data structures of Step 3 and run as many meiosis simulations as desired, in order to generate two pools of gametes: one to store the fathers spermatozoids; and one to store the mothers ovules (see Section III-C).

Step 5. Generation of the genomic structures of the offspring.

Use the pools of gametes generated in Step 4 and simulate the fertilization process, doing all the possible fecundations (see Section III-D), in order to generate the offspring.

Step 6. Selection of reference model.

Compare the models of the offspring generated in Step 5 with the model of the missing individual constructed in Step 2. From the offspring models, select the one, which is the

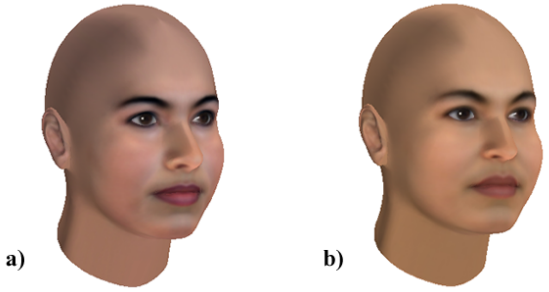

Figure 6. a) Selected model in step 7. b) Generated model in step 9.

closest to the missing individual at reference age (Step 2). Save the model and its genomic data structure as reference model (see Figure 6 a)).

Step 7. Parents virtual models at target age.

Similarly to what was done in steps 1 and 2, construct 3D virtual models for both parents, using selected photographs at the target age.

Step 8. Updating the genomic structures of parents.

This step is identical to Step 3. Thus, using the 3D virtual models constructed in Step 7, take the anthropometric measures and update the genomic data structures (equations 1 to 4) for both parents at target age.

Step 9. Construction of the missing persons model at target age.

From the genomic data structures of both parents, updated in Step 8, update the genomic data structure of the reference model of Step 6 to reflect the genomic information of the missing individual at the target age. Then, using that updated data structure, construct the missing persons model at target age. Based on this model, new plausible models can be constructed to take into account the epigenetic factors (see Figure 6 b)).

V. TESTS AND RESULTS

The tests were based on two family groups (composed of father, mother and daughter) of which it was possible to gather the necessary photographic sequences.

The models were constructed with FaceGen Modeler 3.1 (http://www.facegen.com), which generates good 3D facial models from 2D images and guarantees a point-to-point association between every two models. This association is necessary because all models have a common topological base. All the generated meshes for this study possess 6,215 vertices.

A. *Missing woman: Family group 1*

In this case, the problem to be solved is to find a woman that disappeared at the age of 20 (the reference age), after 20 years (target age of 40). The proposed methodology, consisting of the 9 steps described in Section 4, was applied to this problem. The sets of selected photographs at reference and target ages are shown in Figure 7 a).

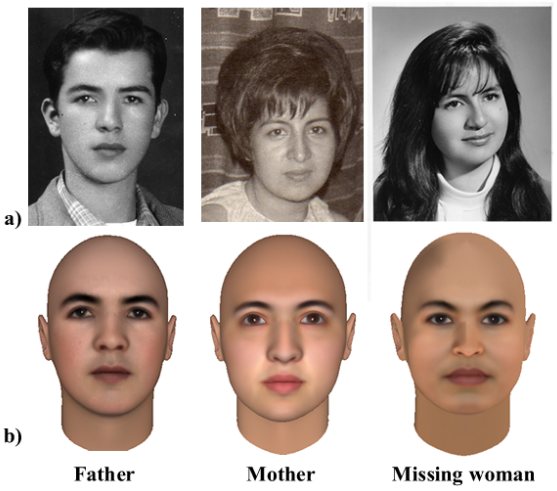

Figure 7. a) Selected photographs of family group 1. b) Parental models at the reference age.

The virtual 3D models constructed in Step 2 are depicted in Figure 7 b), and represent the individuals at the age of 20 (missing woman, her father and mother). For this particular case, the textures were adjusted manually since the images used for generating the models were black and white. The parental genomic data structures for the reference age are determined, as described in Step 3 (see reference [1] for details on how to map the anthropometric measures to genes). 30 meiosis simulation runs (Section III-C) for each parent generated the two pools of gametes (Step 4): one with 120 spermatozoids and the other with 120 ovules). The total number of children generated in Step 5 would be 14,400, but, since the missing person is a female, only the female offspring were generated. Due to the lack of space, only the offspring models, which are the closest to the missing womans model shown in Figure 8, were displayed in Figure 9. Notice that the changes in each of the children are correlated to the models geometry. Figure 9 shows which model was selected as the reference model

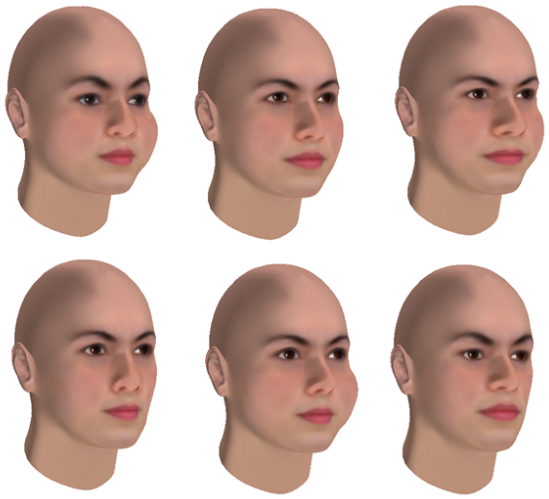

Figure 8. a) Daughters models generated from the paternal models in the initial age.

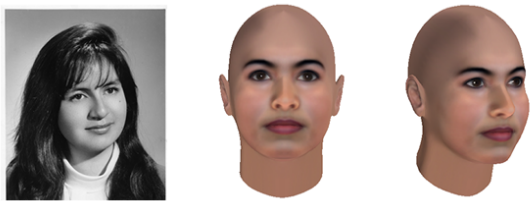

Figure 9. a) Selected model in the age of disappearance.

(Step 6). The parents virtual models at target age (Step 7) are shown if Figure 10. Based on those new models, the parents genomic structures are updated (Step 8). Since the missing womans reference model and genomic data structure were saved in Step 6, it is possible to update the genomic data structure of the missing woman at target age, by traversing its genomic structure and updating each pair of genes (alleles) copying the corresponding genes from the updated genomic structures of the parents at target age (done in Step 8). When the missing womans genomic structue at targe age is updated, its 3D virtual model can be generated, as shown in Figure 11. For comparison purposes and to demonstrate the efficacy of the proposed method, a photograph of the missing woman at target age is also shown in Figure 11.

B. *Missing woman: Family group 2*

Similarly, in the second test, parental models were generated at the ages of 20 (reference age) and 30 (target age). The process executed for the second group family can be seen in its totality in Figure 12.

Figure 10. Parental models at target age (age of 40).

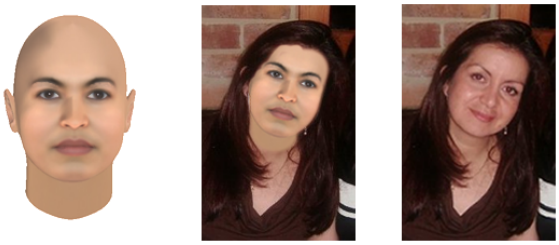

Figure 11. Virtual model of the missing woman at target age and her real photograph at age 40.

VI. Conclusions and considerations

This paper presented a methodology to aid the search of missing persons. The proposed methodology was presented in 9 steps and uses the technique of virtual characters generation by simulated reproductions to build an updated model of the missing person. The quality of the resulting model depends directly upon the parents facial models at reference and target ages. The variability of the offspring is related to the genomic date structure (number of chromosomes and number of genes in each chromosome). It is expected that even better results can be obtained if the number of control parameters (the number of genes in the model) increases a more sophisticated facial model. The results are also influenced by the quality of the 3D virtual model of the missing person at reference age. In the current stage of the research development, the parental models and the initial missing persons model are constructed from photos, with the software FaceGen. This process works properly only if the selected photographs are perfectly frontal photographs. This is a very undesirable restriction for the selection of appropriated pictures. Techniques of images processing to correct small angulations need to be implemented to make this restriction less severe.

It is known that the growing and aging processes are not influenced by genetic factors only. However, researchers agree that including epigenetic factors in age progression models is not a realistic goal. Therefore, modifications around a plausible model generated by the proposed progression model are recommended. For example, different hairstyles give a better perception of the result to the user. Other modifications such as the inclusion of accessories have not been discussed in this paper.

Despite the mentioned restrictions, the obtained results with the proposed technique were very promising. At this time the inclusion of more facial characteristics in the chromosomal structure of the model; the use of image processing to correct for angular deviations from frontal photographs; improvement of texture combination processing to be applied to the offspring and to the final model are objects of further studies.

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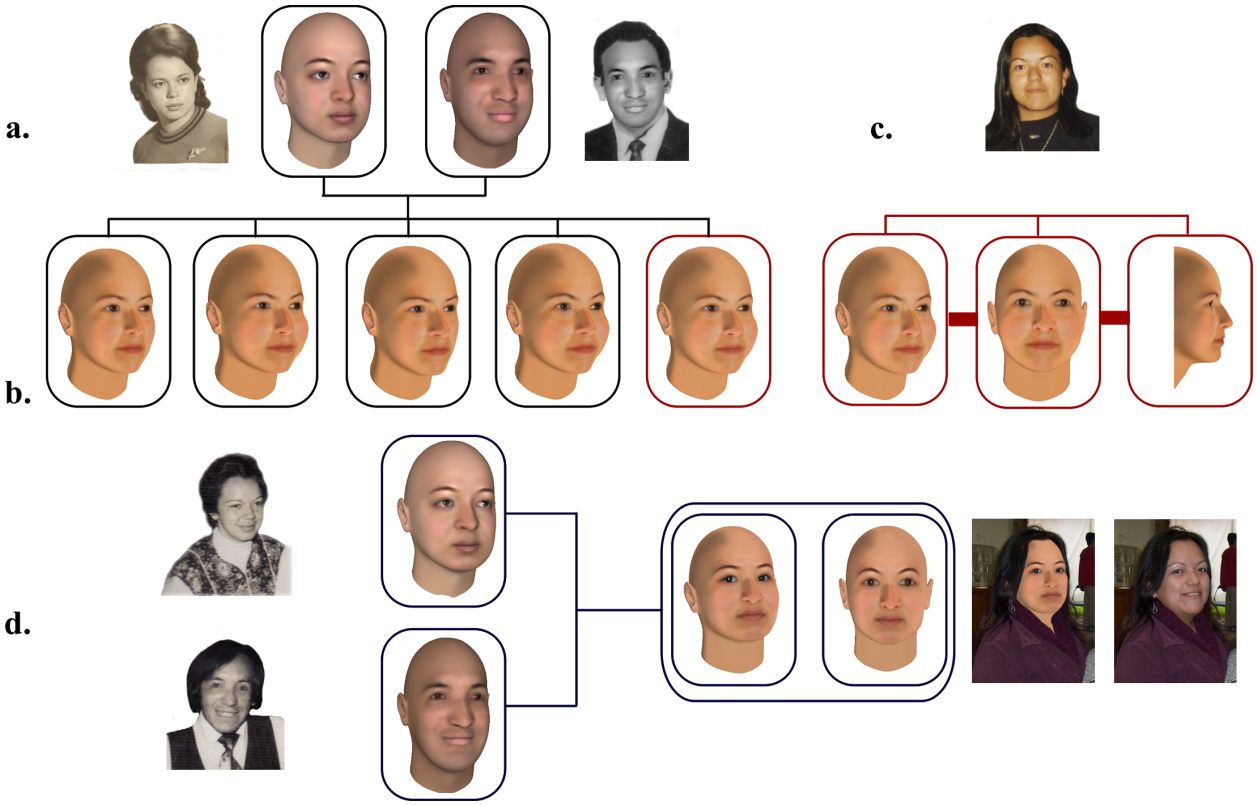

Figure 12. a) Selected photographs and 3D models of parents. b) Daughters models generated from the paternal models in the reference age. c) Selected model in the age of disappearance. d) Missing woman and parental models at target age.

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