Poster Session THU-PM-034



StyleGene: Crossover and Mutation of Region-level Facial Genes for Kinship Face Synthesis

Hao Li¹, Xianxu Hou^{2,5}, Zepeng Huang¹, Linlin Shen^{1,2,3,4*}

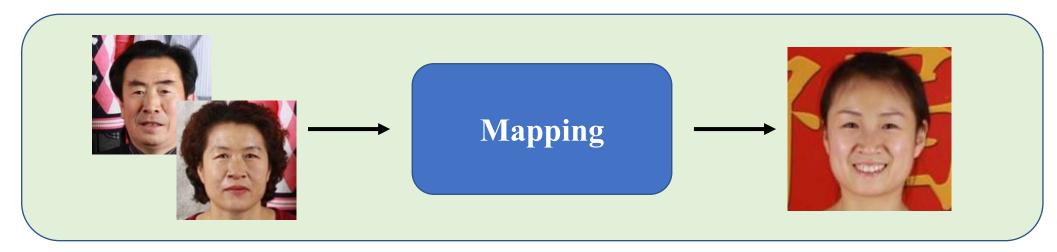
¹Computer Vision Institute, College of Computer Science and Software Engineering, Shenzhen University ²National Engineering Laboratory for Big Data System Computing Technology, Shenzhen University ³Shenzhen Institute of Artificial Intelligence and Robotics for Society ⁴Guangdong Key Laboratory of Intelligent Information Processing, Shenzhen University ⁵School of AI and Advanced Computing, Xi'an Jiaotong-Liverpool University

Github: https://github.com/CVI-SZU/StyleGene



Quick Preview

• Synthesizing Descendant Faces using Parental Images

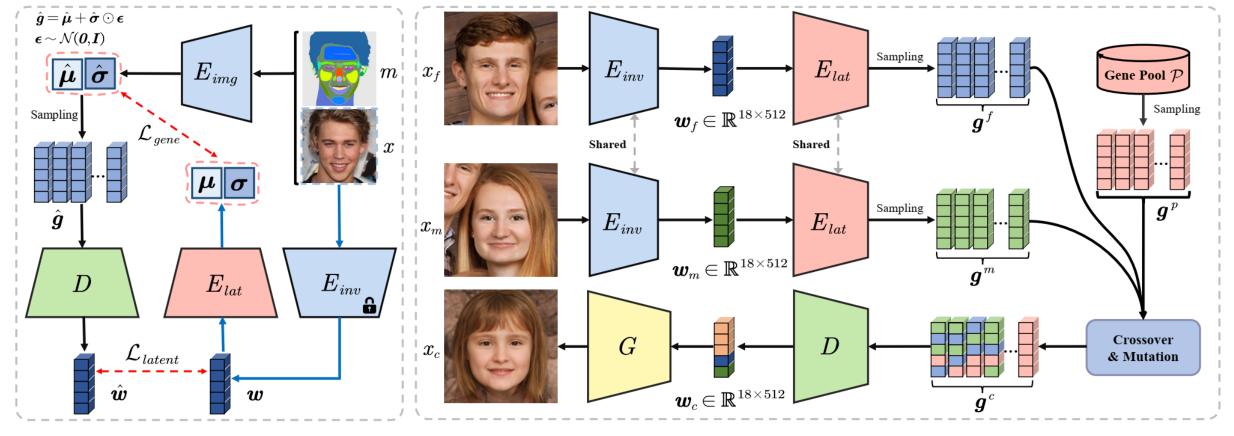


Applications:

- Finding missing children
- Building family trees
- Criminal pursuits
- Social media analysis



Quick Preview



(a) Training Stage

(b) Inference Stage



Motivation

Challenges:

- Missing large-scale, high-quality kinship datasets make visual genetic relations learning difficult.
- Data limitations lead to overfitting in learned genetic relations, resulting in limited diversity among generated descendants.

Objectives:

- Reducing reliance on kinship annotation during the training stage.
- > Enhancing facial genetic region controllability and interpretability.
- Improving the diversity of facial mutation traits.
- Minimizing training complexity and overhead.



Contribution

StyleGene Framework:

Synthesizing high-fidelity kinship faces with controllable facial genetic regions.

Novel Genetic Strategy:

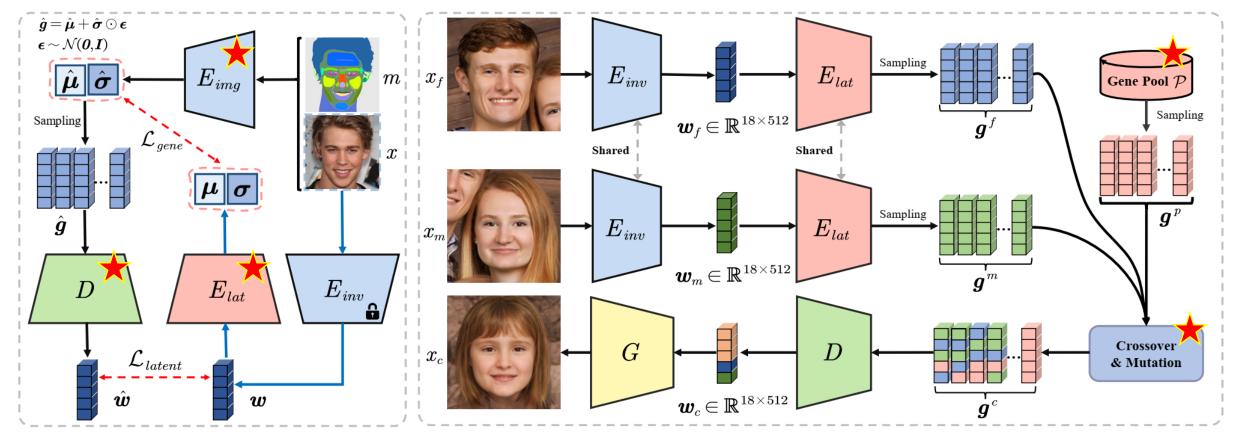
Simulating crossover and mutation to generate region-level facial genes (RFGs) for descendants.

Gene Pool Enhancement:

Increasing kinship face diversity through the Gene Pool concept.



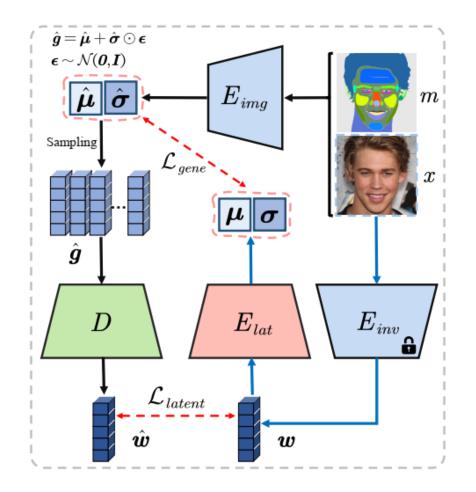
Proposed Method



(a) Training Stage

(b) Inference Stage

Learning Region-level Facial Gene



Reconstruction loss

$$\mathcal{L}_{latent} = \parallel \boldsymbol{w} - \boldsymbol{\hat{w}} \parallel_2,$$

Head

Decouple latent loss

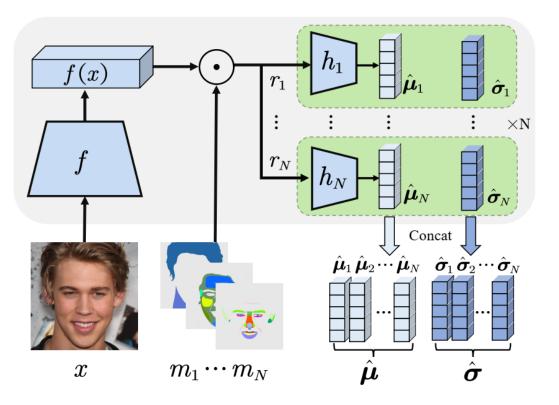
$$\mathcal{L}_{gene} = \sum_{i=1}^{N} \Big[\parallel oldsymbol{\mu}_{i} \parallel_{2} + \parallel oldsymbol{\sigma}_{i} - oldsymbol{\hat{\sigma}}_{i} \parallel_{2} \Big],$$

Joint training of all modules $\mathcal{L} = \mathcal{L}_{latent} + \lambda \mathcal{L}_{gene},$

[1] Zhang, et al. Datasetgan: Efficient labeled data factory with minimal human effort[C]//CVPR 2021

Architecture

Image-based Gene Encoder (IGE) E_{img}



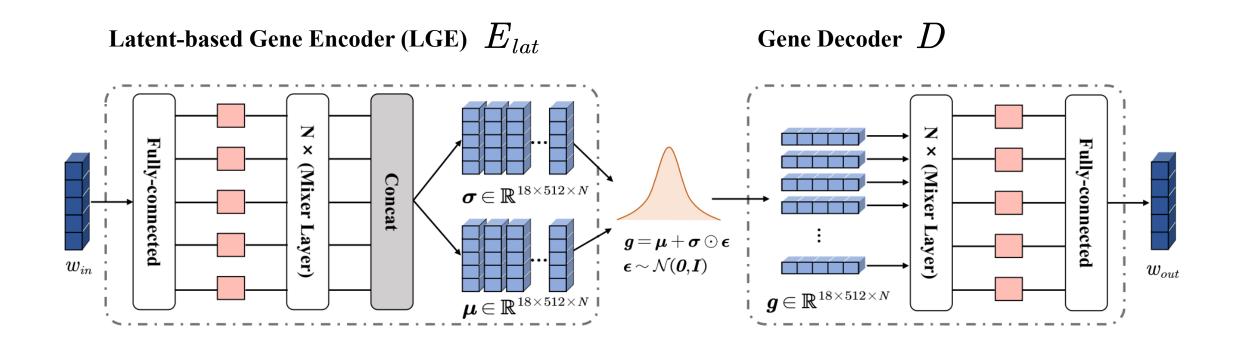
RFG is sampled from a Gaussian distribution:

$$\boldsymbol{\hat{g}}_i \sim q(\boldsymbol{\hat{g}}_i | \boldsymbol{r}_i) = \mathcal{N}(\boldsymbol{\hat{g}}_i; \boldsymbol{\hat{\mu}}_i, \boldsymbol{\hat{\sigma}}_i^2 \boldsymbol{I}), \ \boldsymbol{\hat{g}}_i \in \mathbb{R}^{18 \times 512}$$

Reparameterization trick: $\hat{g}_i = \hat{\mu}_i + \hat{\sigma}_i \odot \epsilon, \epsilon \sim \mathcal{N}(0, I),$

Concatenate all regions RFG: $\hat{\boldsymbol{g}} = [\hat{\boldsymbol{g}}_1, \cdots, \hat{\boldsymbol{g}}_N] \in \mathbb{R}^{18 \times 512 \times N}$

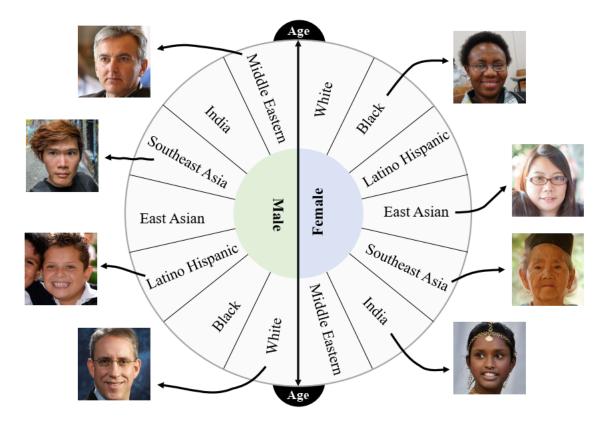
Architecture



Building a Gene Pool

Step1: Extract RFGs from FFHQ dataset Step2: Group RFGs by attributes

- Age: 0-2, 3-4, 10-19, 20-29, 30-39, 40-49, 50-59, 60-69, and over 70 years old
- Race: White, Black, Indian, East Asian, Southeast Asian Middle Eastern, and Latino
- Gender: Male and Female



Crossover & Mutation

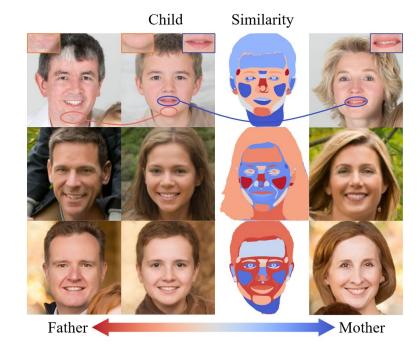
Given a pair of parental face images, x_f and x_m , we first apply LGE to obtain a set of RFGs $g^f = [g_1^f, \dots, g_N^f]$ and $g^m = [g_1^m, \dots, g_N^m]$. The RFGs of descendants $g^c = [g_1^c, \dots, g_N^c]$ can be calculated by

Gene Crossover:

$$\boldsymbol{g}_{i}^{c} = \alpha_{i} \boldsymbol{g}_{i}^{f} + \beta_{i} \boldsymbol{g}_{i}^{m}, \quad \alpha_{i} + \beta_{i} = 1$$

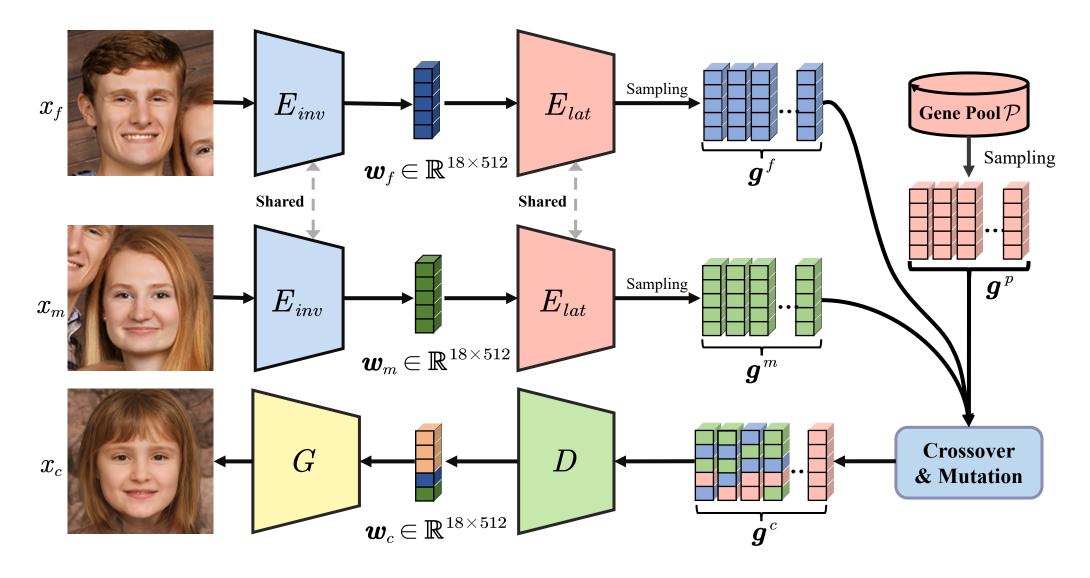
Gene Mutation:

$$\boldsymbol{g}_{i}^{c} = \begin{cases} \boldsymbol{g}_{i}^{p}, & t_{i} = 1 \\ \alpha_{i} \boldsymbol{g}_{i}^{f} + \beta_{i} \boldsymbol{g}_{i}^{m} + \gamma \boldsymbol{g}_{i}^{p}, & t_{i} = 0 \end{cases},$$



where $\alpha_i + \beta_i = 1 - \gamma$, $\boldsymbol{g}_i^p = S(\mathcal{P}_c)$, $S(\cdot)$ is the random sampling operator.

Inference Stage



Experiments

Qualitative evaluation

> FIW dataset



Father Mother Real Child Ours StyleDNA ChildPredictor ChildGAN DNA-Net

Qualitative evaluation

> FF-Database



Father Mother Real Child Ours StyleDNA ChildPredictor

Qualitative evaluation

> TSKinFace dataset



Father Mother

StyleDNA

ChildPredictor

CDFS

Quantitative evaluation

Kinship Verification

Table 2. Kinship verification accuracy (%) on the TSKinFace [31], FF-Database [47], and FIW [34] dataset.

Methods	TSKinFace	FF-Database	FIW
StyleDNA [26]	53.15	55.11	49.47
ChildPredictor [47]	58.24	59.62	51.81
StyleGene (Ours)	81.74	80.38	62.29

Diversity Evaluation (LPIPS metric)

Table 3. Quantitative comparison of the diversity of the generated descendants. * means we cropped the face i.e. no hair.

Methods	TSKinFace	FF-Database	FIW
StyleDNA* [26]	0.0756	0.0763	0.0736
ChildPredictor [47]	0.1697	0.1723	0.1750
StyleGene (Ours)*	0.1748	0.1735	0.1740
StyleDNA [26]	0.1559	0.1542	0.1573
StyleGene (Ours)	0.3270	0.3418	0.3279

User Study

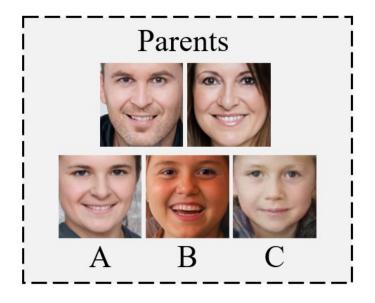


Table 4. The rank of different approaches in user study.

	ChildPredictor	StyleDNA	StyleGene (Ours)
Avg. rank	2.46	2.22	1.32

Distribution of Synthesized Children

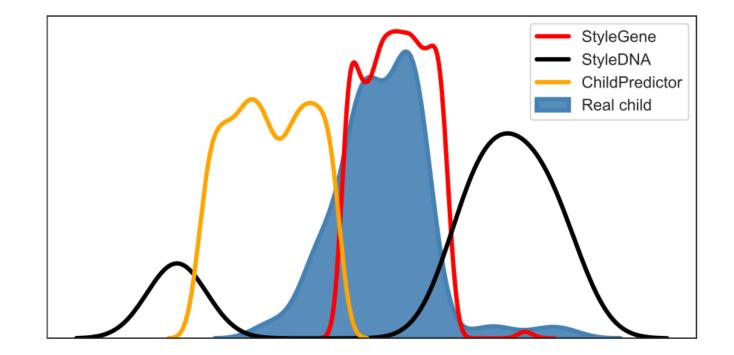


Figure 9. Distribution of real children (blue) and children generated using StyleDNA (black), ChildPredictor (yellow), and ours (red). Best viewed in color.

Conclusion

- StyleGene is a proposed method for synthesizing high-fidelity kinship faces with controllable facial genetic regions.
- ➤ A novel genetic strategy is introduced to simulate the crossover and mutation process to generate the facial genes of descendants.
- ➤ A Gene Pool is used to increase the diversity of the kinship face during the mutation process.
- ➢Experimental results demonstrate superior realness, similarity with parents, and diversity compared to existing methods.