

Figure 1. Face aging/rejuvenation results of IPCGAN [7] and S<sup>2</sup>-IPCGAN (IPCGAN with our S<sup>2</sup>-module).



Figure 2. Continuous face aging by S<sup>2</sup>-IPCGAN.

## Supplementary Material for S<sup>2</sup>GAN

### 1. Using S<sup>2</sup>-module as IPCGAN [7] Plug-in

As mentioned in the manuscript, the S<sup>2</sup>-module in the proposed method is orthogonal to the existing methods. Therefore, the S<sup>2</sup>-module can be used as a plug-in to methods with a transformation network such as [2, 7, 8, 3] to reduce their computational consumption as well as enable the continuous aging, while still keeping their own advantages. Specifically, for methods with distinct models for each pair of age groups such as [8, 3], the S<sup>2</sup>-module can reduce their model number to only one. For all these methods [2, 7, 8, 3], which takes  $nt_e + nt_d$  time to generate aged images of all  $n$  age groups, the S<sup>2</sup>-module can reduce their prediction time to  $t_e + nt_d$  ( $t_e$  and  $t_d$  denote the prediction time of encoder and decoder respectively).

For better illustration, we insert our S<sup>2</sup>-module into IPCGAN [7] without modifying any other hyper-parameters, which is referred to as S<sup>2</sup>-IPCGAN. Fig. 1 and Fig. 2 show the visual results of IPCGAN and S<sup>2</sup>-IPCGAN, and Table 1 shows the model parameters and the prediction time for generating aged images of all 5 age groups. As can be seen from Fig. 1, the S<sup>2</sup>-IPCGAN achieves comparable visual quality to the original IPCGAN. Moreover, as can be seen from Table 1, the prediction time of S<sup>2</sup>-IPCGAN is 40% less than the original IPCGAN with only a bit more parameters. Furthermore, by employing the S<sup>2</sup>-module, the S<sup>2</sup>-IPCGAN is applicable for continuous face aging rather than the original discrete group aging, as shown in Fig. 2. All these benefits demonstrate the superiority of the S<sup>2</sup>-module in our method.

### 2. Preservation of Personalized Characteristics

We also investigate the performance of preserving personalized characteristics. 50 random images with scar or

mole from MORPH are chosen as input, and the three methods respectively generate  $50 \times 4 = 200$  images for 4 age groups. Then, three volunteers are asked to judge whether the scar or mole is kept on the generated image. For each method, Table 2 reports the proportion of the generated images which well preserve the scar or mole, averaged over the three volunteers. As shown, our method better preserves the personalized characteristics than the competitors.

### 3. Generalization Capability

We also investigate the generalization capability of the proposed method by training on MORPH or CACD then testing on LFW. As shown in Table 3, our method achieves much better aging accuracy, with comparable face verification rate and image quality (FID) to IPCGAN.

### 4. To Understand the Personalized Basis

To illustrate the functionality of the basis, we use a model with 8 basis vectors and change the coefficient of a single basis vector at one time. As shown in Fig. 5, when changing the coefficient of basis #1, the network adds more beard; when changing the basis #2, the network grays hair and makes the laugh line wrinkle deeper and longer (the skin color looks weird probably because such coefficients are not being seen at training). As expected, the basis contains personalized aging factors.

### 5. Additional Visual Results

Additional face aging/rejuvenation results of our S<sup>2</sup>GAN are shown in Fig. 3 and Fig. 4.

### 6. Network Architectures

See Fig. 6.





Figure 3. Face aging results of our  $S^2$ GAN on MORPH [5]. The test images are wrapped in red boxes. Best viewed in color and zooming in.

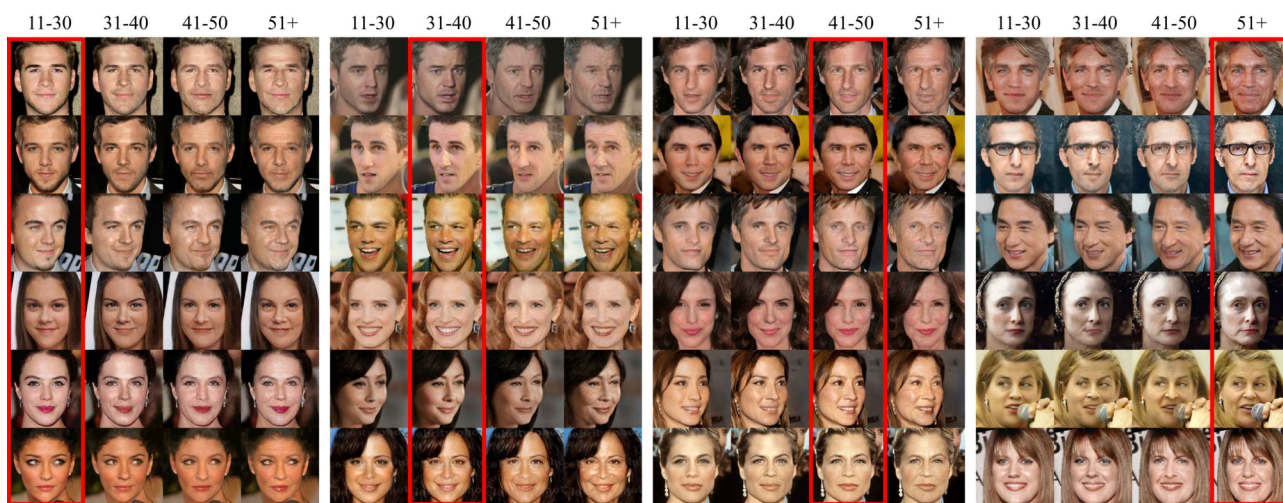


Figure 4. Face aging results of our  $S^2$ GAN on CACD [1]. The test images are wrapped in red boxes. Best viewed in color and zooming in.

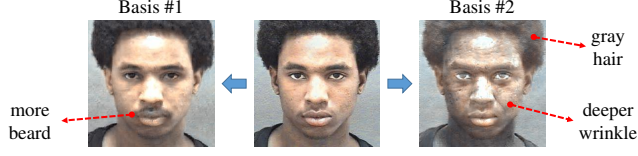


Figure 5. Changing coefficient of single specified basis vector.

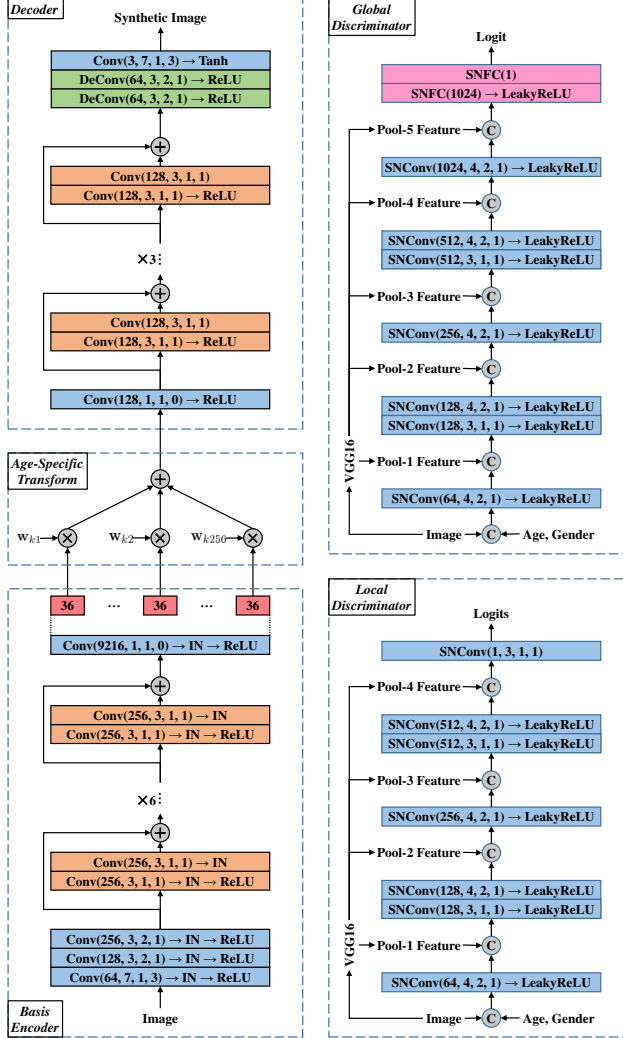


Figure 6. Network Architectures. Conv(d, k, s, p) and DeConv(d, k, s, p) respectively denote convolutional layer and transposed convolutional layer with d as dimension, k as kernel size, s as stride and p as padding size. SNConv and SNFC respectively denote convolutional layer and fully connected layer with spectral normalization [4]. IN is instance normalization [6]. © is the concatenation.

| Method                 | GPU Time / Image | Parameters |
|------------------------|------------------|------------|
| IPCGAN [7]             | 5.1 ms           | 7.58 MB    |
| S <sup>2</sup> -IPCGAN | 3.1 ms           | 7.83 MB    |

Table 1. Computational cost of IPCGAN and S<sup>2</sup>-IPCGAN.

| Method     | Scar/Mole Preservation |
|------------|------------------------|
| CAAE [9]   | 0%                     |
| IPCGAN [7] | 71%                    |
| Ours       | 95%                    |

Table 2. Scar/mole preservation rate.

| Method     | MORPH → LFW |     |      | CACD → LFW |     |      |
|------------|-------------|-----|------|------------|-----|------|
|            | A.          | V.  | F. ↓ | A.         | V.  | F. ↓ |
| CAAE [9]   | 48%         | 56% | 87   | 40%        | 59% | 60   |
| IPCGAN [7] | 48%         | 99% | 10   | 60%        | 96% | 11   |
| Ours       | 67%         | 99% | 11   | 88%        | 96% | 9    |

\* A. = Aging Accuracy, V. = Face Verification Rate, and F. = FID (lower is better).

Table 3. Generalization capability.

## References

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