Achieving Better Kinship Recognition Through Better Baseline

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Abstract—Recognizing blood relations using face images can be seen as an application of face recognition systems with additional restrictions. These restrictions proved to be difficult to deal with, however, recent advancements in face verification show that there is still much to gain using more data and novel ideas. As a result face recognition is a great source domain from which we can transfer the knowledge to get better performance in kinship recognition as a source domain. We present new baseline for automatic kinship recognition task and relatives search based on RetinaFace[1] for face registration and ArcFace[2] face verification model. With the approach described above as the foundation, we constructed a pipeline that achieved state-of-the-art performance on two tracks in the recent Recognizing Families In the Wild Data Challenge.

I. INTRODUCTION

Face recognition using neural networks and RGB image data is still on the rise thanks to the abundance of raw data on the Internet, more public data [3], [4], [5], and popular computational frameworks being open source. Algorithms in this field reach new records [6], [7] both in quality and resource consumption which were unimaginable several years before.

Automatic kinship recognition using visual information is very similar to face verification and thanks to growing Families In the Wild (FIW) [8] dataset is getting more attention in the research community [9].

Annual Recognizing Families In the Wild (RFIW) Data Challenge tries to bring the difficult problem closer to have a solution applicable to the real-world tasks. And every year contestants show new approaches based on metric learning [10], [11], ensembling different facial features [12] and the introduction of additional data pre-processing [13]. We decided to take a step back and start with a better baseline model and then gradually apply different approaches to improve performance. To our surprise, basic fine-tuning happened to be enough to achieve better performance than other competitors. In this work we make three main contributions:

1) We propose a new baseline for evaluating kinship recognition methods, which is based on recent advancements in the face recognition field.
2) We designed a pipeline for the fine-tuning face verification models for visual kinship recognition task based on the new baseline.
3) We show that our approach1 achieves the best performance in Recognizing Families In the Wild Data Challenge (Tracks 1&3).

The rest of this paper is organized as follows: in section II we briefly review existing methods that are useful for our task of kinship recognition and family search, in section III we explain our proposed baseline and pipeline, in section IV we evaluate our approach on RFIW challenge dataset, in section V we conclude our work and discuss further possible improvements.

II. RELATED WORK

Our task is to recognize a binary feature (kin, non-kin) given two face images. There are several different approaches we can use to tackle this problem: from hand-crafted features to generative methods for data augmentation. But we will focus on closer work in similar fields.

Convolutional neural networks (CNN) became the backbone in the variety of methods in computer vision tasks. Since the introduction of AlexNet [14] hand-crafted features had been quickly replaced by better and sometimes even faster algorithms based on CNNs.

Face recognition is an example of a fast-moving field in computer vision. The progress is due to novel datasets [3], [5], [4] for training and evaluation, introduction of different architectures and learning methods [15], [16], [17], [2], more data challenges [18], [19] and industrial interest [7]. Similarity with visual kinship recognition tasks makes the face recognition models a good candidate for fine-tuning for our task. And it was shown [9] that better base models can achieve much higher performance than carefully tuned older ones.

Image retrieval also had a success incorporating CNNs. The deep representation from the penultimate layer was shown [20], [21] to be a good feature extractor. Typically methods were tuned for retrieval task with metric learning [22] but classification approach using proxies [23], [24] became a new promising design.

III. PROPOSED PIPELINE

In [9] fine-tuned SphereFace [16] was proposed as the best baseline benchmark for our task. However, better algorithms were proposed in recent years. ArcFace [2] achieved better performance in face verification and was widely recognized in Github community with several re-implementations easily obtainable in every popular framework. Thus, we tried to use it as a new baseline and foundation for our design.
A. Extracting Face Embeddings

We could use images from FIW dataset without the special preparations to obtain the image embedding, but facial recognition models work differently based on the different face alignment techniques that were used during their training. Moreover, better face detection and registration further improve model performance [1]. Knowing this, we re-detected faces in the challenge’s dataset and aligned them with landmarks from the RetinaFace [1] detector. At this step, some faces were not detected with the selected confidence threshold and were removed from the training and validation set. For the test set, such images were just resized to fit into the face recognition model. There were a total of 4 images removed from the training set, 3 images from validation, and 4 problematic images that occurred in the test set.

The ArcFace [2] model was used for features extraction. This model was pre-trained on cleaned MS-Celeb-1M [3] dataset and has the embedding dimension of 512.

To compare two images \( u_i \) and \( u_j \) we used cosine distance between their computed embeddings \( x_i \) and \( x_j \):

\[
d(u_i, u_j) = \frac{x_i^T x_j}{\|x_i\|_2 \|x_j\|_2} \tag{1}
\]

B. Transfer Learning

The main difference between face and kinship recognition tasks is in the relative distance between different people. While face recognition cares mostly about pictures of the same person being close in embedding space, kinship recognition is trying to achieve a much harder task. In the later different people must be closer to each other than the other groups of people, ideally forming family clusters. The difference in the available labeled data and similarity between the tasks makes face recognition a great source domain for transferring to the kinship recognition domain.

In the previous iterations of RFIW, the metric learning was used as a transfer learning approach and achieved a great performance [10]. However, it requires pairs of images to be carefully sampled to confidently estimate the distribution of all distances in the metric space. Another concern is that it requires a significant amount of time to train the final model.

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Given the information for each person about their family association, we can construct a family classification problem. For every kind separately. Alas, we could only submit 15 results of our three submissions for the final phase.

We sampled 5,000 positive and 5,000 negative pairs selected uniformly between all families from the validation set using algorithm 1.

Using this approach validates our model without the issue of popular families that have lots of images. We used AUC ROC metric on the validation pairs (see fig. 1) for choosing the best model for submission Another problem occurs though: as we select uniformly between the families, families with low member count are given higher priority. We chose to resolve this issue with a higher binarization threshold.

C. Forming Validation Pairs

In track 1 of RFIW Data Challenge images are divided between families. As the distribution between persons and between families in challenge’s data is non-uniform, we need to be careful with sampling the pairs, as validating model offline is crucial given the limited number of submissions. We sampled 5,000 positive and 5,000 negative pairs selected uniformly between all families from the validation set using algorithm 1.

D. Choosing Binarization Threshold

Given a comparison of two image embeddings using cosine distance (1) we need some binarization function to get the needed result. In our case, a simple binarization by threshold was used. The threshold can be chosen based on the trade-off between the false positive rate and the true positive rate. As we had no prior knowledge of how the test pairs were selected we chose target false positive rate based on our three submissions for the final phase.

Given the information about the pair’s possible kind of kinship relation, we could have chosen the threshold for every kind separately. Alas, we could only submit 15 results and some kinds of relations had a low number of pairs to confidently select threshold. We further discuss this in section IV.C.

E. Using for Retrieval

The retrieval task can be reduced to a series of verification tasks. Every probe image is matched with every gallery image

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**Algorithm 1: Sampling validation image pairs**

**Input:** \( N \) number of families

\( k \) number of image pairs to sample

**Result:** \( k \) positive pairs and \( k \) negative pairs

1. \( \text{positive_pairs} \leftarrow [\] \)
2. \( \text{negative_pairs} \leftarrow [\] \)
3. \( A \leftarrow \text{uniform}(1, N, \text{size} = k) \) # anchor families
4. forall \( i = 1, \ldots, k \) do
5. \( A \leftarrow \text{families without } A_i \)
6. \( \text{anchor_person} \leftarrow \text{sample random member from } A_i \)
7. \( \text{positive_person} \leftarrow \text{sample other random member from } A_i \)
8. \( \text{negative_person} \leftarrow \text{sample random member from } O \)
9. \( \text{anchor_face} \leftarrow \text{sample random image from } \) anchor_person
10. \( \text{positive_face} \leftarrow \text{sample random image from } \) positive_person
11. \( \text{negative_face} \leftarrow \text{sample random image from } \) negative_person
12. append (anchor_face, positive_face) to positive_pairs
13. append (anchor_face, negative_face) to negative_pairs
14. **end**

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1Clean dataset can be downloaded from [https://github.com/deepinsight/insightface/wiki/Dataset-Zoo](https://github.com/deepinsight/insightface/wiki/Dataset-Zoo)
image to construct a retrieval matrix (every row contains a retrieval result for the probe image). Our task also has more than one image for every probe person, and we can solve this in different ways. One way is creating an aggregated feature for each probe person. We can do this by averaging all the embeddings from their images. Thus we reduced our task to a single feature per probe and can form a retrieval matrix.

The other way is using all matching results from all images. We need to add aggregation function \( g(\cdot) \) that would consolidate distances between images to adapt to this. Given a gallery image \( u \) and a probe person \( P \) with \( m \) images \( \langle p_1, \ldots, p_m \rangle \) we can sort the gallery images using the distance:

\[
d_{aggr}(P, u) = g\left( \langle d(p_1, u), \ldots, d(p_m, u) \rangle \right)
\] (3)

Aggregation function should take a vector with an arbitrary number of elements and return a single real number. There are different options for such function but we tested only mean and max in this challenge.

With this approach, we need to compare embeddings for every probe image with every gallery image. It can be difficult to compute with reasonable resources when there is a large number of images per person. There is a variety of approaches [22] for that purpose: from reducing latent space [25], [26] to constructing special structures [27] but in this work we will only show (see IV-D) that getting a mean embedding for a person is comparable with searching using the aggregated function \( g(\cdot) \).

**IV. EXPERIMENTS**

**A. Recognizing Families In the Wild Data Challenge**

The Recognizing Families In the Wild Data Challenge (RFTW2020) focuses on determining blood relations based on visual facial similarities. For that, it has 20867 images from 763 families for training and validation sets. This year there were a total of three tracks: one-to-one kinship verification (track 1), two-to-one kinship verification (track 2), and family search and retrieval (track 3). Our team chose to participate in tracks 1&3 so we will focus only on them.

In track 1 there were 39743 pairs for the final testing. Methods were evaluated based on the average accuracy of binary classification (kin, non-kin) over all of the testing pairs. Additional measurements were provided separately for every kinship type.

Track 3 is the image retrieval problem with one family member as a query (or probe) and other family members with distractors as a gallery. There were 190 probe subjects (each with a different number of images) and 3897 images in the gallery. Methods were evaluated based on mean average precision (mAP) and rank@k metrics.

**B. Implementation Details**

We used Mxnet [28] for the implementation of our pipeline. For detection and feature extraction insightface python package was used. In particular, retinaface_r50_v1 which is RetinaFace implementation with ResNet50 as the backbone and arcface_r100_v1 which is modified ResNet101 trained with ArcFace loss on cleaned MS-Celeb-1M dataset.

Re-detected and aligned (as described in III-A) faces were given to the feature extractor model to obtain image embeddings. Performance of this approach (pretrained on fig. 1) was used as a baseline to test our hypotheses.

First, we tried to add a simple classification layer and finetune the whole model on the train set with stochastic gradient descent with base learning rate of 0.0001, momentum 0.9, linear warmup for first 200 batches of size 64, linear cooldown for last 400 batches, multiplying learning rate by 0.75 on epochs 8, 14, 25, 35, 40 and gradient clipping 1.5 for 50 epochs. Random color jitter and random lightning with parameter 0.15 were used for the data augmentation. No random cropping or similar technique was used to not confuse the model that was trained on similar aligned images. After that, we added L2 normalization of the embeddings and retrained the model starting with pre-trained weights. Performance of these two models on our sampled validation pairs (see III-C) can be seen in fig. 1

**C. Verification Results**

We needed to binarize our predictions to submit for test verification on track 1. We chose threshold such that we had true positive rate (TPR) of 0.75 on our sampled validation images for our first submission (pretrained in table I). Next submissions were tested with different thresholds and between several strategies, the one that showed the best average performance was to choose the threshold such that the method would have a false positive rate (FPR) of 0.2. Other entries in table II are provided with that strategy of choosing the binarization threshold.

We tested the simple fine-tuning using a classification layer (+classification) with a similar approach where the embeddings are normalized to have a unit L2 norm before the classification layer (+normalization). Both on our validation data and test set the second approach was superior. This indicates that consistency with our cosine distance metric
that we use for image comparison is crucial for fine-tuning the model for kinship verification.

From comparison table I we can see that our approach performs poorly on grandparents-grandchildren type of kinship because there is a small number of images with this type of relationship in the training set, but we can mitigate this bias through a different threshold for every kind of relationship. Sadly, we could not test this idea due to the lack of time, but we provide a proof of this hypothesis with different thresholds submission where we improved the performance for grandmother-grandson relationship by lowering binarization threshold.

We should note that though our approach scores first on average it is not by a far margin and mostly due to our great performance on sibling pairs. Having an 0.78 average accuracy at best, automatic kinship recognition still needs the opportunity to show this work.

V. CONCLUSIONS AND FUTURE WORKS

In this work we show that using better face verification models is crucial for improving kinship recognition due to more available data. We presented the new baseline for kinship verification and retrieval tasks, which is based on more accurate face recognition model than the previous baseline. Furthermore our designed pipeline for the verification task improved this result and achieved the best performance in the recent challenge.

In future work we plan to provide a more thorough analysis of methods suitable for the automatic kinship recognition task. Different feature extractors and ensembling are the most promising next steps from our perspective.

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