Visual Kinship Recognition: A Decade in the Making

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Abstract—Kinship recognition is a challenging problem with many practical applications. With much progress and milestones having been reached after ten years since pioneered - it is now that today we are able to survey their research and create new milestones. We list and review the public resources and data challenges that enabled and inspired many to hone-in on one or more views of automatic kinship recognition in the visual domain. The different tasks are described in technical terms and syntax consistent across the problem domain and the practical value of each discussed and measured. State-of-the-art methods for visual kinship recognition problems, whether to discriminate between or generate from, are examined. As part of such, we review systems proposed as part of a recent data challenge held in conjunction with the 2020 IEEE Conference on Automatic Face and Gesture Recognition. We establish a stronghold for the state of progress for the different problems in a consistent manner. We intend for this survey will serve as the central resource for work of the next decade to build upon. For the tenth anniversary, demo code is provided for the various kin-based tasks. Detecting relatives with visual recognition and classifying the relationship is an area with high potential for impact in research and practice.

Index Terms—ML survey, facial recognition, benchmarks and evaluation, deep learning, data challenges, visual kinship recognition.

1 INTRODUCTION

About a decade ago, pioneers in visual kinship recognition research published the seminar work in detecting family relationships with face images [1]. Let us now look back at this progress: reflect on the trends, successes, and failures of the past ten years. Furthermore, let us highlight the key challenges, practical use-cases, and promising future directions for research. By doing so, we provide a single resource to compare state-of-the-art (SOTA) methods on many tasks recorded and examined.

1.1 So what? Who cares?

Kinship recognition has a multitude of practical and scholarly uses - relationships provide rich information in sociology, anthropology, and genetics; privacy protections/concerns and potential use-cases can be found in social media, personal discovery, entertainment, and more described later. Besides its entrepreneurial value, visual kinship recognition has significant non-commercial (or humane) value as well. For instance, in cases of missing children, reconnecting families split across refugee camps, border control / customs, criminal investigations, ancestral-based studies, and even genome-based research. Socially, family gives a sense of belonging (i.e., membership, connection). Per Furstenberg,

... important function of family systems receives far less attention in the literature than it merits: The family ... social arrangement responsible for giving its members a sense of identity and shared belonging ... not only those inside the natal family household but also among relations living elsewhere as well [2].

Hence, a recent surge in many seeking out their pedigree. With an abundance of visual data online, resources can benefit.

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1. https://github.com/visionjo/pykinship
The main contribution of the paper is a new long-term view of the major milestones clearly defined protocols, accessible data splits, and trained models; hence, all the components needed to reproduce all experiments reported on as part of this survey. We reveal insights in edge cases that challenge current SOTA, all while improving SOTA by examining different settings and training tricks that further our understanding in kin-based detection from facial cues. Baselines are supported by source code.

1.3 Related surveys

The first survey on visual kinship recognition gave an overview on the SOTA methods and data resources of the time [3]. The authors also proposed future directions with emphasis on the lack of labeled data both in sample counts and relationship types. Hence, Wu et al. [3] claim that Convolutional Neural Network (CNNs) were inferior to metric-based methods held true. Soon thereafter, the release of the large-scale FIW dataset enabled the use of contemporary data-driven solutions [4]. Georgopoulos et al. then surveyed kinship and age in face recognition (FR), claiming the two are similar [5]. Although a comprehensive survey, kin-based problems should be treated independently. With that, having prior knowledge of one could benefit the other, and the same holds true for other soft-biometrics (e.g., gender, emotion).

Most recently, Qin et al. surveyed existing kin-based methods, characterizing each as a measure of kinship traits or statistical learning [6]. Then, groups were split further (i.e., low or mid-level features, metric learning, and transfer learning). Additionally, human performance relative to machines was compared throughout. Methods were reported for several kin-based datasets. Furthermore, the authors proposed a standardized vision system based on a four-step framework which provides a generic, modular solution. Complementing the framework in [6], we define the problems in a consistent way across many kin-based tasks, providing benchmarks on the large-scale FIW dataset [7].

1.4 Organization

The remainder of the survey is organized by sub-topic, that is, such sections, although ordered for coherency, are separated with a clear distinction for the topic of discussion. Specifically, we start by reviewing major-milestones found in the literature after the first decade of research in visual kinship recognition (Section 2). Next, we cover task-protocols as defined for visual kin-based problems (i.e., different views of the problem set for laboratory-based evaluation studies). SOTA for each is referenced and later in a report described in great detail (Section 3). Following this, we highlight essential datasets that have supported progress up to this point, while listing direct links and related logistics as are contemporary and with links to outstanding resources (Section 3.1). Then, and in light of the consideration paid to practical use-cases, we examine existing experiments (i.e., protocol definitions) for tangible benefits, such as in theory or practice, or even as useful prior knowledge for a different purpose, problem, and paradigm; without perceived practical value, tasks are dismissed. A more broad perspective of the technologies impact at large (i.e., in our everyday lives and as our capabilities are enhanced) is then discussed– aim here is to give a perspective with consideration of achievable performance, along with, as far as seen in the literature, the most rigorous analysis on the edge cases and common traits of falsely predicted samples, which ends with a discussion on contemporary limitations (Section 4). We describe the core challenges to overcome in both research and practice, while shining light on the inherent difficulties in sufficient data for the problem (Section 5). We then speak on the applications that line up with specific task-evaluations, both existing (i.e., practically existing) and high in potential (i.e., hypothetically possible). We especially and typically provide the most robust model– typically, assuming we can improve the performance with respect to that currently reported in the literature (Section 6). Closing remarks would provide forecasting both short and long-term directions and problems which kinship may take (Section 7).

2 Background Information

The story of visual kinship recognition research can be told through the data. Therefore, we speak of progress through the first decade from the perspective of the resources available (Fig. 1), and show how interest was contingent on the amount and quality of labeled data. We end this discussing the data challenges, workshops, and tutorials organized to motivate researchers.

2.1 The evolution of the problem

An increasing number of researchers have focused their attention on the problem of learning families in photos since the seminal paper published in 2010 [1]. Fang et al. proposed training machinery to visually discriminate between KIN and NON-KIN from various facial cues. Specifically, the authors demonstrated an ability to verify the kinship of a pair of faces. To support this, Fang et al. built and released the first facial image-based kinship database, Cornell Kin, made-up of 150 parent-child pairs from imagery scraped from the web (i.e., public figures, politicians, and other famous persons). Color cues (e.g., skin and hair), facial features (e.g., mouth width and chin shape) and distances (e.g., the distance between eyes and from nose to chin), along with statistical features (i.e., histogram of gradients (HOG)).

Progress in visual kinship recognition can be assessed by the public data released. Critical points in the research stemmed from the respective problem statements supported by the appropriate data. Hence, we first review the experimental design and the resulting benchmarks. As seen in Fig. 1, the rise in the number of annual publications indicates an increase in interest of researchers; the impact on the research community, as a whole, nearly grows exponentially (i.e., citation count). The incentive provided by data challenges, along with the increase in labeled data, influence the attention given to kin-based problems in multi-media. The Publish and Perish application was used to obtain the original paper-pile (Fig 2). For this, a series of queries was executed, each using visual kinship recognition as the keywords: Google Scholar, limited to 1,000 search results per query, was run two times (i.e., 2010-2020 and 2015-2020); Scopus was queried from 2010-2020, as only 48 items were found; CrossRef, with a limit of 200 items per search, was queried by year of publication (i.e., 2010-11 2011-12, , 2015-16, 2016, 2017, , . . . , 2020). Notice that the years were set such that fewest were expected the first year, more in the first half of the decade, and the most in the latter half. Many papers returned were not on automatic kinship recognition in visual media. However, using the TF-IDF document representation, we were able to quickly filter out irrelevant papers by semi-supervised clustering (i.e., side-information-based) cosine-similarity k-means [7] with labels assumed positive for the papers with keywords or titles that contain visual kinship recognition.
Fig. 1: The last decade of research in visual kinship recognition. Top: a timeline showing correlations between the data released (below timeline) and different citation metrics and events to indicate the impact throughout the research community (above timeline). To collect the statistics on citation-metrics, we built a pipeline to scrape the data needed from the web for the plots above: (1) Publish or Perish [8] was installed on a Mac Book Pro to scrape from various sources (i.e., Google Scholar, Cross Ref, and Scopus) and saved as CSV files; (2) CSV files were converted using Python; (3) the Mendeley application was then used the automatically merge duplicates, while keeping as much information as possible amongst the set; (4) queried Google Scholar for all Related Works and Cited By using PyPi’s scholarly (https://pypi.org/project/scholarly/). PyPi’s scholarly both extended the paper-pile and increased the amount of metadata available (scholarly provides richer metadata per query, allowing us to fill in missing abstracts that are critical for the next step). Finally, we clustered the documents by abstract via TF-IDF [9]. The cluster made-up of a majority of papers on kinship recognition in multimedia was clearly identified: this reduced the burden of manual inspection of hundreds of thousands to thousands. It is important to note that only citation metrics were considered here, leaving out other factors of impact like the number of times tweeted, Github stars, and other indicators that arguably influence the impact of research. Bottom: datasets for kinship recognition, along with references, stats, labels types, SOTA, and URLs. Stats are summarized by one or more of the following: Number of faces (f), families (F), pairs (P), samples (S), and individual subjects (I). Best to view electronically.
Fig. 2: Workflow to scrape publication metadata plotted in Fig. 1. From Publish or Perish [8], we queried Scholar for Related works and Cited by, increasing the size of our list nearly 20-fold. Medley merged duplicates, while keeping as much information as possible. Applied NLP to cluster relevant documents.

2.2 Data challenges and incentives

Challenges date back as early as 2011, which was highly controlled multi-modal data of twins collected nearly annually as a part of Twins Day [10]. Also nearly annually starting in 2014 [11], several data challenges on unconstrained face data were hosted. Lu et al. attracted many with a IEEE International Conference on Automatic Face and Gesture Recognition (FG) challenge with Kin-Faces in the Wild (KinFaceW) [12]. Robinson et al. expanded the list of challenges through an ACM MM Data Challenge Workshop on the first large-scale visual kinship recognition challenge [13], followed by FG challenges the next three consecutive years—an annual effort, to this year [14]. In 2019, there even was the more main-stream Kaggle Competition.²

Besides, there have been several tutorials at top-tier conferences (i.e., ACM MM18 [15], CVPR 2019, and FG 2019). As part of the most recent version (i.e., supplemental to this survey), FIW is now archived with a datasheet: “datasheets for datasets” is a concept that sprung up from the view of bias in machine learning (ML) [16]. The idea is to promote transparency and, thus, minimize the doubt from unknown biases that accompany various publicly available data resources. Specifically, datasheets are complete specifications of data, such that all aspects are recorded in depth (i.e., from the data source, to methods for scraping, to the designing of benchmarks, to the potential applications the data carries). There are other variants that were recently proposed with similar motivation as Datasheets for Datasets, such as FactSheets [17] and Model Cards [18]. Nonetheless, we found that the format and motivation of “datasheets for datasets” was best to archive for FIW, which we used to record data specifications.

3 Problem Statements, Data, Protocols

One goal of ours is to clearly define experiments for which to list the respective SOTA: with reputability as a topmost priority. The experimental settings introduced next are supported by demos made for the public. Current SOTA for the different tasks on the different datasets are listed in Table 1. Sample face photos for one of the one-thousand families that make up FIW, the relationship links between them, and a subset of the family photos for which faces are cropped out are shown in Fig. 3. The discrimination tasks included in the discussion were chosen based on popularity and practicality (Fig. 4). Supplemental to this survey and available online is a Data Card describing FIW.

2. https://www.kaggle.com/c/Recognizing-Faces-in-the-Wild
3. https://web.northeastern.edu/smilelab/fiw/cvpr19_tutorial/
4. http://fg2019.org/visual-recognition-of-families-in-the-wild
5. https://web.northeastern.edu/smilelab/fiw/fiw_ds.pdf

Fig. 3: Sample family of FIW [7]. Faces and relationships of the American Football family, the Gronkowski’s (Top). The montage shows less than half of all photos for respective family. Photo types are various, spanning profile faces (top) to images of different subgroups of family members. Furthermore, samples capture different times of life. Note, crops were made to fit montage (Bottom).

3.1 Paired kin-based visual data

A broad view of the various kin-based multimedia data is considered (i.e., visual, audio, or audio-visual). The clear trend that unfolds is in the level of complexity as the problem rises from one year to the next (Fig. 1). Still, milestones were founded on practical motivations whether it had been the byproduct of overall task protocol (i.e., a more difficult problem statement and, thus, evaluation protocol) or a reduction in random from an increase in the number of data points (i.e., with more data came added challenges). In other words, major data releases and protocol updates seemed to have been adopted by researchers in a productive and timely manner.

An interesting view that also motivated a new public image dataset (i.e., UB Face) is leveraging knowledge of age as a prior and conditioned on whether KIN is true or not [19]. The idea was founded on analyzing the type of paired data frequently in the set of false-positive (FP)—specifically, facial pairs of relatives separated by larger age gaps. Thus, based on perceived hard positives, the UB Face dataset provided two images for each parent, one at a younger and the other at an older age. In the
3.2 Kinship verification

The goal of the most popular kin-based task is to determine whether a face pair are blood relatives (i.e., KIN or NON-KIN). Scholarly findings in the fields of psychology and computer vision revealed that different types of kinship share different familial features. From this, the task has evolved into verifying over a broad range of relationship types, like parent-child (i.e., father-daughter (FD), father-son (FS), mother-daughter (MD), mother-son (MS)) or siblings (i.e., brother-brother (BB), sister-sister (SS), brother-sister (SIBS)). Typically, we assume prior knowledge of the relationship type, both during training and testing. Hence, it is typical to train separate models or learn different metrics. Until the release of FIW [4, 13], small sample sets limited experiments. Thus, the larger data-pool of FIW resulted in larger-scale evaluations that better mimicked true distributions of diverse families globally. With it, also came additional relationship types that span multiple generations (i.e., grandfather-granddaughter (GFGD), grandfather-grandson (GFGS), grandmother-granddaughter (GMGD), grandmother-grandson (GMGS)). FIW is made-up of 1,000 disjoint family trees of various structures (i.e., the number of family members range from five to forty-four). Furthermore, subject nodes making up the trees typically contain multiple face samples—not often samples that span over time, with face shots of most family members at different times in their lives. The families are split into five-folds with no overlap between folds. The trees are converted to pairs of various relationship types, with an average of five face samples per family member. The pairs present a variety of additional challenges, as, for instance, a GMGS pair may or may not be with faces of similar age. It could be an image of the grandmother as a child, and the GS as an adult, or even at the time he was a GF.

3.3 Family classification

Family classification, the problem where one family member is set aside, and all other members are used to model the classes (i.e., family), is reviewed next. Hence, the task is to determine the family that the unknown subject belongs to, which is formulated as a closed-form, multi-class classification problem. This one-to-many problem is challenging, and only increases in difficulty with more families. The challenge stems from the large intra-class variations, which was revealed by a performance drop with an increasing number of families. The task has evolved into verifi-

3.4 Tri-subject verification

Tri-subject verification, first introduced in [24] (i.e., Tri-Subject Kinship (TSKIN)), focused on a slightly different view—predict whether a child is related to a pair of parents. In practice, this setting makes the most sense, as knowledge of one parent means the other can likely be easily inferred. Recently, as part of the RFIW data challenge, FIW was used to organize and benchmark tri-subject verification on scales much larger than ever before [14].

3.5 Search and retrieval

This view, the most recent to be introduced [22], formulates the problem of missing (i.e., unknown) children. A search gallery made up of all faces of FIW, but those of the single child held out as the probes for F families. Thus, the input is visual media of an individual, and the output is a ranked list of all subjects in the gallery. This many-to-many task is staged as a closed set problem. Thus, the number of true-positive (TP) varies for each subject, ranging anywhere from [1, k] relatives present in the gallery. In other words, there are always relatives present.
3.6 Multi-modal data

Additional modalities (e.g., video [25] [29] and audio [30]), although limited attempts and fairly new in literature, have proven quite effective. Wu et al. demonstrated that speech can be modeled between deceiver between KIN and NON-KIN. Audio, in particularly, has shown promising, but through minimal attempts. Work to better understand the patterns that allow for speech to work—whether that be jargon used, accents shared, or other acoustical features— we have seen that a kinship detection system can be improved with audio; however, an in-depth look at the model and the salient components between highly matched signals is subject to future work.

Let us consider other signals that can define visual data; let us consider other label types for faces that could also enhance performance (i.e., complement kin-based knowledge). For instance, expressions and mannerisms are often similar for parent and child (e.g., they have the mother’s smile). More complex dynamics for individual expressions and mannerisms can be effectively captured in video data [31]. KinFaceW Videos (KFVW), spawned out of the same group as KinFaceW, meaning notable contributions by these authors at about the half way point and towards the end of the decade (Fig. 1). Hence, added knowledge that complements the visual information has proven useful for boosting kin-based recognition ratings (e.g., 3D facial images [10] or voice [30]).

3.7 Kin-based facial synthesis

Technology to post-process images (or even curate in real-time, i.e., Snapchat filters) have grown popular in the modern-day main-stream. From this alone–kin-based face synthesis for entertainment and digital art is inherently employable. As a concrete example, Snap Inc. introduced the ability to predict the offspring from a pair of faces in the Snapchat app mid-2019. Surely, a natural curiosity. Furthermore, studies support links between DNA and appearance [32], meaning it possible.

Another, nearly default use-case for synthesizing faces based on kinship is in law enforcement to predict the appearance of an unknown perpetrator provided knowledge of kin. Also, nature-based studies where latent variables control the appearance of an offspring in a manner that allows for the analyzer to explore. And, projecting further in time, presumably, is its place in genetics. If genetics allows for, say, tweaking the fusion of male and female chromosomes to avoid deformities about the face of an offspring, the ability to visualize changes in appearance as a function of changes in latency, would likely be needed.

4 Top Visual Kinship Recognizer

For the discussion on current SOTA in visual kinship recognition, our focus is entirely consumed with the largest and most comprehensive facial image dataset. Said to be motivated by a lack of labeled data, FIW grew to be a multi-task set out to support multiple tasks of visual kinship recognition with the data required for modern-day, data-driven complex-modeling (i.e., deep learning). Furthermore, with the annual data challenge providing additional incentive, along with the project being dynamic in regular releases of updated versions was initially released 2016 [4], and later extended [7]. In addition, the latest data was released for a 2020 data challenge [14]).

Note: for the remainder of this section, we hone-in on the story of FIW as seen from the lens of the annual RFIW data challenges; and each of the years (i.e., 2017 [13]-2020 [14], with a premiere Kaggle Competition6 held just prior to the 2020RFIW). Indeed, we will discuss how deep learning modeling approaches were made possible with FIW— a clear factor listed by Robinson et al. in the first publication pertaining to the data and evaluation [4].

6. https://www.kaggle.com/c/recognizing-faces-in-the-wild
TABLE 2: T-1 Counts. Number of unique pairs (P), families (F), and face samples (S), with an increase in counts and types since [13].

|        | BB | SS | SIBS | FD | FS | MD | MS | GFGD | GFGS | GMGD | GMGS | Total |
|--------|----|----|------|----|----|----|----|------|------|------|------|-------|
| Train  | P  | 991| 1,029|1,588| 712| 721| 736| 716 | 136 | 124 | 116 | 114 | 6,983 |
|        | F  | 303| 304  |286 | 401| 404| 399| 402 | 81  | 73  | 71  | 66  | 2,790 |
|        | S  | 39,608| 27,844|35,337| 30,746| 46,583| 29,778| 46,969| 2,003| 2,097| 1,741| 1,834| 264,540 |
| Val    | P  | 433| 433  |206 | 220| 261| 200| 234 | 53  | 48  | 56  | 42  | 2,186 |
|        | F  | 74 | 57   |90  | 134| 135| 124| 130 | 32  | 29  | 36  | 27  | 868  |
|        | S  | 8,340| 5,982|21,204| 7,575| 9,399| 8,441| 7,587| 762 | 879 | 714 | 701 | 71,584 |
| Test   | P  | 469| 469  |217 | 202| 257| 230| 237 | 40  | 31  | 36  | 33  | 2,221 |
|        | F  | 149| 150  |89  | 126| 133| 136| 132 | 22  | 21  | 20  | 22  | 1,190 |
|        | S  | 3,459| 2,956|967 | 3,019| 3,273| 3,184| 2,660| 121 | 96  | 71  | 84  | 39,743 |

Fang et al., in their seminar work, evaluated humans using a subset of the Cornell Kin dataset. The authors found that, on average, humans were about 4% worse than the machinery (i.e., average human performance was 67.19%, with the top performance reaching 90% and the worst at just 50%). Provided the time of this work, during which whether or not faces were a fair cue to discriminate $KIN$ from $NON-KIN$ was still in question, this contribution is perceived as more than just a means to compare with the ML algorithms, but an attempt to get a sense if this task is even possible for humans.

As hinted throughout, the release of FIW in ways marks a turning point for the problem–multiple tasks can be conducted with the same data, allowing for performances to be compared across (i.e., made possible by the rich label types that support the data); modern-day modeling that is defined with higher capacity to learn, demands big data (i.e., sufficient amounts to suffice resource taxing methods that proved to claim SOTA in tasks all throughout machine learning and studies of multimedia); families as seen world-wide more accurately represented (i.e., diverse families supported by many samples was provided by design). Hence, and especially on the latter points on data size and diversity, the architects of FIW re-evaluated humans at a greater scale [7]. Specifically, eleven relationship types, opposed to the four of Cornell Kin, were involved, and at pair counts ten-times that organized in 2010.

4.2 Results of RFIW annual challenges

Let us now summarize the latest-and-greatest methods on the large-scale FIW dataset, as reported in the White Paper on the FG data-challenge, i.e., 2020 RFIW [14].

Furthermore, we are close to achieving a performance-rating necessary for some applications (Section 6). From this, we perceive that bridging the gap separating research-from-reality (i.e., transitioning from research-to-practice) is approaching. Upon a clear assessment of the state of progress in research, we highlight barriers still in need of overcoming, along with sharing edge cases as means of highlighting common errors. Hence, we aim to inspire by explicitly depicting weaknesses in current SOTA systems.

The proceeding subsection provides a comprehensive overview on the SOTA for the large-scale FIW dataset. A recent data challenge summarized top performers across the three tasks in the events white paper [14]. We review the reported protocols, experimental settings, and the SOTA methods for each of the tasks. For completeness, we list SOTA performances for the most recent and widely benchmarked kin-data. Experiments on FIW were regenerated and are available as part of this survey - other datasets, and the respective SOTA, are listed per the most recent literature.

4.3 Task Evaluations, Protocols, Benchmarks

RFIW 2020 supported three tasks: kinship verification (T-1), tri-subject verification (T-2), and search & retrieval of family members for missing children (T-3). Following the same outline, we next describe each task separately: the problem statement and motivation, data splits and protocols, and benchmark experiments (i.e., baselines). A brief section on the common experimental settings precedes the detailed descriptions of settings unique to the task and follow in separate subsections.

4.3.1 Experimental settings

The FIW dataset provides the most extensive set of face pairs for kin-based face recognition. FIW provides the data needed to train modern-day data-driven deep models [22], [38]–[40]. FIW was split into three parts: train, val, and test. Specifically, 60% of the families were assigned to the train set; the remaining 40% was split evenly between val and test. The three sets are completely disjoint in family and identity. Labeled train and unlabeled val were first released with servers open for scoring (Phase 1). Then, ground-truth for val was made available (Phase 2). Finally, the “blind” test set was released at the start of Phase 3. Phase 3 which lasted for ten days to allow teams to process and make final submissions for scoring. Teams were asked to only process the test set when generating submissions and any attempt to analyze or understand the test pairs was prohibited.

As part of pre-processing, faces for all three sets were encoded via ArcFace CNN [33] (i.e., 512 D). All pre-processing and the
model weights were from the original work. Also common is the use of cosine similarity to determine closeness of a pair of facial features $p_1$ and $p_2$ [41]. This is defined as

$$
CS(p_1, p_2) = \frac{p_1 \cdot p_2}{\|p_1\| \cdot \|p_2\|}.
$$

Scores were then either compared to threshold $\gamma$ (i.e., $CS(p_1, p_2) > \gamma$ infers $\text{KIN}$; else, $\text{NON-KIN}$) or sorted (i.e., ranked list). This concludes the common experimental settings.

Teams were allowed up to six final submissions per task. Submissions were accompanied by a brief (text) description of the system used to generate results.

### 4.3.2 Kinship Verification

Kinship verification aims to determine whether a pair of faces are blood relatives. This classical Boolean problem has two possible outcomes, $\text{KIN}$ or $\text{NON-KIN}$ (i.e., true or false, respectively). Hence, this is the one-to-one view of kin-based problems. The classical problem can be further extended by considering the type of kin relation between a pair of faces, rather than treating all kin relations equally [15].

Prior research mainly considered parent-child kinship types, $i.e.$, FD, FS, MD, MS. Less attention has been given to sibling pairs, $i.e.$, SS, BB, and SIBS. Research findings in psychology and computer vision found that different relationship types share different familial features [19]. Hence, each relationship type can be modeled and evaluated independently. Thus, additional kinship types would further both our understanding and capabilities of automatic kinship recognition. With FIW, the number of facial pairs accessible for kinship verification has dramatically increased, with a subset of the pair types and face pairs listed in Table 2. Additionally, benchmarks now include grandparent-grandchildren types, $i.e.$, GFGD, GFGS, GMGD, GMGS.

#### Data splits.

FIW supports eleven different relationship types that were used in RFIW (Table 2). The test set had an equal number of positive and negative pairs and with no family (and, hence, subject identity) overlap between sets.

7. https://github.com/ZhaoJ9014/face.evoLVe.PyTorch

### Settings and metrics.

Conventional face verification protocols were followed [42], offering different modes (or settings) to span multiple paradigms of kinship verification. We next list the modes:

1. **Unsupervised:** No labels provided, $i.e.$, the prior knowledge about kinship or subject IDs.
2. **Image-restricted:** Kinship labels ($i.e.$, $\text{KIN}$ and $\text{NON-KIN}$) will be provided for a training set that is completely disjoint from ”blind” evaluation set, $i.e.$, no subject or family overlap between training and evaluation sets.
3. **Image unrestricted:** Along with the kinship labels, subject IDs are provided. This allows for the ability to generate additional negative pair-wise samples.

Verification accuracy is used to evaluate. Specifically,

$$
\text{Accuracy}_j = \frac{\# \text{ correct predictions for } j\text{-th type}}{\text{Total } \# \text{ of pairs for } j\text{-th type}},
$$

where $j \in \{11 \text{ relationship types and } \emptyset\}$ (listed in Fig. 5). Then, the overall accuracy is calculated as a weighted sum ($i.e.$, weight by the pair count to determine the average accuracy).

#### Baseline and results.

The threshold was determined by the value that maximizes the accuracy on the val set. Results are listed in Table 3; sample pairs that either 100% or 20% of all teams got correct are shown in Fig. 6.

#### Table 4: T-2 Counts.

No. pairs (P), families (F), face samples (S).

|   | FM-S | FM-D | Total |
|---|------|------|-------|
| **train** | | | |
| P  | 662  | 364  | 736   |
| F  | 375  | 364  | 739   |
| S  | 8,575| 8,588| 17,163|
| **val** | | | |
| P  | 202  | 177  | 379   |
| F  | 116  | 117  | 233   |
| S  | 2,859| 2,493| 5,352 |
| **test** | | | |
| P  | 205  | 178  | 383   |
| F  | 116  | 114  | 230   |
| S  | 2,805| 2,400| 5,205 |

#### Table 5: Verification scores.

Results for tri-subject ($i.e.$, T-2).

|               | FMS | FMD | Avg. |
|---------------|-----|-----|------|
| Sphereface [33] (baseline) | 0.68 | 0.68 | 0.68 |
| stefhoer [34]       | 0.74 | 0.72 | 0.73 |
| DeepBlueAI [36]     | 0.77 | 0.76 | 0.77 |
| ustc-nelslip [35]   | 0.80 | 0.78 | 0.79 |
4.3.3 Tri-Subject Verification

Tri-Subject Verification focuses on a different view of kinship verification— the goal is to decide if a child is related to a pair of parents. First introduced in [24], it makes a more realistic verification—the goal is to decide if a child is related to a pair of parents. Following the procedure in [24], we create positive (have kin relation) triplets by matching each husband-wife spouse pair with their biological children, and negative (no kin relation) triplets by shuffling the positive triplets until every spouse pair is matched with a child which is not theirs (Table 4). Because the number of potential negative samples far exceeds the number of potential positive examples, we only generate one negative triplet for each positive triplet, again following the procedure of [24].

We post-process the positive triplets before generating negatives to ensure balance among individuals, families, and spouse pairs, since a naive data selection procedure which weights every face sample similarly would result in some individuals and families being severely over-represented due to an abundance of face samples for some identities and families. The post-processing is done by limiting the number of samples of any triplet \((F, M, C)\), where \(F\), \(M\), and \(C\) are identities of a father, mother, and child to 5, then limiting the appearance of each \((F, M)\) spouse-pair to 15, and then finally limiting the number of triplet samples from each family to 30. The test set has an equal number of positive and negative pairs. Lastly, note that there is no family or subject identity overlapping between any of the sets.

Settings and metrics. Per convention in face verification, we offer 3 modes (i.e., the same as in task 1 listed in Section 4.3.2). Again, the metric used is verification accuracy, which is first calculated per triplet-pair type (i.e., FMD and FMS). Then, the weighted sum (i.e., average accuracy) determines the leader-board.

Baseline and results. Baseline results are shown in Table 5, with samples of easier and more challenging samples for both KIN and NON-KIN triplets in Fig. 7 and 8. A score was assigned to each triplet \((F_i, M_i, C_i)\) in the validation and test sets using the formula

\[
Score_i = \text{avg} (\cos (F_i, C_i), \cos (M_i, C_i)),
\]

where \(F_i\), \(M_i\), and \(C_i\) are the feature vectors of the father, mother, and child images respectively from the \(i\)-th triplet. Scores were compared to a threshold \(\gamma\) to infer a label (i.e., predict KIN if the score was above the threshold; else, NON-KIN). The threshold was determined experimentally on the val set and used for test.

4.3.4 Search and retrieval

T-3 is posed as a many-to-many, i.e., one-to-many samples per subject. Thus, we imitate template-based evaluations on the probe side, but faces in the gallery are not labeled by subject. Furthermore, the goal is to find relatives of search subjects (i.e., probes) in a search pool (i.e., gallery).

Kin information, as a search cue, can be leveraged to improve conventional FR search systems, or even as prior knowledge for mining social or family relationships in industries like Ancestry.com. However, the task is most directly related to missing persons. Thus, we formulate it as such.

### Table 6: T-3 Counts. Individuals \(I\), families \(F\), face samples \(S\).

| Probe | Gallery | Total |
|-------|---------|-------|
| train |         |       |
| I     | –       | 3,021 | 3,021 |
| F     | –       | 571   | 571   |
| S     | –       | 15,845| 15,845|
| val   |         |       |
| I     | 192     | 802   | 994   |
| F     | 192     | 192   | 192   |
| S     | 1,086   | 4,030 | 5,116 |
| test  |         |       |
| I     | 190     | 783   | 9473  |
| F     | 190     | 190   | 190   |
| S     | 1,487   | 31,787| 33,274|

The protocol of T-3 could be used to find parents and other relatives of unknown, missing children. The gallery contains 31,787 facial images from 190 families (Fig. 9): inputs are subject labels (i.e., probes), and outputs are ranked lists of all faces in the gallery. The number of relatives varies for each subject, ranging anywhere from 0 to 20+. Furthermore, probes have one-to-many samples—the means of fusing samples of probes is an open research question. This many-to-many task is currently set up in closed form (i.e., every probe has a relative(s) in the gallery).

Data splits. This task will be composed of search subjects (i.e., probes) from different families. Probes are supported by several samples of query subject, text description of family (e.g., ethnicity, some relationships between selected members, etc.), and list of relatives present in the gallery. The test set will only consist of sets of images for the probes. Diversity in terms of ethnicity is ensured for both sets. Again, three disjoint sets were split (Table 6).

Settings and metrics. Each subject (i.e., probe) gets searched independently, with 190 in total; hence, 190 families make up the test set. Probes have one-to-many faces. Following template conventions of other many-to-many face evaluations, facial images for unique subjects are separated by identity, with a gallery containing a variable number of relatives, each with a variable number of faces [43].

Mean average precision (MAP) was the underlying metric used for comparisons. Mathematically speaking, scores for each of the \(N\) missing children are calculated as follows:

\[
AP(f) = \frac{1}{P_F} \sum_{tp=1}^{P_F} \frac{P_{rec}(tp)}{P_{F}} = \frac{1}{P_F} \sum_{tp=1}^{P_{F}} \frac{tp}{\text{rank}(tp)},
\]

where average precision (AP) is a function of family \(f\) with a total of \(P_F\) true-positive rate (TPR). We then average all AP scores to determine overall MAP score as follows:

\[
\text{MAP} = \frac{1}{N} \sum_{f=1}^{N} AP(f).
\]

Additionally, TPR as a function of rank will be traced out for further analysis between different attempts.

Baseline and results. Table 7 and shown in Fig. 10. Submissions consisted of a matrix with a row per probe listing the indices of all subjects in the test gallery as a ranked list.

4.3.5 Common trends

There are many commonalities between the different solutions proposed as part of the RFIW challenge. Typically, a ResNet-based [44] backbone; if not, then together with FaceNet [45]. Nonetheless, the story as seen in the timeline is split in half (i.e., with the latter half dominated by modern-day deep learning
Fig. 7: Sample triplets of T-2. Triplets all teams got correct (left) and mostly incorrect (right) for FMS (top rows) and FMD (bottom).

Fig. 8: Sample triplets of T-2. Triplets all teams got correct (left) and mostly incorrect (right) for FMS (top rows) and FMD (bottom).

Table 7: T-3 results. Performance ratings for SOTA methods.

| Methods                  | mAP  | Rank@5 |
|--------------------------|------|--------|
| Baseline (Sphereface)    | 0.02 | 0.10   |
| DeepBlueAI               | 0.06 | 0.32   |
| HCMUS [notwebb]          | 0.07 | 0.28   |
| ustc-nelslip [53]        | 0.08 | 0.38   |
| vuvko [37]               | **0.18** | **0.60** |

approaches). Nonetheless, and quite significantly, metrics learned on top of hand-crafted features dominated the charts as SOTA for many years [46]. Even so, geometric and distant features in pixel space (e.g., key point coordinates on neutral face [47])—directly related to insufficient data to explore modern-day data-driven machinery (i.e., deep learning). Furthermore, and as mentioned, many of the smaller datasets are limited in diversity (i.e., all similar demographics) and with pairs from the same photos, from which some proposed color-based features [48]. Still, papers that hone-in on the smaller data employ more classical approaches, such as representation learning via binary trees [49]. For an in-depth look at these classic approaches, we refer the reader to a previous survey [5].

Provided a deep CNN trained to classify face identity, the weights, as is, capture much of the target information desired. However, instead of looking for absolute closeness in embedding space as the ideal case for a set of samples of a single class (i.e., identity), in kin-based tasks we hope to detect when similarities between a pair (or group) of faces (i.e., encoded) reflect that of the various relationship-types. For this, many tend to fine-tune models initially trained on a larger FR-based database, such as VGG-Face [45], VGG2 [50], and MSceleb [51].

In [53], Track I and III completed in succession, such that a wider sweep of CNN backbones, loss functions, and fusion methods were assessed in Track I, to both gain deeper understanding to make decisions pertaining to Track III. Mainly, ResNet50 and SENet50 were evaluated separately, each with additional fully-connected layers with two losses on top. Binary Cross Entropy (BCE) and Focal loss. BCE, a widely used loss directly related to insufficient data to explore modern-day data-driven space (i.e., deep learning). Furthermore, and as mentioned, many of the smaller datasets are limited in diversity (i.e., all similar demographics) and with pairs from the same photos, from which some proposed color-based features [48]. Still, papers that hone-in on the smaller data employ more classical approaches, such as representation learning via binary trees [49]. For an in-depth look at these classic approaches, we refer the reader to a previous survey [5].

Yu et al. found that BCE loss outperformed Focal Loss for all fusion schemes and settings in Track I [53]. Intuitively, this makes sense as Track I, a Boolean task, has an equal number of positive and negative pairs—imbalanced data motivated Focal Loss, which is not an issue for verification. Then, transferring over the model, loss, and fusion settings that worked best for Track I to Track III and used as is. The difference is in the ranking scheme (i.e., provided multiple faces per query, the average of all faces and each gallery sample determined the score at the subject-level. Tri-subject pairs near the threshold. We show both correct and incorrect predictions for FMS (top rows) and FMD (bottom).

Besides, most solutions involve the renowned Siamese training model, and many of which still incorporate a cosine loss as in the seminal work done at Bell Lab’s mid-90s [54], i.e., multiple inputs to networks with shared weights for which metric is learned on top (Fig 11). In the simplest form, Siamese-based of CNN models is to map two or more samples by a single CNN to a real-number vector space $\mathbb{R}^d$ (i.e., a function $f(\cdot)$ to encode an image (i.e., facial encoding, embedding, feature) of size $d$, especially in the context of facial representation, all refer to the $f(x_i) = z_i \in \mathbb{R}^d$. Generally, and in most methods proposed in RFIW, the shared model is pre-trained data for another, yet similar task (i.e., facial recognition). With that, the CNN that now serves as an encoder, maps $k$ samples to its $d$-dimensional space learned to discriminate between faces. With the Siamese frozen—whether entire network, with a couple of layers on top set with a small learning rate, or popped off by adding a path that splits off prior to later rejoin or just remove entirely—the goal then is to learn a metric optimal for recognizing family members by face cues. Clearly, there are several design choices— with simple solutions in those with an off-the-shelf CNN with no additional training (i.e., trained for FR, so naively assuming that the best way to detect kinship is to detect faces that look like the source). However simple, and with many cases a fair assumption, the naive approach outperformed previous SOTA methods prior to FIW providing the number of data samples needed to suffice the capacity of most deep learning approaches. In light of this, the CNN then serves as the method for feature...
There is an abundant of publicly available FR datasets (e.g., LFW, VGG, MSCeleb [51]) with some motivated by a specific soft attribute (e.g., age [55], gender [56], attribute, and diverse demographics [57], [58]). With this, and provided the known concept of deep learning tending to learn transferable features [39], the use of fine-tuning pre-trained has been done by many. For instance, a SphereFace loss, which is a multi-class loss, is first used to train a large CNN to do facial recognition on identities of an auxiliary dataset, and then having the layers near the top fine-tuned to recognize the families of the FIW training set via

$$L_{\text{family}}(\theta) = -\frac{1}{B} \sum_{i=1}^{B} \log \frac{\exp W_{yi}^T x_i + b_{yi}}{\sum_{j=1}^{N} \exp W_{yj}^T x_i + b_{yj}},$$  \hspace{1cm} (1)$$

where $B$ is the batch size, $N$ is the number of families, $x_i$ is the face encoding from family $y_i$, $W$ is the weight matrix (i.e., $W_j$ denotes the $j^{th}$ column) and $b$ is the bias term. In the end, verifying kinship between a face pair can be done using the model to encode the faces and cosine distance to measure their closeness. If family labels are unavailable, which is another setting of the verification task, approaches tend to use Siamese concepts on top of the pre-trained CNN (Fig. 11). Specifically, sharing weights for two or more samples, and penalizing based on the closeness between a set of samples upon being encoded by the network, has shown to be an effective means of staging a network for the verification task. In return, Siamese; furthermore, the relationship between the pairs with respect to labels at training differences is in preprocessing, method of fusion (e.g., early versus late).

### 4.4 Deep learning approaches

#### 4.4.1 Fine-tuning

There is an abundant of publicly available FR datasets (e.g., LFW, VGG, MSCeleb [51]) with some motivated by a specific soft attribute (e.g., age [55], gender [56], attribute, and diverse demographics [57], [58]). With this, and provided the known concept of deep learning tending to learn transferable features [39], the use of fine-tuning pre-trained has been done by many. For instance, a SphereFace loss, which is a multi-class loss, is first used to train a large CNN to do facial recognition on identities of an auxiliary dataset, and then having the layers near the top fine-tuned to recognize the families of the FIW training set via

$$L_{\text{family}}(\theta) = -\frac{1}{B} \sum_{i=1}^{B} \log \frac{\exp W_{yi}^T x_i + b_{yi}}{\sum_{j=1}^{N} \exp W_{yj}^T x_i + b_{yj}},$$  \hspace{1cm} (1)$$

where $B$ is the batch size, $N$ is the number of families, $x_i$ is the face encoding from family $y_i$, $W$ is the weight matrix (i.e., $W_j$ denotes the $j^{th}$ column) and $b$ is the bias term. In the end, verifying kinship between a face pair can be done using the model to encode the faces and cosine distance to measure their closeness. If family labels are unavailable, which is another setting of the verification task, approaches tend to use Siamese concepts on top of the pre-trained CNN (Fig. 11). Specifically, sharing weights for two or more samples, and penalizing based on the closeness between a set of samples upon being encoded by the network, has shown to be an effective means of staging a network for the verification task. In return, Siamese; furthermore, the relationship between the pairs with respect to labels at training differences is in preprocessing, method of fusion (e.g., early versus late).

#### 4.4.2 Discriminative

Early on, relative to the rest, and predating the large-scale FIW dataset was a proposed CNN made up of various parts-based CNN in an ensemble learning scheme [60].

Many formulated kinship recognition problems in the visual domain as multi-view, multi-task, and multi-modal, which is typically to increase the amount of information obtainable, even when the final target is among other targets during training (i.e., auxiliary tasks that complement the knowledge obtained from recognition, alone). For instance, the Deep Kinship Matching and Recognition (DKMR) was proposed as a jointly-trained model on top of a graph optimization algorithm [61], [61] [62] [39], [63]–[71] large-margin multi-learn (LM^3L) [72].

A novel Heterogeneous Similarity Learning (HSL) function tackled various views (i.e., tasks) of kin-based recognition as a multi-view learning problem, with the different views assumed to be those of different relationship types [62]. Similarity, Support Vector Data Description-based metric learning (SML) loss function, allowing detailed information to be extracted as geometric and appearance-based features for kinship verification [73]. Furthermore, similar to [62] except with Support Vector Machine (SVM)-based layers fine tuned on top of CNN, which was dubbed multi-view SML (MSML).

Duan et al. proposed a coarse-to-fine scheme for which CNN at different levels (i.e., layers) were transferred from being trained using a FR dataset and then fine tuned for kinship using a loss function based on Neighborhood Repulsed Metric Learning (NRML) [74]. In fact, many recent works leveraged existing FR methodologies (e.g., CNN trained to classify faces) as a prior, the then fine tune using the kin-based image data as the source in a transfer-learning regime [75].

Several lines of research specifically focused on the one-to-one kinship verification problem by learning a face encoder robust in detecting kinship relationship via denoising autoencoder (AE) (DAE) [61], [76] [77] [78]. A recent survey covers some of the deep learning models proposed for automatic kinship recognition [79]. To complement this, we extend on the discussion with the submissions of the 2020 RFIW, along with a few other works that came out most recently. We describe the space as we perceive as the true state– of all the methods, we highlight the commonalities, the shortcomings, the open research questions, and even how the models used to discriminate can be directly related to those used to synthesize (i.e., many recent works discussed in the next section were missing from recent literature reviews and, hence, this made for an imperative in-depth review on the topic).

Besides still-faces, deep learning approaches were also proposed for recognizing kinship pairs using facial cues in video data [80]. A sequence recurrent neural network (NN) was trained for kinship verification in videos using a novel attention mechanism [81]. With videos, there comes more bits of information; however, the range of bits (i.e., the underlying variation of the

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**Fig. 9: Plot of face counts per family in test set of T-3.** The probes have about 8 faces on average, while the number of family members in the gallery nears 20 on average, with a total average of 170 faces.
data) should be optimized to maximize the information gain. In other words, video data introduces another space for fusion in the choosing of the best frame(s) to describe and represent [82].

Of all the proposed methods, there is a common factor: the larger the age gap the higher percentage of FP during evaluation. As mentioned, this was addressed early on with UB Face [19] and, although fundamental to the analysis of results over the years, proposed models tended to acknowledge this as a challenge, but with no added mechanism to make robust to age-variations between parent-child. That is, until Wang et al. proposed using generative adversarial network (GAN) technology to synthesize younger versions of an input face. Specifically, and a clearly effective data augmentation approach, the authors trained generators for both genders to account for this while training a deep CNN with a maximum margin loss to do boolean classification (i.e., KIN / NON-KIN). As formalized in their work, domain $A$, for aged, was the source and domain $Y$, for young, was the target. Provided paired data, the parent aimed to transform $x_i \in A \rightarrow x_j \in Y$ with data distribution $x \sim p_A \rightarrow x \sim p_Y$. Having noticed that FIW, which most closely matches real-world data, does not necessarily have parents at older ages (i.e., aged). Thus, the inputs could very well be parents as juveniles, or even during infancy. To mitigate the problem, for there are no age-labels provided in FIW, focus was directed to constrain the output such to influence younger aged faces less so, than if faced with an elderly parent.

Graphical neural network (GNN) with a metric learned on top proved to be one of the most effective deep learning models employed for kin-based vision problems [28].

### 4.4.3 Generative

Many years came and went: years for which we witnessed the first visual kinship benchmark made public in 2010, the attribution of AlexNet in 2012 [83] and the deep learning revolution that spawned from it, the introduction of the now renowned GAN in 2014 [84], and, finally, the release of FIW in 2016 (Fig. 1). We then had the components needed to inspire the methods discussed next. In the end, there were many milestones, both discussed and omitted, in face synthesis that made the attempts to predict child faces from a parent inevitable. However, it is when both parents are input as prior knowledge for the generative model that things become more unique to kinship itself, as should be made clear shortly. Such a two-to-one problem, like we have seen throughout the domain, then becomes a question on how to best fuse knowledge from a pair of faces. In nature, we are not simply products of our parents averaged—again, a gross, objectively inappropriate assumption. As an example that would be in line with assuming a). From this, face synthesis conditioned on kin-based relationships has been founded in several works [85]–[87].

The first literate attempt to leverage deep learning modeling for synthesizing a child from a prospective parent was in [85]. These authors proposed to use a Gated AE to learn a latent mapping function as weights as part of the encoding process, which was later decoded and penalized per pixel difference (i.e., face image reconstruction error). A byproduct of such a learning scheme and, hence, representation from a learned mapping to latent space provided a means to measure salience (Fig 12). Such a mapping was dubbed genetic features by the authors. Where this name is a fair nickname provided the context, it is an oversimplification.

![Fig. 10: T-3 sample results (Rank 10). For each query (row) ≥ 1 face(s) as the probe returns the corresponding samples from the gallery (i.e., top 10). FP are labeled with x (red), while true predictions show the relationship type (green): P for parent; C for child; S for sibling.](image-url)
we opt to formally refer to these salience mappings as more misleading than accurate in definition or in nature. Thus, bring up the aforementioned jargon. In all cases, such naming is in the more advanced DNA-Net). Hence, we the authors condone much room for improvement in the generative realm.

generalization performance has definitively improved, there is still the problem is even started. Noticing this, [86], [87]. Although the problem with just one parent is insensible– it takes two to changes from one sample-to-the-next. Nonetheless, trying to solve is, for the variation embedded in many complex factors nearly be matched up to the visual system (i.e., cortex) of a human (even in the more advanced DNA-Net). Hence, we the authors condone such labeling as informal name schemes for the sake of high-level discussion. However, it is simply an analogy that grossly simplifies biological systems of humans. For consistency with literature, we bring up the aforementioned jargon. In all cases, such naming is more misleading than accurate in definition or in nature. Thus, we opt to formally refer to these salience mappings as genetic features. Regardless, Dehghan et al. pioneered the foundation of future generative modeling attempts and experiments [85].

KIN-GAN aimed to synthesize a child’s face from a sample of a single parent [88]. The problem is inherently difficult as is, for the variation embedded in many complex factors nearly changes from one sample-to-the-next. Nonetheless, trying to solve the problem with just one parent is insensible– it takes two to tango in nature and, thus, such a formulation is out of scope before the problem is even started. Noticing this, [86], [87]. Although generalization performance has definitively improved, there is still much room for improvement in the generative realm.

The end-to-end framework proposed by Gao et al. aims to mimic the nature of reproduction [86]. The resulting system, dubbed DNA-Net, fuses latent representation of a parent pair at the feature-level, which is used as input to conditional adversarial AE (CAEE) model trained on top (Fig. 13). The chose in CAEE made it so the generator could synthesize children as a function of age and sex (i.e., interpolating latent vector such to synthesize from young-to-old and from more mescaline to more feminine). Sample results are shown in Fig. 14. Note that treating sex as a continuous spectrum, opposed to discrete labels, is both appropriate and more precise (i.e., provided an extreme pair, one female and the other male, there exists many cases in between, which is, in fact, where most of society falls [89]). As a part of the work to support DNA-Net, the authors compared salience in detecting kinship of type parent-child at specific facial features (i.e., eyes, nose, mouth, and chin). Hu invariant moments were used as the shapes of the four facial parts localized by detection [90], from which the accumulative cosine distances yielded heritability maps (Fig. 15).

### 4.5 The RFIW challenge series

RFIW series was motivated by means to promote FIW with a platform for experts to publish and junior scholars to get started. With the first edition dating back to 2017 [13] as a data challenge workshop held in conjunction with the ACM Conference on Multimedia, both the problem and amount of interest has progressed each year since (i.e., 2018-20 held in conjunction with FG as a data challenge). We next discuss several of the top work that resulted from the series. Specifically, we first look back at all years up to the latest, and then hone-in on the latest 2020 RFIW, where interest seems to have peaked in all tasks.

#### 4.5.1 Pre-RFIW 2020

Prior to the last RFIW challenge, there were several honorable mentions. As part of the 2017 RFIW (i.e., first edition), Yong et al. used an ensemble of deep CNN with data augmenting and mining techniques. Specifically, the authors proposed to train an ensemble (i.e., four resnet models with 80, 101, 152, and 269 layers) for facial recognition and then fine-tune for kinship verification using a triplet loss that targets relationships within each family [39]. Furthermore, KinNet, as dubbed by the authors, included the use of image processing (i.e., gamma correction, down/up sampling of pixels, and blurring with Gaussian noise) to augment data during training (i.e., motivation was an equal sample count for all families to later use to fine-tune each model of the ensemble), and were assigned triplets using a hard-negative mining scheme. In the end, KinNet was the top performing submission of the 2017 RFIW with an impressive average of 74.9%. It is important to note that, although KinNet performed well relative to the eight submissions and provided baselines, the grandparent-grandchild type and more pairs for the returning types (i.e., parent-child and sibling types) in the proceeding RFIW challenges. Thus, a direct comparison in reported metric would be unfair.

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**Fig. 12:** Activation responses from mapping image-to-latent space (visualization from [85]). For visualization purposes, the salience mapping produced by transforming via activation response is super-imposed on the average face. Family101 dataset was used for this experiment [21]. The end result depicted here was dubbed the genetic features from latent space of a trained Gated AE.

**Fig. 13:** 

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**Fig. 11:** Generic Siamese network. Approaches tend to follow the Siamese model, differing in method of fusion, i.e., black-box, middle. Specifically (from top-to-bottom), an image pair shot $x_1$ and $x_2$.

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concatenation of features from prospective parents, the father and mother are fused (i.e., $h_f$ and $h_m$) before passed as input to the CAAE model. Point is, generating the input to pass to the second stage of DNA-NET. Note that DNA-Net was dubbed by the authors in the effective work proposed; however fair when speaking in general terms (i.e., infrequent situation in research), we suddenly see naming schemes such as this, genetic features, among few others is too strong. Nonetheless, there is a clear analogy, so for the sake of story-telling and system depiction, Gao et al. rightfully dubbed this 

$$R^2 \times R^{2d} \rightarrow R^d$$

as the latent representation of deep NN. Authors also implement ArcFace [33] - a family of loss functions - binary cross-entropy and focal loss. Finally, they fused the feature vectors with two algebraic formulae leading to $2 \times 2 \times 2 = 8$ independent "models." A unique feature was the construction of a "jury system" to combine outputs of different models to improve accuracy. With [35] the top-scorer in T-2.

Yu et al. also used a Siamese network, i.e., encoded features from face images via a CNN with shared weights [35], ResNet50 or SENet50 was used as the backbone, both pre-trained on VGG-GFace2 [50]. In addition, team ustc-nelsip also employed two loss functions - binary cross-entropy and focal loss. Finally, they fused the feature vectors with two algebraic formulae leading to $2 \times 2 \times 2 = 8$ independent "models." A unique feature was the construction of a "jury system" to combine outputs of different models to improve accuracy. With [35] the top-scorer in T-2.

[52] competed in Tracks I (kinship verification) and III (kinship search and retrieval). For extracting features the authors use a Siamese CNN with FaceNet (Inception-ResNet-v1) and with VGG-Face (Resnet-50) as the pre-trained models. FaceNet uses Triplet Loss as the main loss function in the training phase. The authors also implement ArcFace [33] - a family of loss functions based on the geodesic distance between feature vectors which aim to discriminate the latent representation of deep NN.

4.6 Summary of SOTA

Proposed solutions for the 2020 RFIW FG challenge tended to use backbone networks trained for conventional FR, then fine tuned for kin-specific face tasks. Each submission for all three tasks surpasses the simple baseline provided as part of the challenge organization. We next summarize results of each team separately.

4.7 Limitations of SOTA

A majority of solutions for visual kinship recognition assume prior knowledge of the relationship type. In some cases, this would be practical. For instance, given a source of a known subject with knowledge of the relationship type. In some cases, this would be practical. For instance, given a source of a known subject with knowledge of the relationship type. In some cases, this would be practical. For instance, given a source of a known subject with knowledge of the relationship type. In some cases, this would be practical. For instance, given a source of a known subject with knowledge of the relationship type. In some cases, this would be practical. For instance, given a source of a known subject with knowledge of the relationship type. In some cases, this would be practical. For instance, given a source of a known subject with knowledge of the relationship type.

5 Technical Challenges

Like conventional FR, when working with unconstrained faces in the wild [42] the problem becomes more difficult. In other words,
imagery collected from sources outside a controlled laboratory environment is subject to more variations in pose, illumination, and scale. For faces, there are even more variables to further complicate the problem, such as expression and age. Furthermore, preparing to run such benchmarks to mimic real-world use-cases (i.e., designing experiments and preparing the data) is, in itself, a challenge. Inheriting these challenges, but adding even more variations inherent in nature and in true data distributions of kinship, it is unsurprising that visual kinship recognition is a difficult problem. Nonetheless, great efforts over the last decade have been spent not just on solving the problems in kinship recognition, but also critiquing kinship research and its direction. We now elaborate on the challenges to keep this technology from making the transition of research-to-reality.

5.1 The nature
A near radical piece of its time, Goode [94] surveyed family structure as more of a complex system than the ‘conjugal family form’ of many traditional cultures (e.g., Western, Chinese, Arab). Besides, ways to best weight (or fuse [95]) different relationship types remains unanswered. Even simple questions have soft, varying solutions [96] like *Do we look more like our father?*

Aging as a function of life experiences can influence the similarity in appearances when comparing family members with large a age-gap. Wang *et al.* demonstrated a clear benefit in having a face image synthesized at younger ages [76]. In fact, their ablation study revealed cumulative improvements as $x \sim p_Y$ was bounded to $>20$ years of age, then to $>30$, and up to $>50$. With increasing the size of the domain (i.e., the respective age considered young, which is orthogonal to those considered old) came improved results. Fig. 16 depicts samples of the faces of parents synthesized for the kinship verification task. Other types of data augmentation, like transforming faces to their basis to then invert, rotate, and modify the ocular geometry [97], have proven as an effective mean to broaden information for the sample.

5.2 The environment
The challenges from age variations in FR not only intensify in kin-based problems, but also change in novel ways. For instance, let us assume a comparison in the faces of a grandmother and a prospective grandson. The age of each and age gap between the two are subject to variation. In other words, the problem inherits the same challenges of FR such that considerations for directed relationships of concern—the grandmother might be in her early years when the picture was captured, just as the grandson might even be a grandfather himself at the time the picture was taken.

Nurture adds additional challenges to the problem: For instance, a pair of brothers inherited the nose from their mother; one boy experienced a broken nose perhaps more than once; suddenly, that boy no longer has a nose that resembles the mother. Where such challenges exist in conventional FR, the relative cost of losing a distinguishable feature is greater in kin-based problems when how that could be the one inherited from a prospective parent(s).

Biology-based research has focused on the problem of kinship recognition from a vast array of viewpoints. For instance, work
that precedes the work done in machine vision, focused on a
human’s ability to recognize kinship—specifically, the ability of
younger siblings to better distinguish between KIN and NON-KIN
in strangers [98] (i.e., having seen the first-born their entire lives
trains them). An interesting hypothesis indeed, which is supported
in the reported experiments (minimal sample set, but typical of
human evaluations done in face-based research). Intuitively,
the contrary could also be true (i.e., the role of the older sibling,
watching after their younger sibling would better train for this
ability). In any case, the authors propose a theory conditioned
on age; difference in age could play a significant role in such a
study, as we agree this could be the case for a much older sibling
(i.e., already developing an ability to discriminate between faces),
the same argument of realizing the key differences as a means of
recognizing kin in a sibling at a young age could be argued both
ways. Furthermore, the authors discarded samples of subjects with
no siblings and more than two siblings—on the one hand the intent
to control the experiment with less variation is understandable—on
the other, subjects without siblings would serve as a meaningful
baseline, while those with a number of siblings only strengthens
the case for the oldest being the most keen on recognizing kin
(i.e., having grown watching over their younger siblings).

### 5.3 The data and its distribution

Within-family variations are vast. As such, one cannot infer
that the inherited traits from one father-son pair might mimic
inherited traits of another father-son pair. Furthermore, the factors
introducing added complexity vary across different ethnic groups.

To capture the true data distributions of visual kinship as
seen around the world is a great challenge, where many efforts
have exhibited exploitable flaws. For instance, using color features
claimed SOTA on the KinFaceW dataset, as faces of true-relatives
often were cropped from the same photos [100] [101]. The same
motivation ushered in a different paradigm as means to measure
unintended data leakage in the unnatural domain inherited by
samples being of the same image or different. To say the least - this
was a crafty piece of work that acquired an abundance of cheap
data by image-level constraints that impose faces in the same
photo as matches, which means it is a binary problem with classes
for the same and different photo. In other words, by the paired data
acquired by finding images with one-to-many faces from the web
(Fig. 17), Dawson et al. proposed training a detector to determine
whether a face pair was from the same or different photo. Then,
the boolean class model was directly evaluated on kin-based image
sets, with the only difference in the target classes (i.e., same
and different assumed to be KIN and NON-KIN). Thus, showing SOTA
ratings on a majority of existing kinship data—again, hypothesis
that public benchmarks were subject to unintended data leakage,
and one that is intrinsic to the distribution of classes (i.e., KIN
and NON-KIN). In the end, FSP proved competitive on KFW-I, KFW-
II, Cornell KF, and TSKIN; however, FSP lacks sufficient training
to perform well on the multi-image FIW data (i.e., 58.6%, which
was the first, smallest version of the FIW dataset). In fact, at the
core of FIW specifications, as defined in its earliest paper [4],
the concept of same and different photo was one considered in the
creation of FIW—mentioned as part of motivation for the data in
other recent literature reviews on kin-based image datasets [99].

Other challenges that are present, but explored, are issues of
bias in using FR for kinship recognition. Robinson et al.
has recently shown variations in sensitivities in score space for
different subgroups, like gender and ethnicity [57]: a study that
should be conducted on existing kin-based data.

### 6 Applications

There are an abundance of practical uses for kinship recognition
technology, which we will review next.

**Entertainment and personal knowledge.** AncestryDNA claims
to have over 15 billion people in its DNA network: their >3M
paying subscribers (and >16M people DNA tested), resulted in
the establishment of 100M family trees that form 13B connec-
tions across 80 countries. As of 2019, Ancestry launched
AncestryHealth as a means to infer inheritable health conditions
via DNA. Clearly, there is high interest in learning about one’s
family roots—which started from curiosity (i.e., knowing where
one fits, recalling the aforementioned words of Furstenberg [2]),
but now includes learning about one’s health from their DNA.
Acquiring sufficient data to support both DNA and imagery would
be difficult, at best; however, provided more reliable kinship
recognition capabilities, there is no doubt that such technology
can further enhance popular services such as those provided by
billion dollar companies (e.g., ancestry.com).

**Missing children.** Identifying unknown children being exploited
online; reconnecting families separated by the modern-day refugee
crisis [102]; finding unknown relatives, whether directly or in-
directly, via platforms like Ancestry. Statistics show that people
want to learn of missing family ties. Furthermore, unfortunate
scenarios can leave family members desperate to reconnect with a
lost member or member(s) they were split from.

**Soft attribute as prior knowledge for traditional FR.** Whether
it be to enhance FR capabilities [103], to learn to discriminate
between hard negatives (e.g., brothers), or to narrow the search
space (e.g., FR failed to identify the bombers of the 2013 Boston
Marathon) - but had we known they were brothers, the search
space could have been drastically reduced. Hence, kinship pro-
vides a powerful cue to help boost existing FR systems.

**Nature-based studies.** Near the start of the new millennium, 3D
scans allowed the facial appearances of ten pairs of twins to be
compared via landmark features (i.e., anteroposterior and vertical
facial parameters) [104]. About ten years later, this work inspired
Dehghan et al. to raise the question: **Who do I look like?** And then

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8. www.ancestry.com/corporate/about-ancestry/company-facts
attempt to solve the question using computer vision technology or specifically, using a gated AE [85].

**Kin-based face synthesis.** An early attempt to predict the appearance of a child from a pair of prospective parents was in [105]. Specifically, Frowd et al. proposed EvoFit, which used classic shape-based modeling and *eigenfaces* to project a pair of faces via statistical appearance-based modeling. In all fairness, the generative task was heavily influenced by [106], as many face synthesis tasks were throughout the years, and especially in 2006 the EvoFit came out. In short, EvoFit learned its weights from face samples collected in a tightly controlled setting—per the requirement that 223 landmarks were precisely marked for all faces. As seminar as EvoFit was in its own right, this early attempt to predict the appearance of children was seemingly ahead of its time, in available machinery (lacking the data-driven, highly complex modeling techniques of today), in resources available to reproducible *(i.e., no public data released with paper)*, and in the problem statement itself. In other words, considering EvoFit was proposed before our 2010 timeline means it predated the first benchmark in kinship verification. With that, we believe the small impact of this work was due to its timing and, in return, the lack of complete support for the problem, so if others did want to partake they too would have to collect data. Meaning, it was impossible to reproduce results directly. Regardless how minimal the impact was in citations and usage of other researchers, the work certainly showed promise considering the results were from a minimally-sized data pool. Thus, had a widely used benchmark been practiced, or provided the data constraints were handled *(i.e., inability to generalize + inability for others to reproduce)*, then EvoFit could have attracted much more attention. Perhaps, our 2010 time-line would have had to start a few years prior. Nonetheless, this is only speculation and, therefore, we can only hypothesize the *what ifs* after the fact.

7 **Discussion**

7.1 **Broader impacts**

The fourth RFIW gained fair attention. T-1, kinship verification, saw the most (10+ submissions). T-2 *(i.e., tri-subject)* and T-3 (search and retrieval) were both supported for the first time by RFIW, are more complex than the classic task of T-1, and are practically motivated. All submissions outscored baselines.

The scope of kin-based problems spans much wider than RFIW. Specifically, in application *(e.g., generative-based tasks [86], [88]) and experimental settings *(e.g., with privacy a concern [107])*. Tasks of RFIW were thought to be appropriate, provided the difficulty and practicality; the question how best to formulate the problem is an open research question, in itself. Nonetheless, as one of the goals of this survey set to convey, we aim to provide a stronghold on the laboratory-style evaluations as seen appropriate in the modern day.

7.2 **Where are we going?**

It is an exciting and opportunistic time in the kinship problem domain for researchers and practitioners alike. First and foremost, there is a lot of room for improvements in performances of current SOTA, and even improving the experiments in design, purpose, and extent. This includes, but is not limited to, additional label types *(i.e., other soft attributes like expression, age, and ethnicity)*, different data splits and protocols *(e.g., given a father, daughter, and grandparents from the side of the mother, determine the mother)*, and practical use-cases *(e.g., applications to create coherent family photo-albums)*. Besides, generative-based tasks hold another array of promising directions to take next; whether improved predictive capability of a child’s face - provided a pair of parents, or a more fine-grained view of predicting any node in a family tree - provided samples of all other family members - then the room for improvement and potential for growth is furthered.

In most cases, both existing and considered, the underlying question remains. *How to best fuse prior knowledge?* For instance, in tri-subject verification, an active research question concerns the fusion of the features from the two parents. Flipping this very problem around *(i.e., given parents, generate the face of the child)*, the question of feature fusion is still prominent. Looking ahead at attempts to solve the fine-grained problem of populating family trees, regardless if viewed as discriminate or generative, the question remains: *how to best leverage prior knowledge of additional family members relatively of different types and degrees?*

Another area deserving of attention is that of privacy concerns. As is the case for many ML tasks, privacy has motivated researchers. Recently, Kumar et al. proposed using a graphical neural network (GNN) to first achieve SOTA in family classification, and to then add noise to encrypt the data, and demonstrating that a variant of the model safely encapsulates the learned knowledge *(i.e., an ability to accurately deceive)* [107].

Although the number of methods is great—whether metric-learning, deep features, a variant of both—most recent attempts only differ in the broad sense. Bottom-line, successes in all tasks have been tributes of systems based on a Siamese network(s) that encodes inputs from image-to-feature space. The feature space learned typically differs in the point and method of fusion. Specifically, paired samples are usually split evenly *(i.e., the number of pair-types of type KIN and NON-KIN for each relationship type is split fifty-fifty)*. Provided a Siamese network, often pretrained on auxiliary face recognition dataset, act as face encoders. In order to transform from feature-to-score space, either a metric, fusion technique, or both are applied—this tends to be where methods differ, yet the same conventional coarse system holds (Fig. 11). In summary, it is the Siamese net to encode faces, followed by some means of feature-fusion that are stove-piped to a metric or learning objective. Hence, some relevant aspects of such a system produce current SOTA from which we had drawn.
conclusions, and especially in identifying research trends and open issues. We consider the most relevant among aspects for achieving effective systems as follows: (1) effective method for fusion; (2) representation that considers the relationship’s direction; (3) detecting other attributes (e.g., age and gender) and knowledge of the higher-level scene (e.g., face detected in picture with car styles that hint the picture was taken in the 1970s).

Surveying a decade of research in visual kinship recognition showed increasing interest with an increase in data resources. Clearly, the problems alone are challenging, even when compared to other machine-vision tasks (e.g., conventional FR). Furthermore, the task of designing, collecting, and annotating labels is exceptionally difficult for kin-based problems. Thus, as contributions in data are proposed, interest seems to spike in response. With the release of the large-scale FIW dataset, for the first time, a data resource attempts to closely mimic data distributions of families around the globe. Moreover, FIW provides the data needed for the modern day, deep learning models. FIW, having had many existing datasets to learn from, remains the largest and most dynamic.

7.3 Conclusion

However, the release of FIW was only the beginning, as efforts were then spent on annual challenges (i.e., four consecutive years, 2017-2020), and also a Kaggle competition. With the resource and incentive provided by challenges, motivation for researchers to engage is ever so high and thus, we present this survey— not only as a means to realize the aspects that have been effective and vice versa— but also to provide a solid foundation for the next decade to build upon well-defined protocols and problem statements, each supported with source code in a single location, enabling even a wider audience to get started and contributing to the problem.

This brief survey met the following: (1) reviewed research progress in the kin-based vision domain; (2) emphasized milestones that helped guide us to where we are today; (3) defined problem statements to lay a foundation for consistent and fair comparisons moving forward; (4) compiled a single resource accessible online. In the end, we encourage all readers to see the open-source project to use, reference, or contribute. We challenge the experts and invite newcomers to take on the challenges, and to consider the next steps highlighted. Let us continue moving forward on this unique biometric problem.

The deep learning revolution has only begun for visual kinship recognition— how to embed, how to fuse, how to interpret— how do experts across disciplines engage by leveraging for a deeper understanding in inheritance as a science (i.e., anthropology)! Hence, the right tools for the right scholar. Considering the many benchmarks with great overhead for improvement, along with the many social and relational data mining that is made possible with soft-attribute labels such as those in FIW, it is an exciting time for junior, senior, and practical researchers to reap benefits alongside its place with pure business, product, and patent design.

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