

Recognizing Families In the Wild (RFIW): The 4th Edition

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Abstract—*Recognizing Families In the Wild (RFIW)*— an annual large-scale, multi-track automatic kinship recognition challenge supporting visual kin problems on scales larger than before. Organized in conjunction with the 15th IEEE International Conference on Automatic Face and Gesture Recognition (FG), RFIW provides a platform for publishing original work and the gathering of experts for a discussion of the next steps. This paper summarizes the supported tasks (*i.e.*, kinship verification, tri-subject verification, and search & retrieval of missing children) in the evaluation protocols, which include the practical motivation, technical background, data splits, metrics, and benchmark results. Furthermore, top submissions (*i.e.*, leader-board stats) are listed and reviewed as a high-level analysis on the state of the problem. In the end, the purpose of this paper is to describe the 2020 RFIW challenge, end-to-end, along with forecasts in promising future directions.

I. INTRODUCTION

Automatic kinship recognition has numerous uses. For instance - as an aid in forensic investigations, automated photo library management, historical lineage and genealogical studies, social-media-based analysis, tragedies of missing children and human trafficking, and concerns about immigration and border patrol. Nonetheless, the challenges in such face-based tasks (*i.e.*, fine-grained classification in unconstrained settings), are only amplified in the kin-based problem sets, as the data exhibits a high degree of variability in pose, illumination, background, and clarity, along with soft bio-metric target labels (*i.e.*, kinship), which only further exacerbates the challenges with consideration for the directional relationships. Hence, the usefulness brought by the practical benefits of enhancing kinship-based technology is matched by the challenges posed by the problem of automatic kinship understanding. This motivated the launching of the *Recognizing Families In the Wild* (RFIW) challenge series: a large-scale data challenge in support of multiple tasks with the aim to advance kinship recognition technologies. We intend for RFIW to serve as a platform for expert and junior researchers to present and share thoughts in an open forum.

The *Families In the Wild* (FIW) dataset [25], [26], [31]— a large-scale, multi-task image set for kinship recognition— supports the annual RFIW.¹ The aim of the RFIW challenge is to bridge the gap between research-and-reality using its large scale, variation, and rich label information. This makes modern-day data-driven approaches possible, as has been seen since its release in 2016 [3], [5], [8], [15], [33].

We summarize the evaluation protocols— practical motivation, technical background, data splits, metrics, and

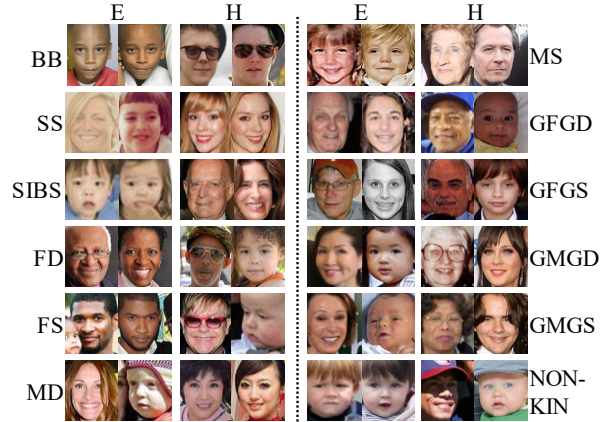


Fig. 1. Sample pairs for the categories of T-1, kinship verification. For each, sample pairs with similarity scores near the threshold (*i.e.*, hard (H) samples), along with highly confident predictions (*i.e.*, easy (E) samples).

benchmarks— of the 2020 RFIW challenge. Specifically, this manuscript serves as a white-paper of the RFIW held in conjunction with the 15th IEEE International Conference on Automatic Face and Gesture Recognition (FG). Additional and information supplemental on the challenge website.²

The remainder of the paper is organized as follows. The three tasks that make-up RFIW2020 are introduced separately (Section III-B, III-C, and III-D). For each task, a clear problem statement, the intended use, data splits, task protocols (*i.e.*, evaluation settings and metrics), and benchmark results are provided. From there, we bring up the discussion (Section V) on broader impacts and potential next steps. Then, we conclude (Section V-B).

II. RELATED WORKS

Kinship recognition, as seen in the machine vision, started in [7], where minimal data and low-level features set the stage for the task of kinship verification between parents and child. Soon thereafter, [34] took a gender specific view of the problem— moreover, the problem was viewed as a low rank transfer subspace problem, where the source and target are set as faces of the parent at younger and older ages, respectively [30]. Family101 [6] was the first facial image dataset with family tree labels; at about the same time, KinWild [18] was released and used to organize data challenges [17]. The task of tri-subject kinship verification (*i.e.*, Track 2), was inspired by the work that came next,

¹RFIW project page, <https://web.northeastern.edu/smilelab/fiw/>.

²RFIW2020 webpage, <https://web.northeastern.edu/smilelab/rfiw2020/>.

TABLE I

COUNTS FOR T-1: NUMBER OF UNIQUE PAIRS (**P**), FAMILIES (**F**), AND FACE SAMPLES (**S**), WITH AN INCREASE IN COUNTS AND TYPES SINCE [27].

		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	2790
	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

in [23], for which data (*i.e.*, TS-Kin) and benchmarks were released. Until the release of FIW in 2016 [25], deep learning models were not widely applied to the kin-based domain, with the minimal exception (*i.e.*, [37]), as the data capacity of their more complex machinery was not met by previous datasets. As part of the first RFIW [27]), FIW was further extended [26], [31], making ever more kin-based problems possible to approach [8], [14]. A major focus of this (*i.e.*, RFIW 2020) is to establish a record of state-of-the-art for the latest-and-greatest version of the FIW image-set.

III. 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). We next describe each task separately, following the same outline: the problem statement and motivation, data splits and protocols, and benchmark experiments (*i.e.*, baselines). A brief section on experimental settings common to all tasks precedes the detailed descriptions of each task in separate subsections.

A. 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 [4], [15], [31], [33]. 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* 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 Sphreface Convolutional Neural Network (CNN) [16] (*i.e.*, 512 D). All pre-processing and the model weights were from the original work.³ Also common, is the use of cosine similarity to determine closeness of a pair of facial features p_1 and p_2 [20]. This is defined as

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

³<https://github.com/wyliu/sphreface>

Scores were then compared to threshold γ (*i.e.*, score $> \gamma$ infers KIN; else, NON-KIN) or sorted (*i.e.*, T-3).

Scores were then either compared to threshold γ (*i.e.*, $\text{cossim}(p_1, p_2) > \gamma$ infers KIN; else, NON-KIN) or sorted (*i.e.*, to rank in T-3). This concludes experimental settings common to all tasks.

B. Kinship Verification

Kinship verification aims to determine whether a pair of faces are blood relatives. This classical Boolean problem has two possible outcomes, KIN or 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 [24].

Prior research mainly considered parent-child kinship types, *i.e.*, father-daughter (FD), father-son (FS), mother-daughter (MD), mother-son (MS). Less attention has been given to sibling pairs, *i.e.*, sister-sister (SS), brother-brother (BB), and brother-sister (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 I. Additionally, benchmarks now include grandparent-grandchildren types, *i.e.*, grandfather-granddaughter (GFGD), grandfather-grandson (GFGS), grandmother-granddaughter (GMGD), grandmother-grandson (GMGS).

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

2) *Settings and metrics*: Conventional face verification protocols were followed [11], 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.*, KIN/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.

TABLE II
AVERAGED VERIFICATION ACCURACY SCORES FOR T-1 OF RFIW.

Methods	FD	FS	MD	MS	GFGD	GFGS	GMGD	GMGS	BB	SS	SIBS	Avg.
Sphereface [16] (baseline)	0.61	0.66	0.69	0.62	0.66	0.71	0.73	0.68	0.57	0.64	0.50	0.64
stefhoer [12]	0.77	0.80	0.77	0.78	0.70	0.73	0.64	0.60	0.66	0.65	0.76	0.74
ustc-nelslip [35]	0.76	0.82	0.75	0.75	0.79	0.69	0.76	0.67	0.75	0.74	0.72	0.76
DeepBlueAI [38]	0.74	0.81	0.75	0.74	0.72	0.73	0.67	0.68	0.77	0.77	0.75	0.76
vuvko [29]	0.75	0.81	0.78	0.74	0.78	0.69	0.76	0.60	0.80	0.80	0.77	0.78

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,

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

where $j^{th} \in \{\text{all 11 relationship types}\}$. Then, the overall accuracy is calculated as a weighted sum (*i.e.*, weight by the pair count to determine the average accuracy).

3) *Baseline Experiments*: The threshold was determined by the value that maximizes the accuracy on the *val* set. Results are listed in Table II, with samples in Fig 1.

C. 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 [23], it makes a more realistic assumption, as having knowledge of one parent often means the other potential parent(s) can be easily inferred.

Triplet pairs consist of Father (F) / Mother (M) - Child (C) (FMC) pairs, where the child C could be either a Son (S) or a Daughter (D) (*i.e.*, triplet pairs are FMS and FMD).

1) *Data Splits*: Following the procedure in [23], 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 III). 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 [23].

We post-process the positive triplets before generating negatives to ensure balance among individuals, families, and

TABLE III
COUNTS FOR T-2. NO. OF PAIRS (P), FAMILIES (F), FACE SAMPLES (S).

		FM-S	FM-D	Total
train	P	662	639	1,331
	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

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.

2) *Settings and metrics*: Per convention in face verification, we offer 3 modes (*i.e.*, the same as in task 1 listed in Section III-B.2). The metric used is, again, 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.

3) *Baseline Results*: Baseline results are shown in Table IV. A score was assigned to each triplet (F_i, M_i, C_i) in the validation and *test* sets using the formula

$$\text{score}_i = \text{avg}(\cos(F_i, C_i), \cos(M_i, C_i))$$

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 γ to infer a label (*i.e.*, predict KIN if the score was above the threshold; else, NON-KIN). The threshold was found experimentally on the *val* set. The threshold was applied to the *test* (Table IV).

D. 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

TABLE IV
TRI-SUBJECT VERIFICATION ACCURACY SCORES FOR T-II BENCHMARK.

	FMS	FMD	Avg.
Sphereface [16] (baseline)	0.68	0.68	0.68
stefhoer [12]	0.74	0.72	0.73
DeepBlueAI [38]	0.77	0.76	0.77
ustc-nelslip [35]	0.80	0.78	0.79

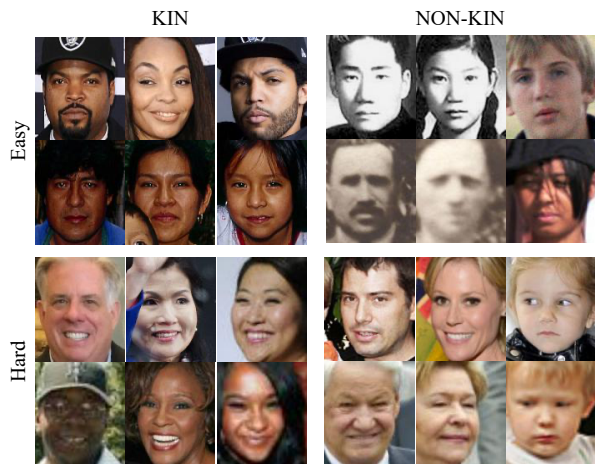


Fig. 2. Tri-subject pairs near the threshold, and for correct and incorrect predictions. Each shows FMS (top rows) and FMD (bottom).

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.

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. 3): 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 setup in closed form (*i.e.*, every probe has relative(s) in gallery).

1) *Data Spits*: 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 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 V).

2) *Evaluation Settings*: 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

TABLE V

COUNTS FOR T-3: 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	9d73
	F	190	190	190
	S	1,487	31,787	33,274

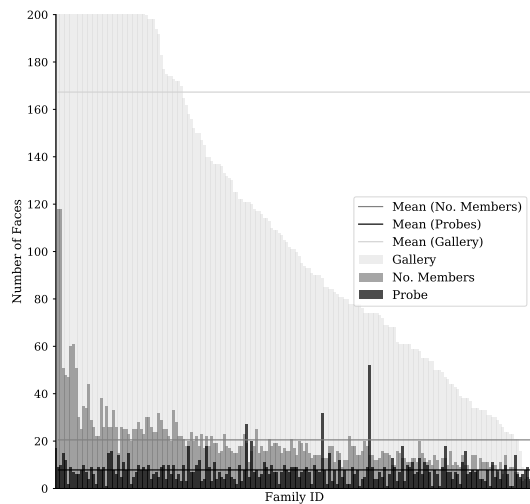


Fig. 3. Plot showing the face counts for each family in test set of T-3. The probes have about 8 faces on average, while the number of family members in the gallery nears 20 on average, with an average of 170 faces in total.

evaluations, facial images for unique subjects are separated by identity, with a gallery containing variable number of relatives, each with a variable number of faces [32].

Teams were allowed to submit up to six final submissions, with each submissions being a ranked-list of all subjects in the gallery. Submissions were accompanied by a brief (text) description of the system used to generate results. With that was a ranked list per probe in the test. Per RFIW rules, participants were permitted to analyze test results, as this was the purpose of the 192 families provided as the val set.

a) *Evaluation Metric*: MAP was the underlying metric used for comparisons. Mathematically speaking, scores for each of the N missing children are calculated as follows:

$$AP(f) = \frac{1}{P_F} \sum_{tp=1}^{P_F} Prec(tp) = \frac{1}{P_F} \sum_{tp=1}^{P_F} \frac{tp}{rank(tp)},$$

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:

$$MAP = \frac{1}{N} \sum_{f=1}^N AP(f),$$

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

3) *Baseline Results*: Table VI and shown in Fig. 4.

TABLE VI

PERFORMANCE RATINGS FOR TRACK 3.

Methods	mAP	Rank@5
Baseline (Sphereface) [16]	0.02	0.10
HCMUS notweeb [21]	0.07	0.28
DeepBlueAI [38]	0.06	0.32
ustc-nelslip [36]	0.08	0.38
vuvko [29]	0.18	0.60

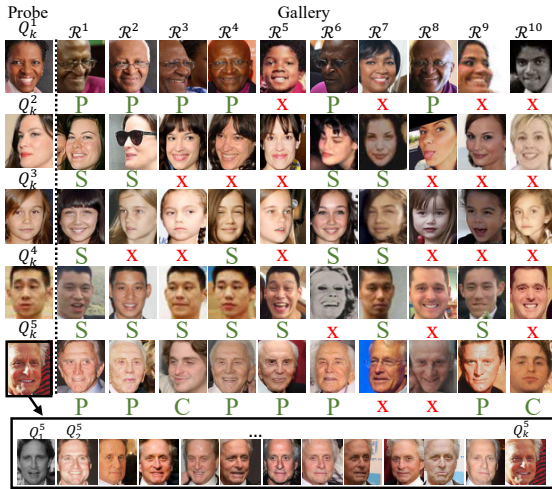


Fig. 4. T-3 sample results (Rank 10). For each query (row) one or more faces of the probe returned the corresponding samples of gallery as top 10. Here, **x** (red) depicts false predictions, while true predictions displays the relationship type (in green): **P** for parent; **C** for child; **S** for sibling.

IV. SUMMARY OF SUBMISSIONS

Solutions for the tasks of the 2020 RFIW FG challenge tended to use backbone networks trained for conventional face recognition (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.

A. Team Vuvko

Team Vuvko [29] treated the different relationship types as a multi-task problem and trained a local expert for each type on top of a ResNet50 [10], simultaneously. This multi-task model, trained and evaluated for kinship verification (Table II), was deployed for the other tasks as well (Table IV and VI). Another method applicable to all tasks was using different fusion techniques in deep feature space [35], [36].

Sample pairs in the T-1 challenge that were unanimously correctly and incorrectly classified are shown in Fig. 5. Similarly, sample triplets that all teams got correct or incorrect in T-2 are shown (Fig. 6, left and right column, respectively).

Team Vuvko scored the highest average in T-1 (Table II) as well as the highest ranking for T-3 (Table IV).

B. Team DeepBlueAI

Team DeepBlueAI used two pre-trained CNNs (*i.e.*, VGG-Face [28] trained on VGG2 [1] and FaceNet trained on MSCeleb [9]) [38]. The CNN were used to encode each face— the two face encodings were then concatenated using different types of arithmetic [35], [36]. In [38], the distance between faces was then determined using euclidean distance. Also, SENet [13] was swapped in for ResNet50 as the backbone for a modest boost in performance on the validation, but dropped on the test. Much like in [26], [38] fine-tuned a CNN using families as the classes (*i.e.*, the difference was the authors used Arcface, opposed to Sphereface as in [26]).

Team DeepBlueAI tied for second in kinship verification, T-1 (Table II), and second to best in T-2 (Table IV).

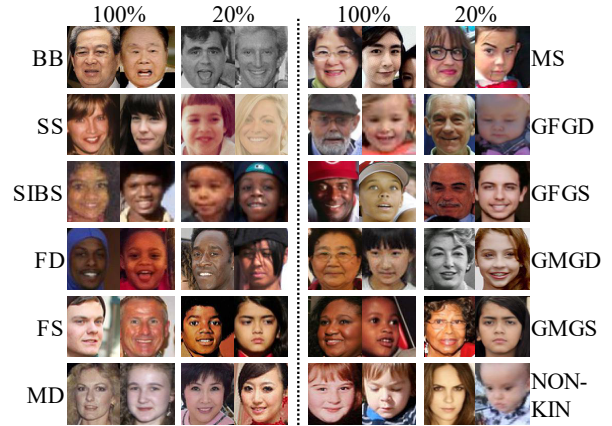


Fig. 5. Sample pairs of T-1 that all teams got correct or incorrect.

C. Team Ustc-Nelslip

Team Ustc-nelslip [35] also used a Siamese network, *i.e.* encoding features from images in parallel with weights shared across the two image processings. ResNet50 or SENet50 was used as the backbone, both pre-trained on VGGFace2 [1]. In addition, team ustc-nelslip 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.

Team Ustc-nelslip scored highest in T-2 (Table IV).

D. Team Stefhoer

Team Stefhoer [12] placed particular emphasis on the the dependence of family identification accuracy for cross-gender versus same-gender pairs of images. These researchers constructed a Kinship *comparator* module that consisted of eleven separate "local expert networks" connected in series. These eleven networks corresponded to the eleven types of family relationships (*e.g.*, father-son and brother-sister) in the challenge. Perhaps as a result of this focus team Stefhoer registered the highest score in the subcategories of father-daughter and mother-son identification (within T-1).

E. Team HCMUS

Team HCMUS [21] 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 [2] - a family of loss functions based on the geodesic distance between feature vectors which aim to discriminate the latent representation of deep NNs.

V. DISCUSSION

A. A Broader Impact

The fourth *Recognizing Families In the Wild* (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

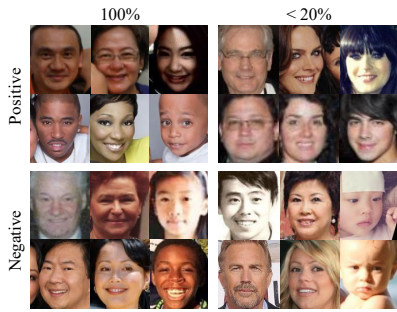


Fig. 6. Sample triplets of T-2 that all teams got correct (left) or mostly incorrect (right). Each shows FMS (top rows) and FMD (bottom).

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 [8], [22]) and experimental settings [14], focuses on particular views of the visual kinship recognition problem. 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.

B. Conclusion

This paper presented the 2020 RFIW challenge organized in conjunction with the 15th IEEE International Conference on Automatic Face and Gesture Recognition (FG). The 2020 challenge is the fourth edition of the RFIW annual evaluation. For this, we added 2 new tracks, tri-subject verification and search & retrieval of missing children; the traditional kinship verification task continued to be supported as well. The *Families In the Wild* (FIW) dataset was used to pose each of the challenge tracks. As challenging it may be, many entries outperformed the “vanilla” baselines in all tasks. Regardless, in all three cases, there still exists much room for improvement. Accuracy on the Verification and Tri-subject has just begun to approach the 80%; Search & Retrieval further behind. Baseline code at github.com/visionjo/pykinship. As we see it, the story of FIW is still in its infancy.

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