

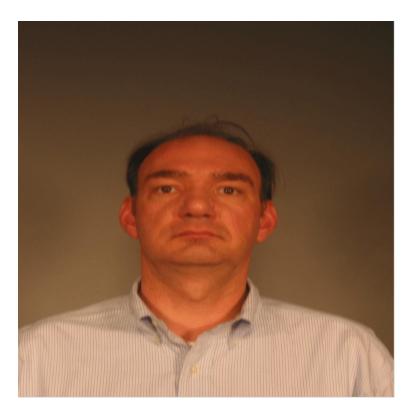
Modeling an Anonymous Identification System

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Suppose a biometric system encounters some number of individuals*.



Encountered Individual

- Presume no prior information about any of these individuals / identities.
- The actual identity of the individual observed is unknown to the system (identification).
- The system is also not acquiring information pertaining to the identity of encountered individuals.





Motivation

Suppose all we wish to know is has this person been encountered previously by the system.



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Has this person been encountered?



Encountered Individual





Motivation

Suppose all we wish to know is has this person been encountered previously by the system.



CITeR

Has this person been encountered?



Encountered Individual

Yes, this person has been previously encountered.

*Face images sampled from from MBGC Dataset



Anonymous Identification

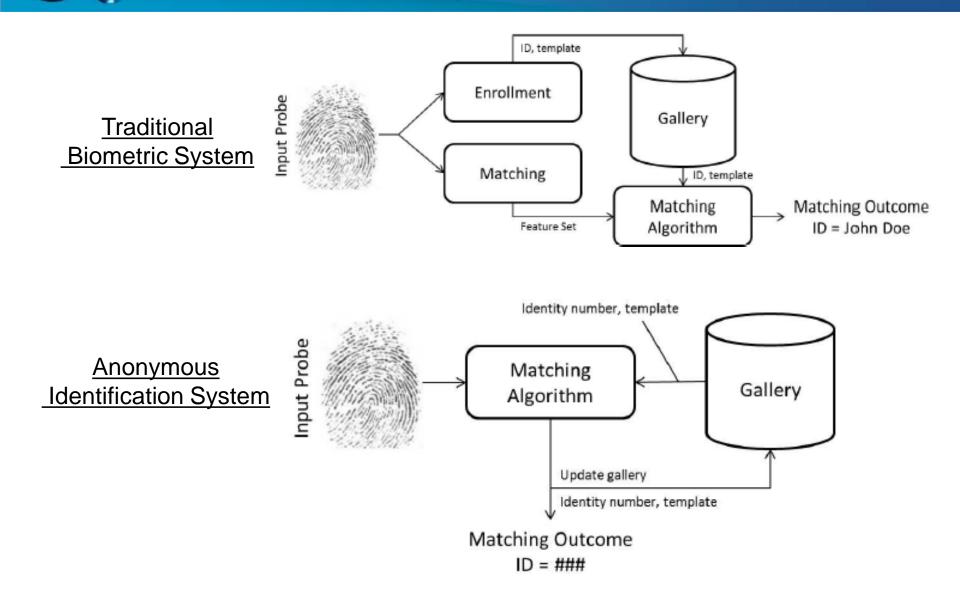
Anonymous identification system

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- Variant of a classical biometric system.
 - No explicit enrollment process.
 - Biometric templates in the gallery are not labeled with the identity of individuals.
- Comparison process
 - System observes the input (probe) biometric data and determines if a match exists in the gallery.
 - Addresses the question: "Has this person been encountered before?"

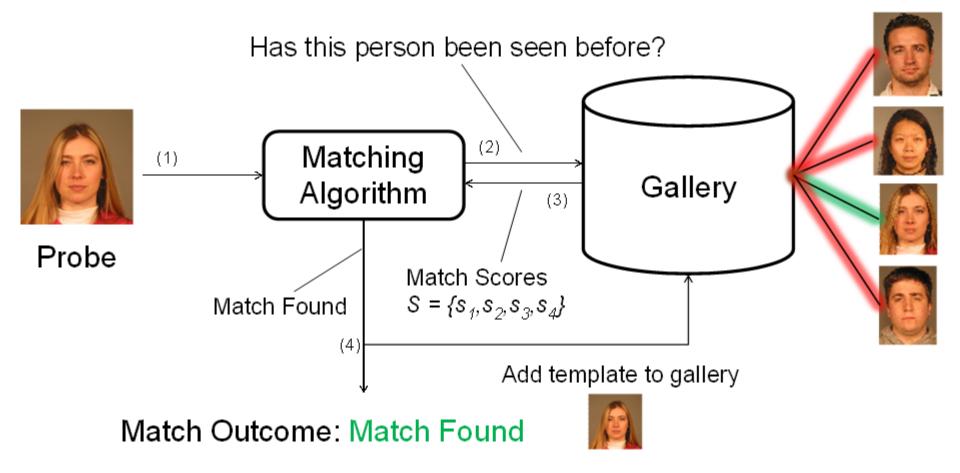


Visual Comparison

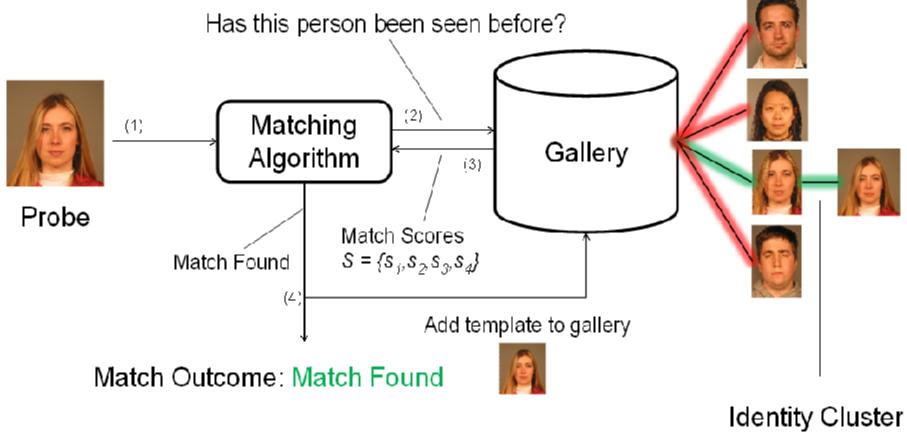








Visual Example: Match Outcome

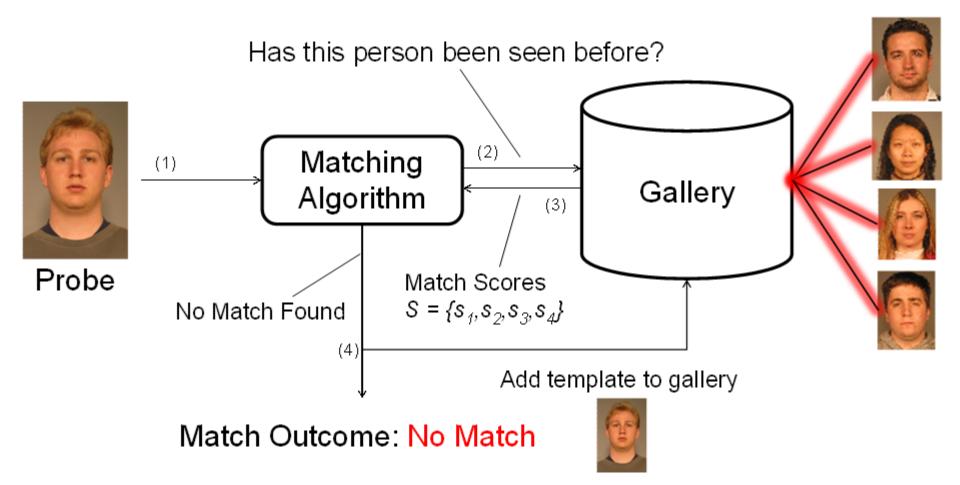


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Updated



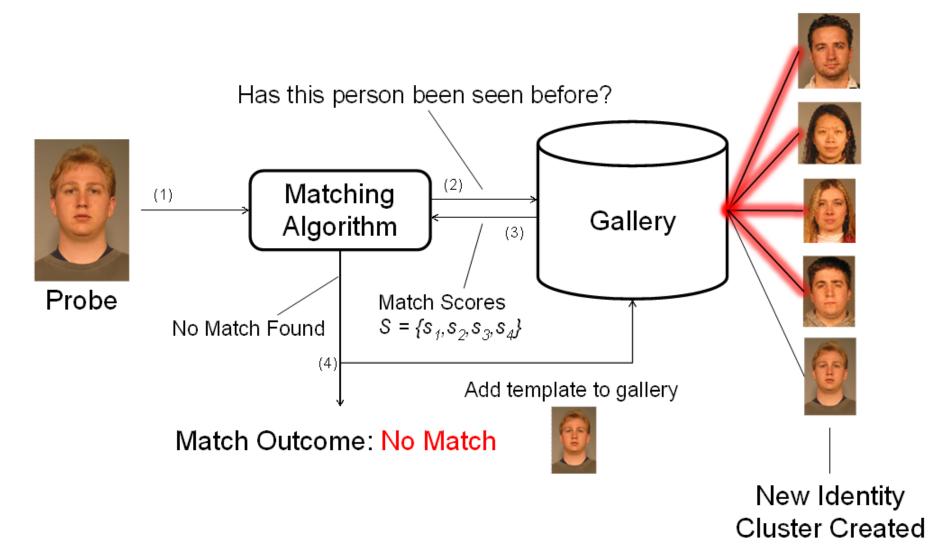


*Face images sampled from from MBGC Dataset





Visual Example: Non-match Outcome



*Face images sampled from from MBGC Dataset



Potential Applications

- De-duplication
 - The de-duplication problem invokes searching through a database to solely determine if the probe matches to an entry in the gallery.
 - i.e., not concerned with the identity of the match.
 - De-duplication contrasts to classical identification, since gallery entries may not be accurately labeled.
 - Problem gaining traction in the context of national scale ID programs*.
- . Surveillance
 - Allows for real-time updating of a gallery.

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- Identity profiles can be newly created or updated following each encounter.
- Covert operation.
 - Subjects do not need to be enrolled in order to be later recognized.

*UIDAI, "Role of Biometric Technology in Aadhaar Enrollment" Government of India, Tech. Rep. January 2012.



• Traditional system

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- Error is computed using a fixed set of gallery and probe images.
- Anonymous system
 - Since the gallery expands, the error rate changes depending on the current gallery and future probes.
- How?

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- In a traditional analysis, probe p_k is absolutely associated with a specific set of gallery entries.
- In an anonymous identification system, the actual identity pertaining to probe p_k may or may not have been previously encountered.
- Further, if the proper identity has been encountered, it may exist in multiple identity clusters due to decision error.

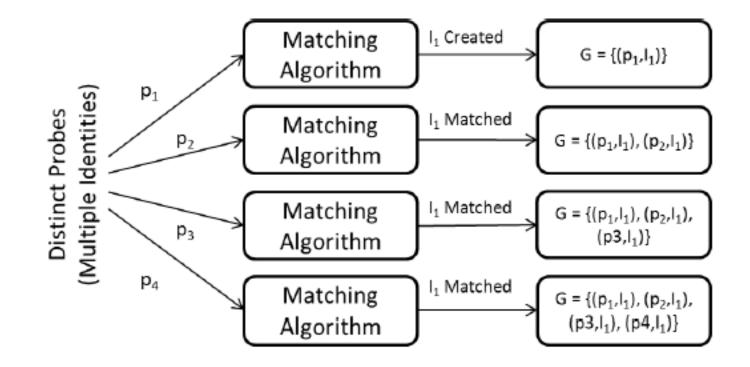


- False Dynamic Match (FDM)
 - Occurs when a probe incorrectly matches to an identity cluster that does not contain an entry belonging to the encountered individual.
- False Dynamic Non-Match (FDNM):
 - Occurs when a probe, which should match to at least one existing identity cluster, does not match to any identity cluster.
 - Thus, if the individual has not been seen by the system, a false dynamic non-match cannot occur.
 - A false dynamic non-match does not occur when a probe correctly matches to an identity cluster consisting of the true identity, in addition to other identities.





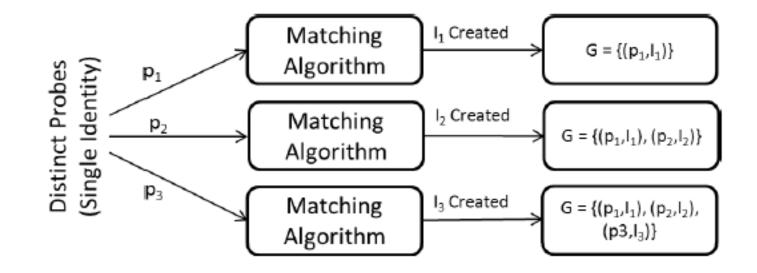
False Dynamic Match: Visualization







False Dynamic Non-Match: Visualization





- Analytical Error Prediction
 - Derive an analytical approach for estimation of FDMR (False dynamic match rate) and FDNMR (False dynamic non-match rate) given a set of test data.
- Constraints
 - Assume all probes have an equal probability of being observed.



Error Prediction – False Dynamic Match

• False Dynamic Match

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- Occurs when a probe is incorrectly matched to an identity cluster who entries do not contain the true identity of the probe.
- . Events
 - **Event A**: When p_k is matched against G at encounter e_k , there are no genuine scores generated and at least one impostor score is greater than γ .
 - γ = decision threshold
 - Event B: When p_k is matched against G at encounter e_k, both genuine and impostor scores are generated, and there is at least one impostor score that (a) exceeds γ and (b) is greater than all genuine scores.

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FDM - Mathematical Representation

Mathematical Representation

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 $- P(FDM|p_k, e_k) = P(A|p_k, e_k) \cup P(B|p_k, e_k)$

$$- P(A|p_k, e_k) = \sum_{z=1}^{N_I^{\gamma}} \frac{\binom{N_I^{\gamma}}{z} \binom{K-N_I^{\gamma}}{k-z-1}}{\binom{K}{k-1}} * \frac{\binom{N_G}{0} \binom{K-N_G}{k-1}}{\binom{K}{k-1}}$$

-
$$P(B|p_k, e_k) = \sum_{\forall C} \sum_{z=1}^{\zeta} \frac{\binom{\zeta}{z}\binom{K-\zeta}{k-z-1}}{\binom{K}{k-1}} * \frac{\binom{K-N_G}{k-C_\ell-1}}{\binom{K}{k-1}}$$

- Auxiliary Variables
 - N_G = Number of genuine probes in G
 - N_I^{γ} = Number of potential* imposter scores above γ .
 - *C* = Set of genuine probe combinations (e.g. {1,2,4}, {3,4}, {2},...)
 - ζ = Number of potential* imposter scores above the maximum

*Inclusive to entities outside the gallery.



- . False Dynamic Non-match
 - A probe does not match to a genuine gallery entry and any impostor probes that could procure a match have not been observed.
- . Events
 - **Event C**: When p_k is matched against G at encounter e_k , all genuine scores generated are below γ .
 - = **Event D**: When p_k is matched against G at encounter e_k , all impostor scores generated are below γ .

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FDNM - Mathematical Representation

Mathematical Representation

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 $- P(FDNM|p_k, e_k) = P(C|p_k, e_k) \cap P(D|p_k, e_k)$

$$- P(C|p_k, e_k) = \sum_{z=1}^{\rho} \frac{\binom{\rho}{z} \binom{\omega}{0} \binom{K-N_G}{k-z-1}}{\binom{K}{k-1}}$$

$$- P(D|p_k, e_k) = \frac{\binom{N_I^{\gamma}}{0}\binom{K-N_I^{\gamma}}{k-1}}{\binom{K}{k-1}}$$

- Auxiliary Variables
 - N_G = Number of genuine probes in G
 - N_I^{γ} = Number of potential* imposter scores above γ .
 - ρ = Number of potential* genuine scores below γ .
 - ω = Number of potential* genuine scores above γ .

*Inclusive to entities outside the gallery.



Expected Error Rates

• Expected Error Rates - $E(FDMR) = \frac{100}{K} \sum_{e_k} \sum_{p_k} P(FDM|p_k, e_k)$ - $E(FDNMR) = \frac{100}{K} \sum_{e_k} \sum_{p_k} P(FDNM|p_k, e_k)$

*Expected FDMR and FDNMR over K encounters



Experiments

. Datasets

- WVU face dataset
 - 5 frontal face images for 240 subjects.
 - Similarity scores computed from VeriFace.
- WVU fingerprint dataset

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- 5 fingerprint images corresponding to the R1, R2, L1 and L2 fingers for 240 subjects.
- Similarity scores computed from VeriFinger.
- CASIA Iris Version 3 dataset
 - Subset using 5 left iris images for 122 subjects.
 - Similarity scores computed using an open source IrisCode algorithm.



Experiments

. Datasets

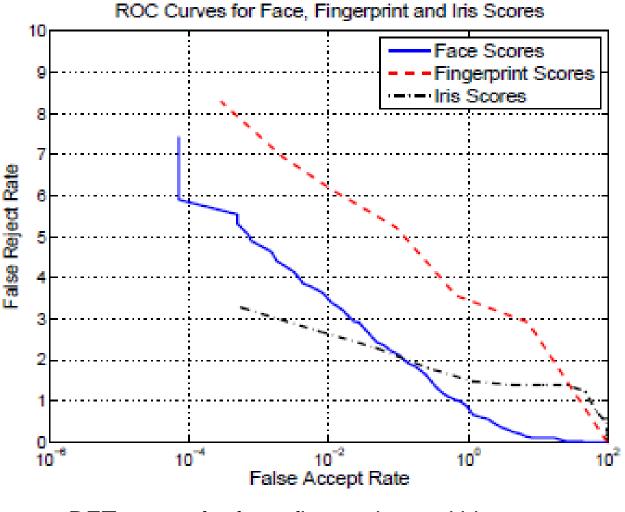
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- CASIA Iris Version 3 dataset
 - Subset using 5 left iris images for 122 subjects.
 - Similarity scores computed using an open source IrisCode algorithm.
 <u>Note</u>: We are interested in the *meaning* of the numbers, rather than the value(s).



DET Curves for Match Score Sets



DET curves for face, fingerprint, and iris scores.



Evaluating the Prediction Model

- Model Prediction
 - Evaluate the ability of the model to accurately predict error rates given a set of test scores.
- Experimental setup
 - Create a bootstrapped test set of 300 probes

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- Each bootstrapped test set contains 5 genuine probes for 60 identities.
- Allows for variation in the test data for evaluating the model performance.
- Aids in mitigating numerical errors from computing very large combinatorics.
- Compare theoretical and observed FDMR and FDNMR.

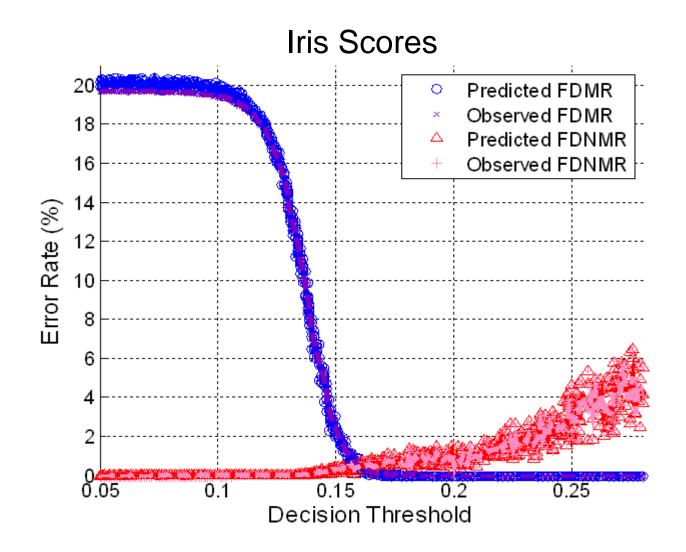


Evaluating the Prediction Model

Fingerprint (R1) Scores **Face Scores** 22 20 Predicted FDMR Predicted FDMR 0 0 20 Observed FDMR Observed FDMR х 18 Predicted FDNMR Predicted FDNMR 18 Δ Observed FDNMR 16 Observed FDNMR 16 14 Error Rate (%) Error Rate (%) 14 12 12 10 10 8 8 6 6 04 0.1 0.4 0.5 0.02 0.04 0.08 0.2 0 0.06 0.1 0.3 Decision Threshold Decision Threshold



Evaluating the Prediction Model

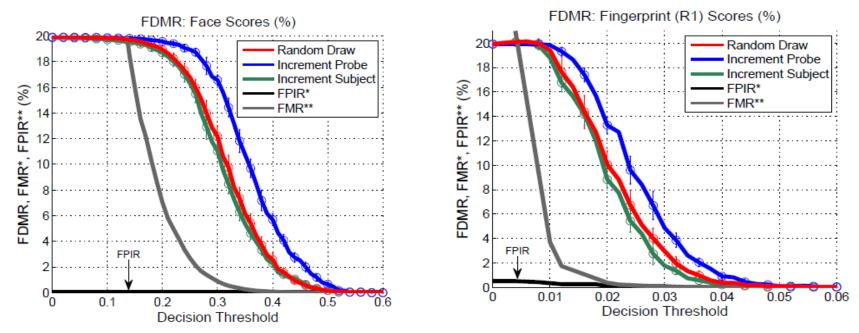




- Anonymous Identification
 - Discussed the concept of an anonymous identification system.
 - This approach does not ask for unique identity information and only determines if a person has been encountered before.
- Error Dynamics
 - Defined the types of error in an anonymous identification system.
- Error Prediction
 - Developed a prediction model for estimating the expected error, provided a test set of match scores.
 - The prediction model accurately predicted observed error rates within $\pm 1.5\%$ for three modalities.



- Other Accomplishments
 - Demonstrated the order in which probes are encountered affects the observed error rates.
 - Traditional metrics for evaluating biometric system performance fail to accurately quantify the dynamics of an anonymous identification system.







Thank You!

Acknowledgments Office of Naval Research WVU Night Biometrics Team



- Anonymous Identification in Literature
 - Dodis *et al.* first defined an anonymous identification system where users enroll in ad-hoc groups and prove membership [1].
 - Bringer *et al.* adopted the term anonymous identification in the context of cancelable biometrics [2].
 - Phrase has come to refer to template protection or quality assurances for privacy.
- Present Form
 - Here, this definition is *not* concerned with template protection.
 - Loosely resembles the work of Dodis *et al.* [1], as the matching process does not necessarily deduce identity.

[1] Y. Dodis, A. Kiayias, A. Nicolosi, V. Shoup, "Anonymous Identification in ad-hoc groups," *Advances in Cryptology* – Eurocrypt (2002)
 [2] J. Bringer, H. Chabanne, B. Kindarji, "Anonymous identification with cancelable biometrics," *International Symposium on Image and Signal Processing and Analysis* (2009).



- Performance as a function of permutation
 - Demonstrate that the order in which probes are encountered affects the observed error.
- Experimental setup
 - Define three types of permutations
 - Random Draw
 - Draw K probes at random without replacement.
 - Increment Probes (IP)
 - Probes corresponding to a single unique identity repeat every M encounters. (M = Number of distinct identities in test set)
 - Increment Subjects (IS)
 - Probes corresponding to a single unique identity repeat successively.
 - Record observed error rates of each permutation type at many values of γ.
 - Also note the FMR, FNMR, FPIR, and FNIR of each score set for all values of γ. (γ = decision threshold).



Algorithmic Representation

Algorithm 1: Anonymous Identification

Input: Biometric probes p_1, p_2, \ldots, p_K

Output: Gallery *G* comprised of *K* probes with assigned anonymous identity numbers $I = \{I_1, I_2, ..., I_K\}$. *Define*: $S(p_k, p_j)$ as similarity score between p_k and p_j .

Initalize:

 $I_1 = 1 \setminus$ the first probe is automatically assigned cluster number 1. Gallery entries $G = \{p_1, I_1\} \setminus$ the first probe is now placed in the gallery. $I_2 = I_3 = I_K = -1 \setminus$ the rest of the probes are yet to be observed.

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//Begin algorithm

for k = 2 to K do \\ iterate through the rest of the probes.

for j = 1 to k - 1 do \\ upon encountering probe p_k , compare it with the previous set of encountered probes that are in the gallery database.

 $R(j) = S(p_k, p_j) \setminus$ compute similarity between p_k and p_j .

end for

if $max_j \{R(j)\}_{i=1}^{k-1} \ge \gamma$ then

 $I_k = I_m$ where $m = \arg \max_{j \in \mathbb{R}} \{R(j)\}_{j=1}^{k-1} \setminus \{R(j)\}_{j=1}^{k-1} \}$ there is a match with the m^{th} gallery entry.

else

 $I_k = max(I) + 1 \setminus if$ there is not a match, assign p_k an anonymous identity number one higher than the maximum value in I.

end if

 $G = G \cup \{p_k, I_k\} \setminus$ add the new probe, along with its anonymous identity number to the gallery. end for

//End algorithm

Return G



Experiments

Random Draw

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$$\begin{array}{c} P_{3,2} \rightarrow P_{1,1} \rightarrow P_{4,1} \rightarrow P_{1,2} \rightarrow P_{2,2} \rightarrow P_{2,1} \rightarrow P_{4,2} \rightarrow P_{3,1} \\ \hline P_{2,2} \rightarrow P_{3,1} \rightarrow P_{1,2} \rightarrow P_{3,2} \rightarrow P_{4,1} \rightarrow P_{2,1} \rightarrow P_{4,2} \rightarrow P_{1,1} \end{array}$$

Increment Subjects (IS)

$$P_{1,1} \rightarrow P_{1,2} \rightarrow P_{2,1} \rightarrow P_{2,2} \rightarrow P_{3,1} \rightarrow P_{3,2} \rightarrow P_{4,1} \rightarrow P_{4,2}$$

$$P_{3,1} \rightarrow P_{3,2} \rightarrow P_{1,1} \rightarrow P_{1,2} \rightarrow P_{4,1} \rightarrow P_{4,2} \rightarrow P_{2,1} \rightarrow P_{2,2}$$

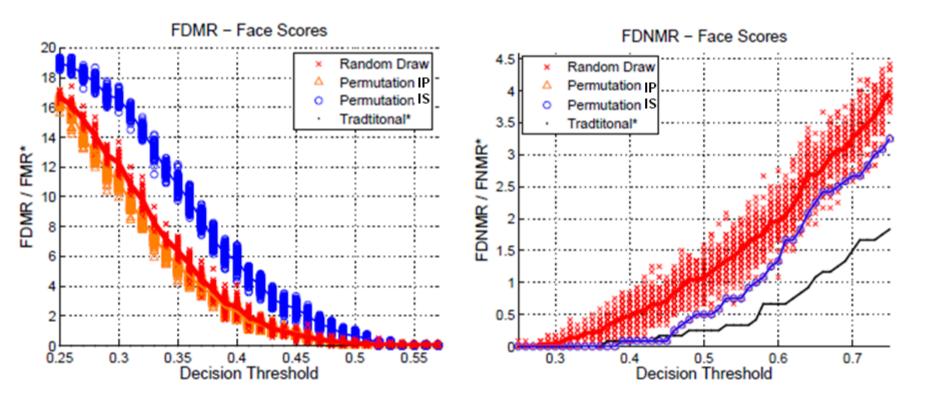
Increment Probes (IP)

$$\begin{array}{c} P_{1,1} \rightarrow P_{2,1} \rightarrow P_{3,1} \rightarrow P_{4,1} \rightarrow P_{1,2} \rightarrow P_{2,2} \rightarrow P_{3,2} \rightarrow P_{4,2} \\ \hline P_{3,1} \rightarrow P_{4,1} \rightarrow P_{1,1} \rightarrow P_{2,1} \rightarrow P_{3,2} \rightarrow P_{4,2} \rightarrow P_{1,2} \rightarrow P_{2,2} \end{array}$$

Figure 7: Observation flowchart of permutations "Random Draw", "Increment Subjects" (IS), and "Increment Probes" (IP), where M = 4 and T = 2. Note that for permutations IS and IP, the first subscript denotes the m^{th} subject and the second subscript denotes the t^{th} probe of that subject. In addition, the first subscript does not necessarily follow 1, 2, ..., M, but rather any combination of 1, 2, ..., M (e.g., 2, 1, 3, 4, or 3, 2, 4, 1).



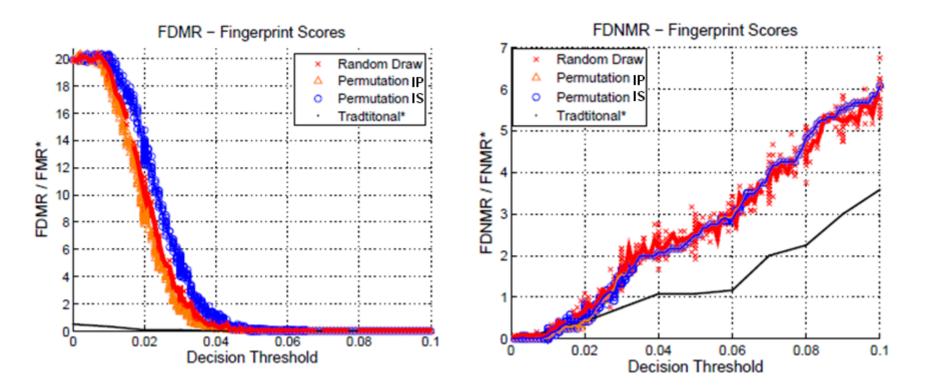
Experiments



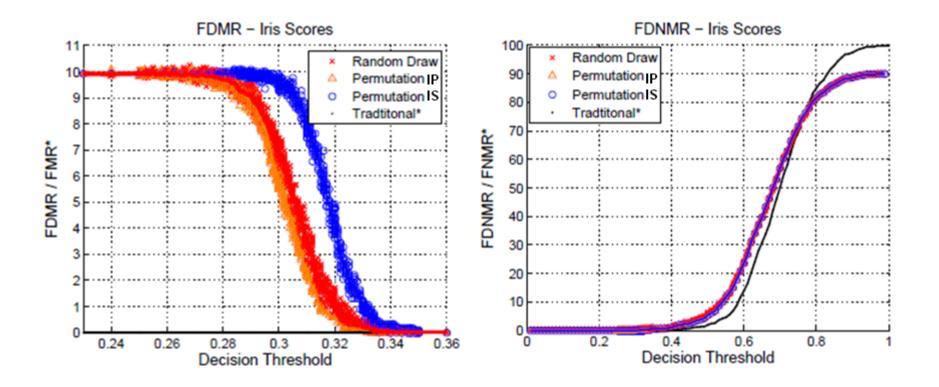
False dynamic match and false dynamic non-match rates for face scores.



Experiments



False dynamic match and false dynamic non-match rates for face scores.



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False dynamic match and false dynamic non-match rates for iris scores.



Traditional vs. Anonymous

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- Shape of performance curves similar.

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- Intersection of FDMR and FDNMR approximately equal to stated EER
- Suggests performance is comparable to the state of art.
- FMR and FNMR are poor predictors of FDMR and FDNMR, respectively.
- Performance as function of encounter
 - Figures demonstrate the probability of observing a false dynamic match can be significantly impacted by probe order.
 - Evidenced in permutation scatter
 - Permutation IS Highest Error
 - Permutation IP Lowest Error
- Error Prediction
 - Accurately predicted observed error rates within +/- 1.5%