# Relating ROC and CMC Curves

Work done with Brian DeCann

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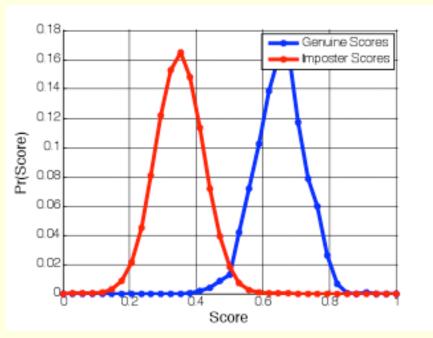
#### Introduction

- Performance of a verification system is summarized using Receiver Operating Characteristic (ROC) curve
- Performance of a closed-set identification system is summarized using Cumulative Match Characteristic (CMC) curve
- Can the CMC curve be derived from the ROC curve and vice-versa?

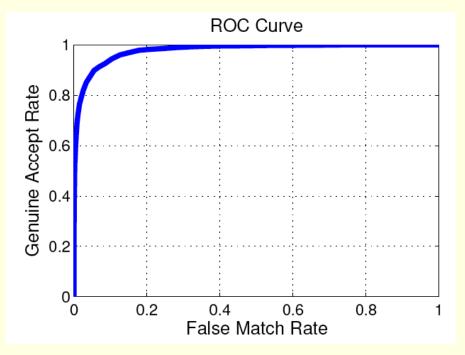
#### **ROC Curve**

- Biometrics samples are compared against each other
- Genuine and impostor scores are generated
- False Match Rate (FMR) and False Non-match Rate (FNMR) are computed at multiple thresholds
- ROC Curve: True Match Rate versus False Match Rate
- ROC Curve: Aggregate Statistics

#### **ROC Curve**



**Match Score Distributions** 

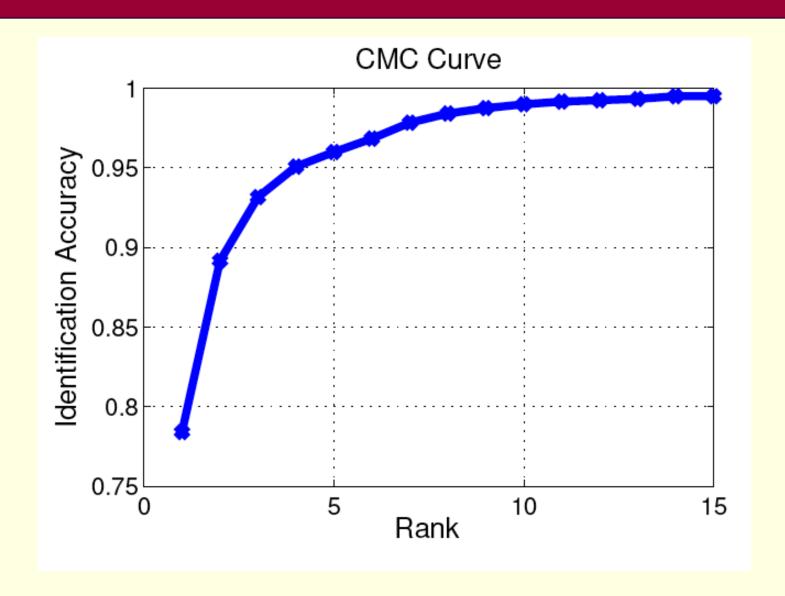


**ROC Curve** 

#### CMC Curve

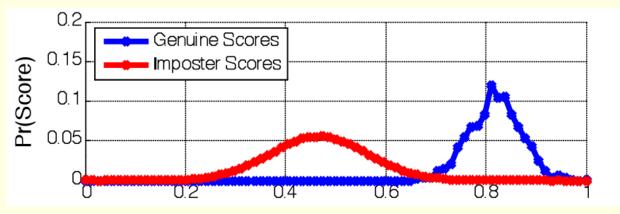
- Each probe biometric sample is compared against all gallery samples
- The resulting scores are sorted and ranked
- Determine the rank at which a true match occurs
- True Positive Identification Rate (TPIR): Probability of observing the correct identity within the top K ranks
- CMC Curve: Plots TPIR against ranks
- CMC Curve: Rank-based metric

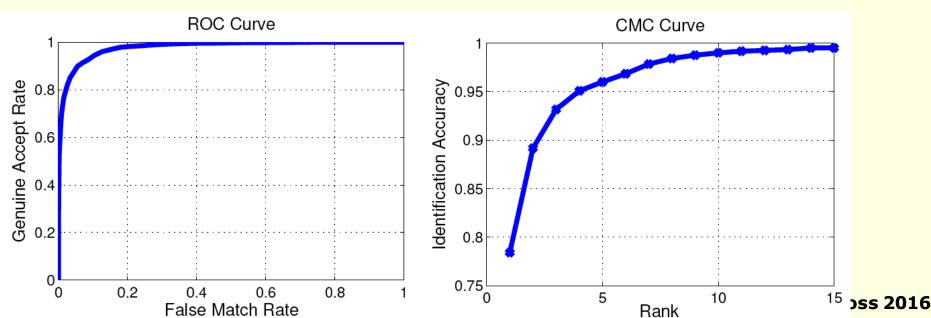
## CMC Curve



#### CMC versus ROC

• It is reasonable to expect a good ROC curve to be associated with a good CMC curve and vice-versa





## Predicting CMC from ROC

- The CMC can be predicted from the ROC data
  - Bolle et. al. (2005), Hube (2006)

$$Rank - n = \sum_{k=1}^{n} {N-1 \choose k-1} \int_{0}^{\infty} F_G(s) FAR(s)^{k-1} (1 - FAR(s))^{(N-k)} ds$$

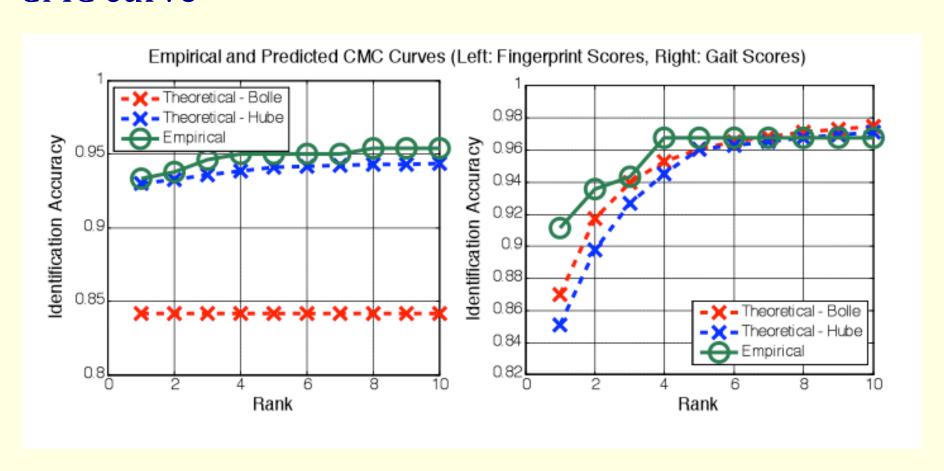
<u>Hube</u>

$$Rank - n = TPR(FAR = \frac{n}{N})$$
, where TPR = (1-FNMR)

- R. Bolle, J. Connell, S. Pankanti, N. Ratha, and A. Senior. The Relation Between the ROC Curve and the CMC. AutoID 2005
- J. Hube. Using Biometric Verification to Estimate Identification Performance. BSYM 2005

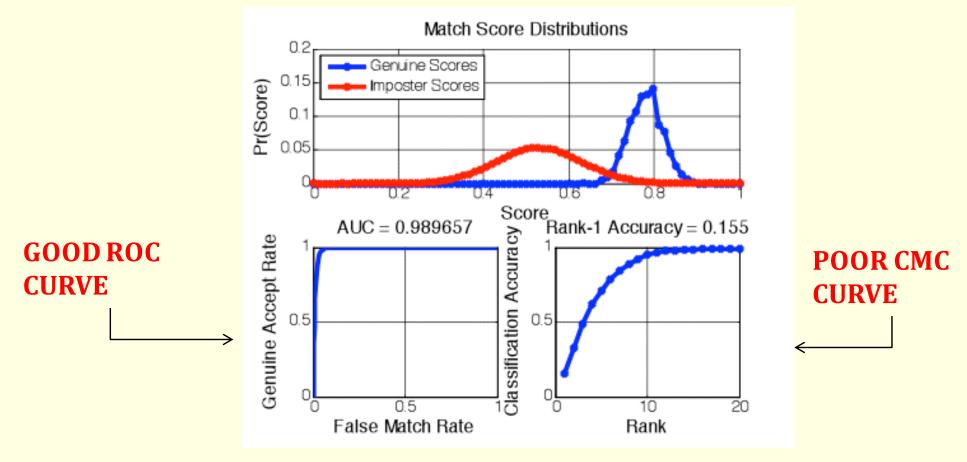
## Predicting CMC from ROC

 But neither model perfectly predicts the empirical CMC curve

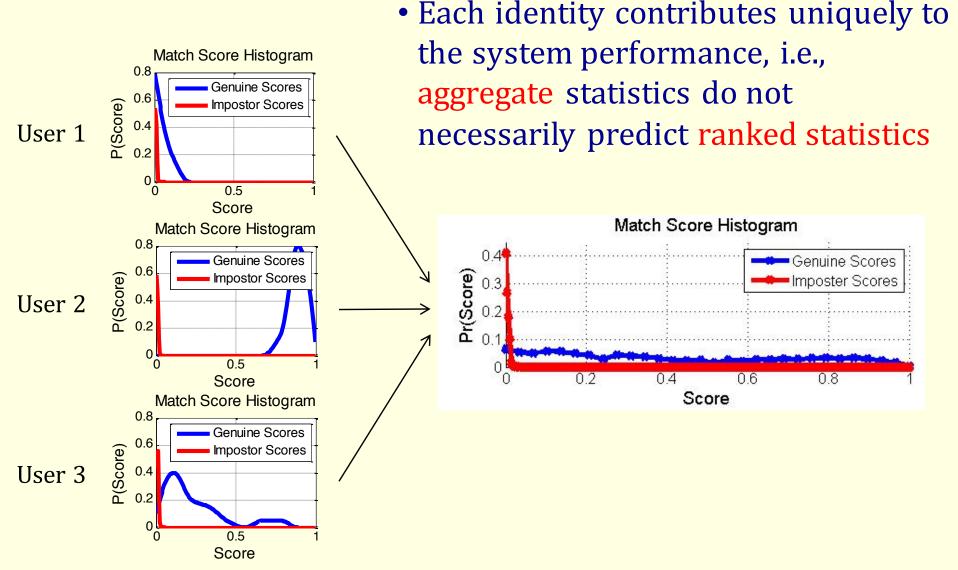


#### ROC versus CMC

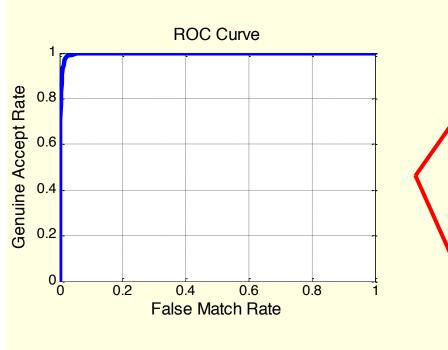
 DeCann and Ross (2012) showed that it is possible for a good ROC curve to be associated with a poor CMC curve and vice-versa

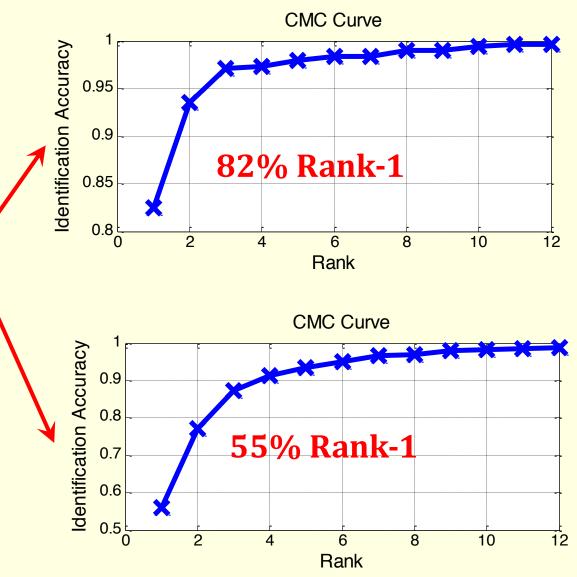


## Why did CMC prediction models fail?



## One ROC Curve: Multiple CMC Curves



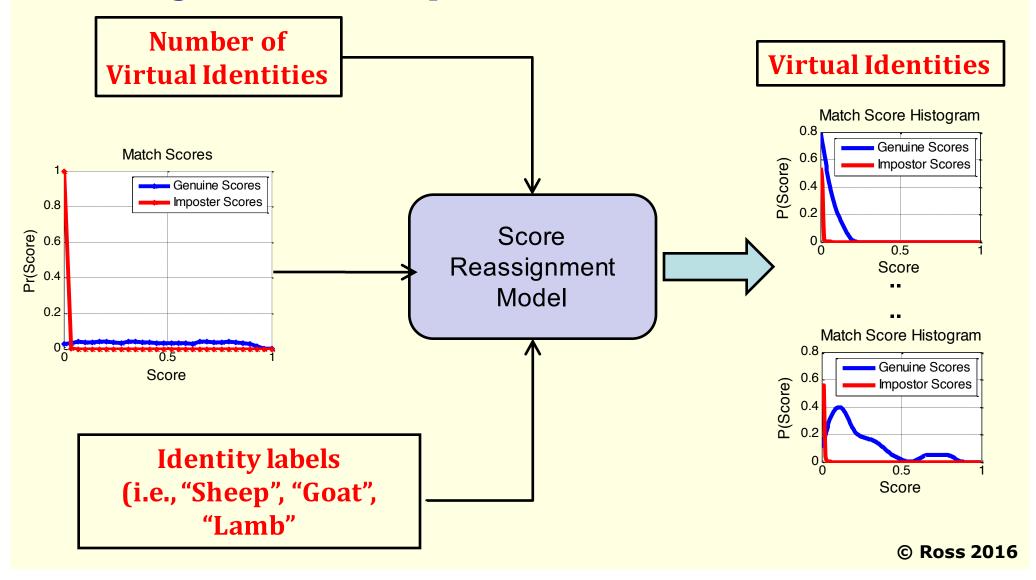


#### Virtual Identities

- Input: Set of genuine and impostor match scores
- Output: Virtual identities with different rank-based statistics
- Method: "Reassign" match scores to virtual identities according to the "Doddington's Zoo" concept
  - Sheep: Low FMR and FNMR
  - Goats: High FNMR
  - Lambs: High FMR

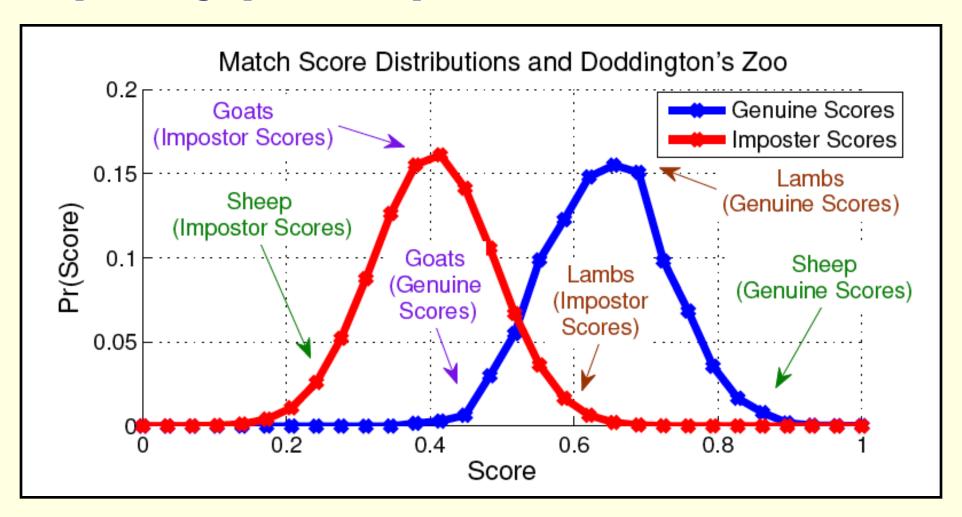
### Reassigning Match Scores

Set of genuine and impostor match scores



## Sampling Match Scores

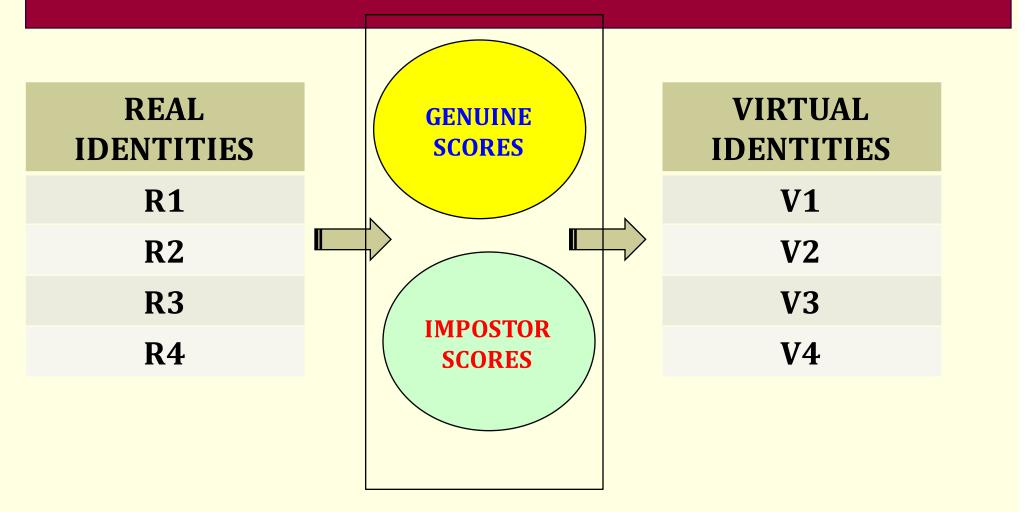
• Depending upon "Sheep", "Goat", "Lamb" labels



## Sampling Rationale

- Genuine Scores: Use the label ("Sheep", "Goat", "Lamb") to assign genuine match scores to a virtual identity
- Impostor Scores: Use the labels of "pairs" of virtual identities to assign impostor match scores to a virtual identity

#### From Real to Virtual



Aggregate Statistics do not change

## Reassigning Genuine Scores

#### **Algorithm 1**: Reassigning Genuine Scores

Input: Vector  $\mathbf{s}_{Gen}$ , containing the genuine scores.

Vector  $\chi$ , a set containing the labels of each identity (e.g., "Sheep", "Goat", "Lamb").

Define:  $\delta$ ,  $\epsilon_{Gen}$ : Scaling parameters.

Output: Matrix S populated with genuine scores.

 $\setminus \setminus$  begin algorithm

Step 1: For each identity, note the assigned label.

Step 2a: Draw a genuine score (without replacement),  $\phi$ ,  $\mathbf{s}_{Gen}$ , from within subset  $\mathbf{s}_{rng}$ , where

$$\mathbf{s}_{rng} = (\mu_{Gen} + \sigma_{Gen}, 1), \text{ if } \chi_n = Sheep.$$

$$\mathbf{s}_{rng} = (0, \mu_{Gen} - \sigma_{Gen}), \text{ if } \chi_n = Goat.$$

$$\mathbf{s}_{rng} = (0, \mu_{Gen} + \sigma_{Gen}), \text{ if } \chi_n = Lamb.$$

#### Reassigning Genuine Scores

```
Step 2b: If \mathbf{s}_{rnq} is a null set, and \mathbf{s}_{rnq} = (a, b),
    set a = \delta \cdot a, b = \frac{b}{\delta} and repeat Step 2a.
Step 3a: Draw \binom{N_G}{2} - 1 scores (without replacement)
    from \mathbf{s}_{Gen} within \phi \pm \epsilon_{Gen}.
Step 3b: If less than \binom{N_G}{2} - 1 scores can be drawn
    set \epsilon_{Gen} = \frac{\epsilon_{Gen}}{\delta} and repeat Step 3a.
Step 4: Store the sampled genuine scores in S.
return S
\setminus \setminus end algorithm
```

## Reassigning Impostor Scores

```
Algorithm 2: Reassigning Impostor Scores
```

Input: Vector  $\mathbf{s}_{Imp}$ , containing the impostor scores.

Matrix S, where sampled genuine scores are stored (from

Alg. 1) and sampled impostor scores will be stored.

Vector  $\chi$ , containing the labels of each identity

(e.g., "Sheep", "Goat", "Lamb").

 $\mathbf{S}_{Gen}^n$ ,  $\mathbf{S}_{Gen}^m$ , Assigned genuine scores for identities n, m.

Define:  $\delta$ ,  $\epsilon_{Imp}$ : Scaling parameters.

Output: Matrix S populated with genuine and impostor scores.

Step 1: For all combinations of n and m (n = 1, ..., N,

 $m=n+1,\ldots,N$ ), note  $\chi_n$  and  $\chi_m$ .

## Reassigning Impostor Scores

Step 2: Draw an impostor score,  $\phi$  from  $\mathbf{s}_{Imp}$ , within interval  $\mathbf{s}_{rng}$ , where

```
\mathbf{s}_{rng} = (0, min\{max\{\mathbf{S}_{Gen}^n\}, max\{\mathbf{S}_{Gen}^m\}\}), if \chi_n = Sheep or Goat, \chi_m = Sheep or Goat.
\mathbf{s}_{rng} = (0, max\{\mathbf{S}_{Gen}^n\}), if \chi_n = Sheep or Goat, \chi_m = Lamb.
\mathbf{s}_{rng} = (0, max\{\mathbf{S}_{Gen}^m\}), if \chi_n = Lamb, \chi_m = Sheep or Goat.
\mathbf{s}_{rng} = (0, 1), if \chi_n = \chi_m = Lamb.
```

Step 3: If  $\mathbf{s}_{rng}$  is a null set,  $\mathbf{s}_{rng} = (0, 1)$ .

## Reassigning Impostor Scores

```
Step 4a: Draw N_G^2 - 1 scores from \mathbf{s}_{Imp} within \phi \pm \epsilon_{Imp}.
```

Step 4b: If less than  $N_G^2 - 1$  scores can be drawn

set 
$$\epsilon_{Imp} = \frac{\epsilon_{Imp}}{\delta}$$
, and repeat Step 4a.

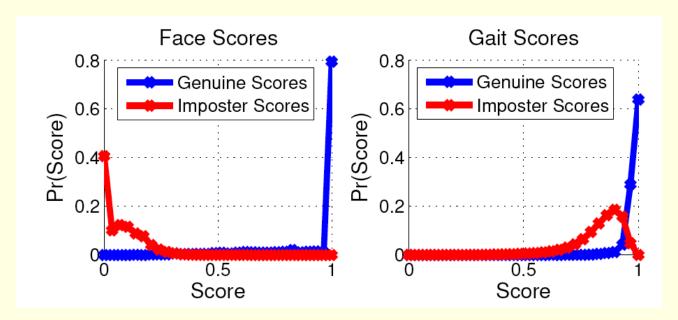
Step 5: Store the sampled impostor scores in S.

return S

 $\setminus \setminus$  end algorithm

#### **Datasets Used**

- Face: WVU Multimodal Dataset
  - 240 subjects, 5 Samples / subject
  - Match scores computed using VeriLook
- Gait: CASIA B dataset
  - 124 subjects, 6 samples / subject
  - Match scores computed using Gait Curves algorithm



#### **Evaluation Criteria**

- ROC data: Area underneath the ROC (AUC)
- CMC data: Weighted Rank-M strategy

#### Generate Virtual Identities

- Generate virtual identities with different input parameters: (% Sheep, % Goats, % Lambs)
- Compute AUC and Rank-M values

Sheep (%)	Goat (%)	Lambs (%)	AUC Face)	Rank-M (Face)		AUC (Gait)	Rank-M (Gait)
100	0	0	0.999	1.0	I	0.980	1.0
82	10	8	0.999	1.0	ı	0.980	0.966
50	26	24	0.999	0.997	I	0.980	0.915
15	10	75	0.999	0.997	i	0.980	0.800
					1		

**Same Aggregate Statistics** 

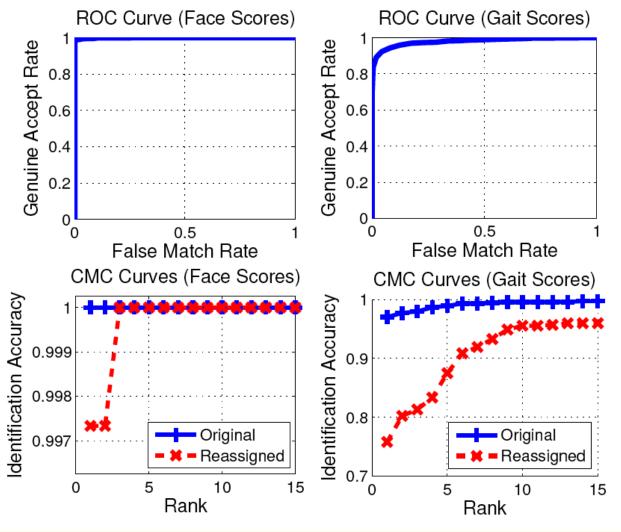
**Different Rank Statistics** 

Note: Increasing the proportion of Goats or Lambs decreases Rank-M performance

#### A Closer Look

- ROC and CMC curves for "Original" and "Reassigned"
- (15% Sheep, 10% Goats, 75% Lambs)

100% to 99.7%



99% to 75%

#### Summary

- It is possible for a single ROC curve to be associated with multiple CMC curves
- The distribution of "Sheep", "Goat", "Lamb" in the target population results in this phenomenon
- Any ROC-CMC prediction model, should account for this variability in user performance
- Soft biometric traits are more likely to exhibit this type of disparity
- Reporting both ROC and CMC curves is recommended
- Note: Closed-set identification

**Project sponsored by ONR** 

## Reading Material

- B. DeCann and A. Ross, "Relating ROC and CMC Curves via the Biometric Menagerie," Proc. of 6th IEEE International Conference on Biometrics: Theory, Applications and Systems (BTAS), (Washington DC, USA), September 2013
- B. Decann and A. Ross, "Can a Poor Verification System be a Good Identification System? A Preliminary Study," Proc. of IEEE International Workshop on Information Forensics and Security (WIFS), (Tenerife, Spain), December 2012