Documentation for ROC Baseline 2016

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Abstract

We present ROC baseline data to support the recommendations in Matey et al [6].

1 Introduction

An ROC curve in the context of biometric identification is a plot of the false non-match rate (FNMR) vs. the false match rate (FMR) with the match criterion as a running parameter. Matey et al [6] recommended that (1) ROC curves be used in papers that make comparisons of biometric algorithms and collection procedures and that such curves include state of the practice baseline curves for comparison with the results of the paper; and (2) organizations with existing baseline data make that data available to researchers in order to enable implementation of recommendation (1). This document and the associated files implement recommendation (2) for face, finger and iris using data and algorithms that were available circa 2013. This document and the associated files will be updated as additional data becomes available.

We request that authors making use of our ROC baseline data cite [6] and the URL for paper and the ROC baseline data, `http://www.nist.gov/itl/iad/ig/rocbaseline.cfm`.

2 Data Sources

This ROC baseline data is from ongoing NIST biometric evaluation efforts; an overview of those efforts can be found at `http://www.nist.gov/itl/biometrics/index.cfm`.

The specific efforts and descriptions of the data and algorithms used here are described in the list below. See table 1 for additional details.

- face: *FRVT 2013* [7] ,
- finger: *PFT II*[1] , and
- iris: *IREX IV*[8].

Although some of these studies reported 1-to-N results; the results here are the result of running the algorithms in 1-to-1 modes or near equivalents. In the case of the IREX IV data, the algorithms were run with parameters set to generate a full candidate list with the match scores for each match. It is possible that some score normalization occurred in this mode, but we do not believe that it significantly changes the ROC data presented here from what we would obtain in a pure 1-to-1 mode.

It is important to note that the performance of all algorithms for all modalities depends on the difficulty of the dataset. It is also important to note that there is no generally accepted method for judging the relative quality/difficulty of datasets across modality and that better data will, in general, give better results. Hence, comparisons of the modalities are, strictly speaking, apples to oranges comparisons. All of the data used in the preparation of these baselines are from operational collections and maybe regarded as examples of what can be achieved in field operations of the types indicated. However, it is certainly possible to collect data of lower quality than is represented here (e.g. mug shots are generally of higher quality than surveillance video). In less challenging environments it is generally possible to collect data of higher quality than in more challenging environments [4] [5] [3].

The datasets used here are sequestered. We plan to provide additional baseline ROC data based on freely accessible datasets.

Table 1: Data Sources

Modality	NIST Report	Dataset Comments
Face	FRVT 2013	Operational data: mug shots
Finger 02: right index 02+07: right and left index	PFT II	Operational data: combination of Azla, DHSS2 Poebva
Iris	IREX IV	Operational data: DoD collection

3 ROC results

The ROC baseline data can be found in table 2 and in the accompanying file ROC_Baseline2016A.txt. Figure 1 presents a plot of that data generated by applying the R [2][9] code reproduced below to that data.

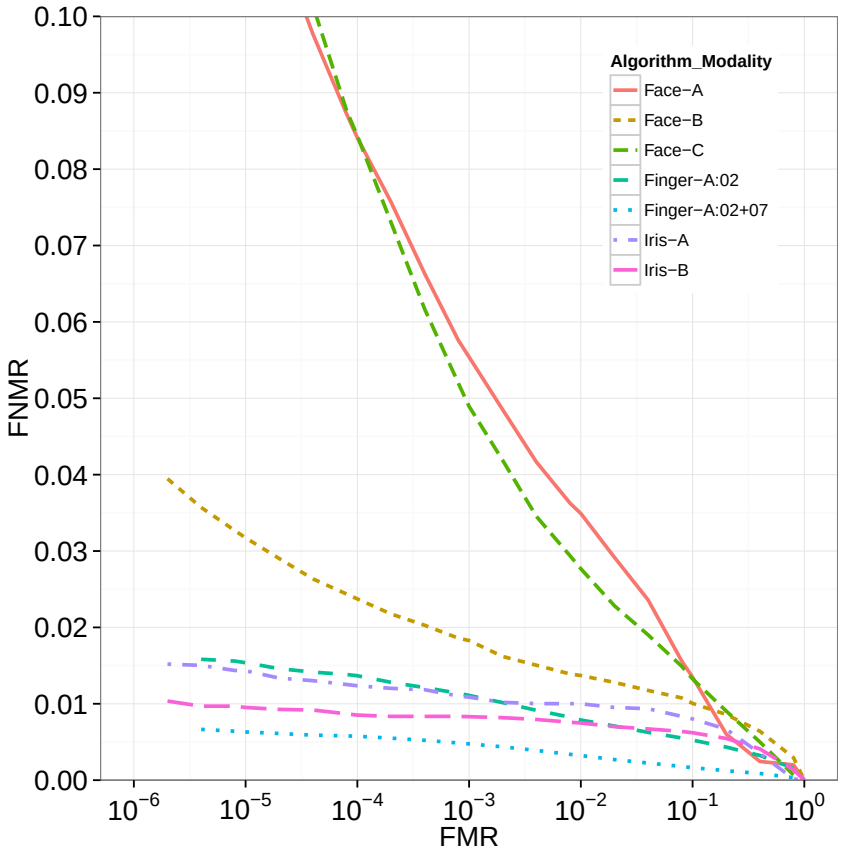

Figure 1: ROC Baselines for face, finger and iris; algorithms circa 2013.

Table 2: ROC baseline data; algorithms circa 2013

FMR	Face-A	Face-B	Face-C	Finger-A:02	Finger-A:02+07	Iris-A	Iris-B
1.00E-06	NA	NA	NA	NA	NA	NA	NA
2.00E-06	0.154	0.039	0.172	NA	NA	0.015	0.010
4.00E-06	0.139	0.036	0.153	0.016	0.007	0.015	0.010
8.00E-06	0.127	0.033	0.136	0.016	0.006	0.014	0.010
1.00E-05	0.123	0.032	0.131	0.015	0.006	0.014	0.010
2.00E-05	0.109	0.029	0.115	0.015	0.006	0.013	0.009
4.00E-05	0.098	0.026	0.101	0.014	0.006	0.013	0.009
8.00E-05	0.087	0.024	0.088	0.014	0.006	0.013	0.009
1.00E-04	0.084	0.024	0.084	0.014	0.006	0.012	0.009
2.00E-04	0.076	0.022	0.073	0.013	0.005	0.012	0.008
4.00E-04	0.066	0.020	0.062	0.012	0.005	0.012	0.008
8.00E-04	0.058	0.019	0.052	0.011	0.005	0.011	0.008
0.001	0.055	0.018	0.049	0.011	0.005	0.011	0.008
0.002	0.048	0.016	0.042	0.010	0.004	0.010	0.008
0.004	0.042	0.015	0.035	0.009	0.004	0.010	0.008
0.008	0.036	0.014	0.029	0.008	0.003	0.010	0.008
0.01	0.035	0.014	0.028	0.008	0.003	0.010	0.007
0.02	0.029	0.013	0.023	0.007	0.003	0.010	0.007
0.04	0.024	0.012	0.019	0.006	0.002	0.009	0.007
0.08	0.016	0.011	0.015	0.006	0.002	0.008	0.006
0.1	0.013	0.010	0.013	0.005	0.002	0.008	0.006
0.2	0.006	0.009	0.009	0.004	0.001	0.007	0.005
0.4	0.002	0.006	0.005	0.003	0.001	0.004	0.004
0.8	0.002	0.003	0.001	0.002	0.000	0.000	0.001
1	0.000	0.000	NA	NA	NA	0.000	0.000

4 R Code to produce ROC figure

```
# ROC-AllModalities.R  20160613
# Generation of ROC (FNMR vs FMR) curve for multiple modalities
# James R. Matey
# NIST
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# ------------------------------------------------------------------------------
# Face data         from Patrick Grother
# Iris data         from George Quinn
# Fingerprint data from Craig Watson and Su Cheng
# ------------------------------------------------------------------------------
# Libraries
library(lattice)
library(ggplot2)
library(scales)
library(reshape2)
# ------------------------------------------------------------------------------
# Setup file paths
# Assume cd to directory containing script and ROCBaselineData.txt is already done
mainDataDirectory <- "./"
outputSubDirectory <- "./Output/"
rocBaselineFile <- "ROCBaselineData.txt"
rocBaselineDataPath <-   unlist(paste(c(mainDataDirectory ,
                         rocBaselineFile), collapse=""))
rocBaselinePlotPath <-   unlist(paste(c(mainDataDirectory , o
                         utputSubDirectory ,
                         "rocBaselinePlot.pdf "), collapse=""))
# ------------------------------------------------------------------------------
# Load data
rocBaselineData <- read.table(rocBaselineDataPath , header=TRUE)

# ------------------------------------------------------------------------------
# Create ROC Curve from rocBaselineData
scientific_10 <- function(x) {
  parse(text=gsub("e", " %*% 10^", scientific_format()(x)))
}

longFormatRocBaselineData <- melt(rocBaselineData , id.vars = "FMR",
                                  variable.name = "Algorithm_Modality",
                                  value.name = "FNMR")
rocPlot <- qplot(FMR, FNMR, data = longFormatRocBaselineData  ,
           geom = "line", linetype=Algorithm_Modality, shape = Algorithm_Modality,
           colour = Algorithm_Modality, size = I(1)) +
    coord_cartesian(ylim=c(0, 0.1)) + scale_y_continuous(breaks=seq(0, 0.1, 0.01))
+
    theme_bw() + theme(legend.position=c(.8, .8)) +
    theme(axis.title.x  = element_text(size=16),
          axis.title.y  = element_text(size=16) ) +
    theme(axis.text.x   = element_text(size=16),
          axis.text.y   = element_text(size=16) ) +
```

```
    scale_x_log10(
        breaks = trans_breaks("log10", function(x) 10^x),
        labels = trans_format("log10", math_format(10^.x))
    )
rocPlot
dev.copy(pdf,rocBaselinePlotPath);
dev.off ();
```

5 Acknowledgments

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References

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