

# Biometrics (CSE 40537/60537)

University of Notre Dame, Fall 2014

## **Assignment 1: Fingerprint recognition**

(Deadline: Friday 9/26/2014, 11:00 AM)

## **1 Introduction**

### **1.1 Important note on biometric data usage**

In each assignment you will use your own biometric samples, collected during practical classes. Your biometric data will be stored by the instructor in the encrypted container, and will be used only for the purpose of this Biometrics course. The data will be permanently deleted after concluding the course.

Using your own biometric data during assignments has many advantages, e.g. you can interact with real biometric systems. However, should you have any doubts related to the data collection or processing, please contact the instructor to work out the alternative solution (e.g. finding appropriate samples in one of the public biometric datasets). Your decision on not using your own biometric data during assignments is fully permissible and it will not influence the grading of your work.

## **2 Software and data distribution**

Due to security reasons, the biometric data and the software will be distributed only during the practical classes, and will not be posted to the webpage.

### **2.1 How to complete the assignments**

1. You will need MATLAB software installed on a Windows machine to complete the assignment. You may use University computers, or download MATLAB from <https://oit.nd.edu/software-downloads> (your netID and the password is required).
2. Read the instructions in Sec. 3 and solve all tasks using the software and biometric data distributed during the class.
3. There is no formal template for providing the answers. Use a tool that you like. I accept:

- a single Word or PDF document incorporating all text answers and the resulting images,
  - an email with the text answers and the resulting images attached as a single zip file,
  - a mixture of the above.
4. Send your answers to `aczajka@nd.edu` by **Friday 9/26/2014, 11:00 AM**
5. Should you have any problems with sending the results, you can bring them personally on the USB flash drive during my office hours (Fitzpatrick 355C), or just before/after the classes.

### 3 Tasks to be solved

1. Your software package contains three folders:
  - `mfiles`: MATLAB scripts prepared by the instructor,
  - `data-raw`: biometric samples collected during class,
  - `data-processed`: processing results (interim and final).

Run MATLAB and go to the `mfiles` folder. Each m-file has a short documentation with calling convention: type the m-file name preceded by `help` command to read this prior using each m-file.

2. Run `BIO_FGP_proc.m`. It will prepare JPG images and minutiae maps. Run `BIO_FGP_proc_results.m` to see the processing results for **one, selected fingerprint image**. What do you see in the resulting images (#2 to #6)?
3. Use `BIO_FGP_singular.m` to localize **singular points** and the **core** on fingerprint images. Select **only one image for each your finger** (i.e. four images in total). You will find the results in `data-processed` folder with `SINGULAR` word added to the name of each selected file. Please attach resulting images to you answer sheet.
4. Provide the Henry's classification for all four images generated in point 3.
5. Use `BIO_FGP_minutiae.m` to look how the minutiae detection software localized the Galton's details for your fingers (type 'auto' as an input parameter). Did the software make any mistakes? If so, what improvements could you propose?
6. Use `BIO_FGP_minutiae.m` to mark minutiae by your own (type 'manual' as an input parameter). Select **one finger** and try to mark all minutiae that you see in **all three images**. Results will be saved in `data-processed` folder as new `.xyt`

and .jpg files with `manual` word added to the name of each selected file. Please attach **only resulting .jpg files** to your answer sheet.

7. Use `BIO_FGP_match.m` to calculate the similarity scores between minutiae maps for the finger selected in point 6. Compare the minutiae maps calculated automatically (you may perform up to three comparisons since you have only three different samples). What is the average matching score? Now, compare the minutiae maps built by your own. What is the average matching score in this case? Who was better: you or the machine? Try to briefly explain why?

8. Use `BIO_FGP_match_all.m` to generate all possible within-class (genuine) and between-class (impostor) scores. Then, use `BIO_FGP_EER.m` to plot the FNMR and FMR curves. What is the EER? How would you interpret the resulting value of EER? Did the algorithm perform well? Would you apply this algorithm in high security scenario? Would you apply this algorithm in scenarios requiring high comfort of use? Please attach the resulting graph `data-processed/EER.jpg` to you answer sheet.