

CS 559 ASSIGNMENT 2

Design and evaluation of Iris Recognition System

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IRIS RECOGNITION:

The iris recognition system consists of an auto-matic segmentation system that is based on Hough Transform. The code used in this is able to localise the ocular iris and pupil region, occluding eyelids and eyelashes and reflections.

- ① The extracted image is then normalised into a rectangular block with constant dimensions.
 - ② Finally, the phase data from 1D Log-Gabor filter was extracted and quantised to four levels to encode the unique pattern of the iris to a bit-wise template.
 - ③ Hamming distance was then employed for classification of iris templates and compared.
- a) Three iris data set were given to us and images taken from same subjects both eyes are stored in same subfolder with right/left eye indications.

Among the data set given we have probes and gallery.

PROBE:

A fresh biometric sample to be recognized is called as probe or query.

GALLERY:-

The set of enrolled identities is called the gallery or watch list.

Here. Database LG2200 2008 are used as gallery

LG4000, LG2200 - used as probes.

In our experiment we have taken 25 cases, and all probes are from both the database given.

b) DESIGN:-

→ We first created the database from the given data set for probes and query.

→ We called the function `createTemplate.m` which creates templates for the image, where noise, segmentation, matching, normalization, encoding templates are created in the diagnostic folder.

Code to load data and get hamming distance - test.m

```

1 - [templatea, maska] = createiristemplate('02463d1916.tiff')
2 - [templateaa, maskaa] = createiristemplate('02463d2896.tiff')
3
4 - [templateb, maskb] = createiristemplate('04233d1706.tiff')
5 - [templatebb, maskbb] = createiristemplate('04233d2627.tiff')
6
7 - [templatec, maskc] = createiristemplate('05033d695.tiff')
8 - [templatecc, maskcc] = createiristemplate('05033d1633.tiff')
9
10 - [templated, maskd] = createiristemplate('04385d1433.tiff')
11 - [templatedd, maskdd] = createiristemplate('04385d2285.tiff')
12
13 - [templatee, maske] = createiristemplate('05450d108.tiff')
14 - [templateee, maskee] = createiristemplate('05450d1043.tiff')
15
16
17 %diagonal elements
18 hdaa = gethammingdistance(templatea, maska, templateaa, maskaa, 0)
19 hdbb = gethammingdistance(templateb, maskb, templatebb, maskbb, 0)
20 hdcc = gethammingdistance(templatec, maskc, templatecc, maskcc, 0)
21 hddd = gethammingdistance(templated, maskd, templatedd, maskdd, 0)
22 hdee = gethammingdistance(templatee, maske, templateee, maskee, 0)
23
24 %other elements
25 hdab = gethammingdistance(templatea, maska, templatebb, maskbb, 0)
26 hdac = gethammingdistance(templatea, maska, templatecc, maskcc, 0)
27 hdad = gethammingdistance(templatea, maska, templatedd, maskdd, 0)

```

script | Ln 39 Col 6

Output:-

```

C:\Users\samru\Documents\MATLAB\iriscode\code
Current Folder
cmc.m
circlecoords.m
canny.m
best_value.m
adjgamma.m
addcircle.m
06266d50.tiff-houghpara.mat
06266d50.tiff
06059d255.tiff-houghpara.mat
06059d255.tiff
05465d111.tiff-houghpara.mat
05465d111.tiff
05463d973.tiff
05463d972.tiff-houghpara.mat
05463d972.tiff
gethammingdistance.m (MATLAB Function)
- returns the Hamming Distance between two iris templates
gethammingdistance(template1, mask1, te...

Command Window
hdee =
    0.3923

hdea =
    0.2843

hdeb =
    0.2692

hdec =
    0.3125

hded =
    0.2500

fx >> new

```

Search diagnostics



	a	b	c	d	e
a	0.200	0.4505	0.4388	0.4113	0.4446
b	0.3253	0.010	0.3596	0.2979	0.3769
c	0.3492	0.2949	0.121	0.3866	0.4269
d	0.3152	0.2550	0.3588	0.2920	0.3923
e	0.2895	0.2692	0.3125	0.2500	0.3333

→ Then we compare the templates of the image by calling the `gethammingdistance-m`.

→ Here Matching is done with hamming distance.

Hamming distance:

It gives the measure of how many bits are same between two bit patterns of the templates. Using the Hamming distance of two bit patterns, a decision can be made as to whether the two patterns were generated from different sources or from the same one.

$$HD = \frac{\text{Sum of disagreeing bits (exclusive OR)}}{N \text{ (total bits)}}$$

$$0 < HD < 1 \quad ; \quad 0.5 - \text{random agreement}$$

0.0 - perfect, but not possible due to noise and other factors

c) → Imposter & Genuine distributions.

The same-subfolder images from the probe and the gallery should give the closest identification value along diagonal. With this the matrix is drawn and distributions are plotted.

		Probe				
		A	B	C	D	E
Gallery	F	<u>0.2</u>	0.45	0.43	0.41	0.41
	G	0.32	<u>0.01</u>	0.35	0.29	0.32
	H	0.34	0.29	<u>0.12</u>	0.37	0.42
	I	0.31	0.25	0.35	<u>0.29</u>	0.39
	J	0.27	0.26	0.31	0.25	<u>0.33</u>

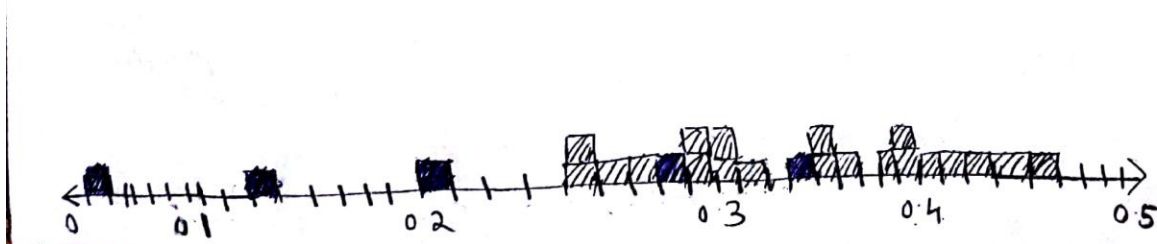
↓

The matrix has the hamming distance calculated for the probe and gallery. Since the diagonal probe (gallery) are from the same subset, the diagonal has less HD (ie) they are the genuine scores-

The genuine & imposter distribution:-

■ - Genuine

▨ → imposter



d) Now to plot the ROC curve we vary the threshold. (E)
and plot the graph between FMR and TMR

$$FMR = \frac{\text{No. of false Match.}}{\text{No. of false identity claims}}$$

No. of false identity claims

$$TMR = 1 - FMR = 1 - \frac{\text{No. of false non-match results}}{\text{No. of True identity claims}}$$

Varying threshold.

① $t = 0.2$

$$FMR = 0$$

$$TMR = 0.6$$

② $t = 0.29$

$$FMR = 0.2$$

$$TMR = 0.2$$

③ $t = 0.18$

$$FMR = 0$$

$$TMR = 0.2$$

④ $t = 0.25$

$$FMR = 0$$

$$TMR = 0.6$$

⑤ $t = 0.32$

$$FMR = 0.4$$

$$TMR = 0.8$$

⑥ $t = 0.4$

$$FMR = 0.75$$

$$TMR = 0$$

⑦ $t = 0.35$

$$FMR = 0.45$$

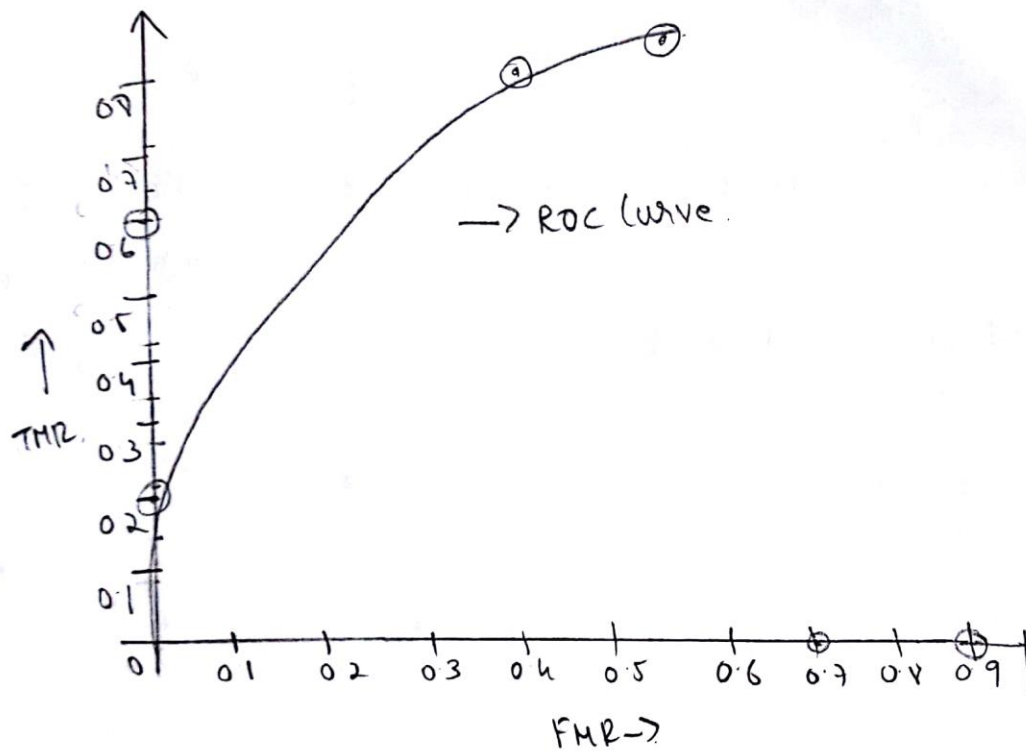
$$TMR = 0.7$$

⑧ $t = 0.45$

$$FMR = 0.9$$

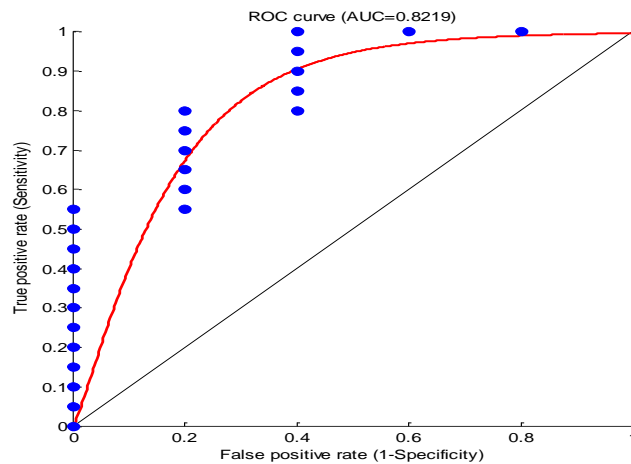
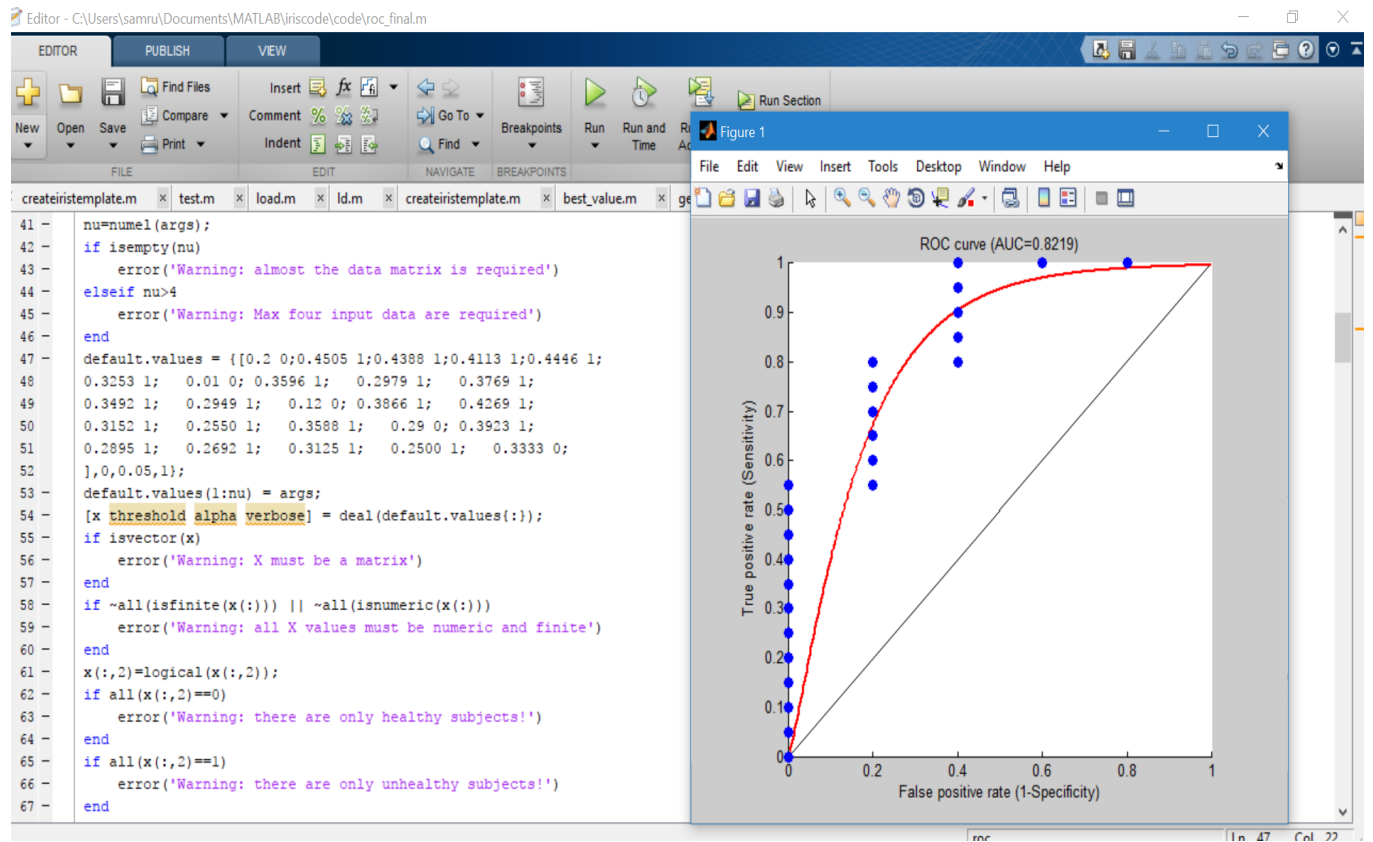
$$TMR = 0$$

(7)



→ We have also coded in matlab to find the ROC curve

→ ROC curve thus found is pasted in screenshot folder.



e) cmc curve.

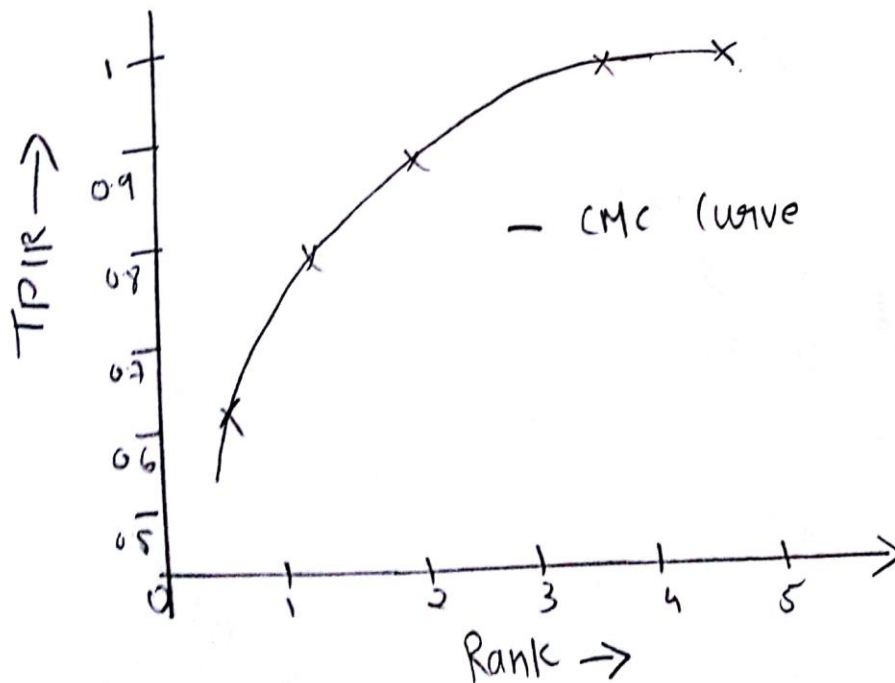
→ In cmc curve each biometric sample is compared to all the gallery samples.

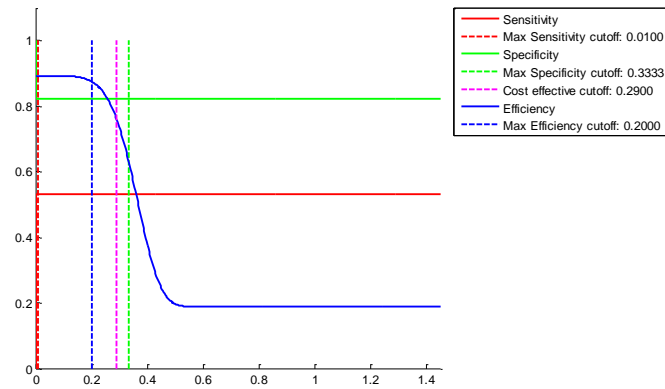
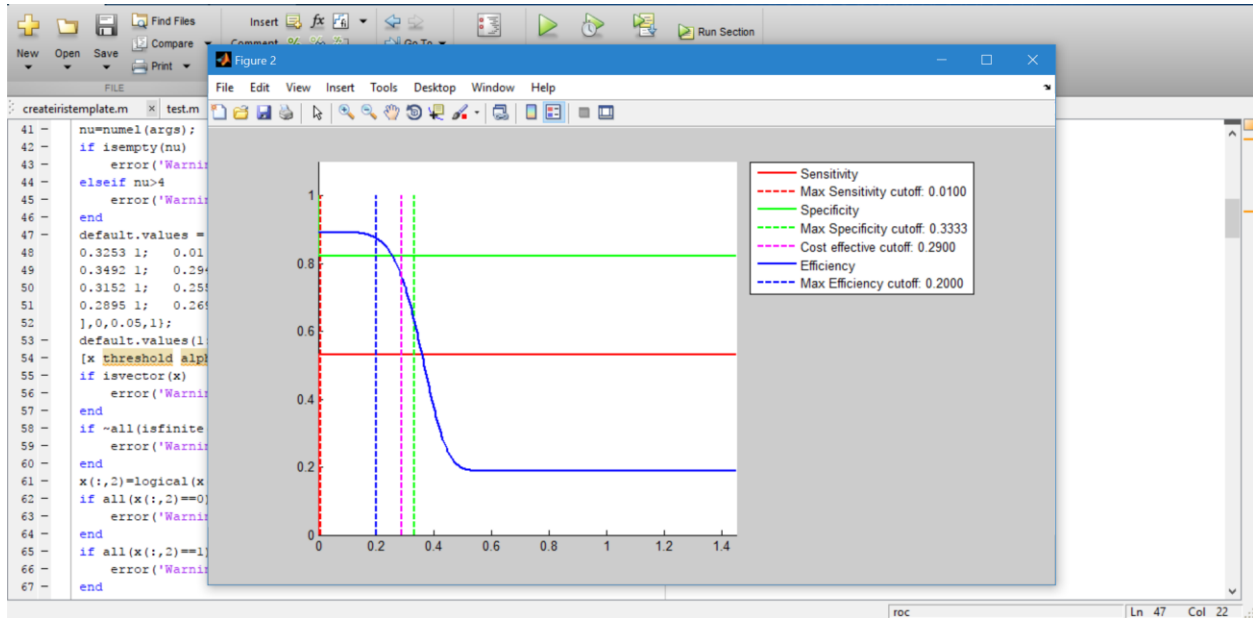
→ The resulting scores are sorted and ranked.

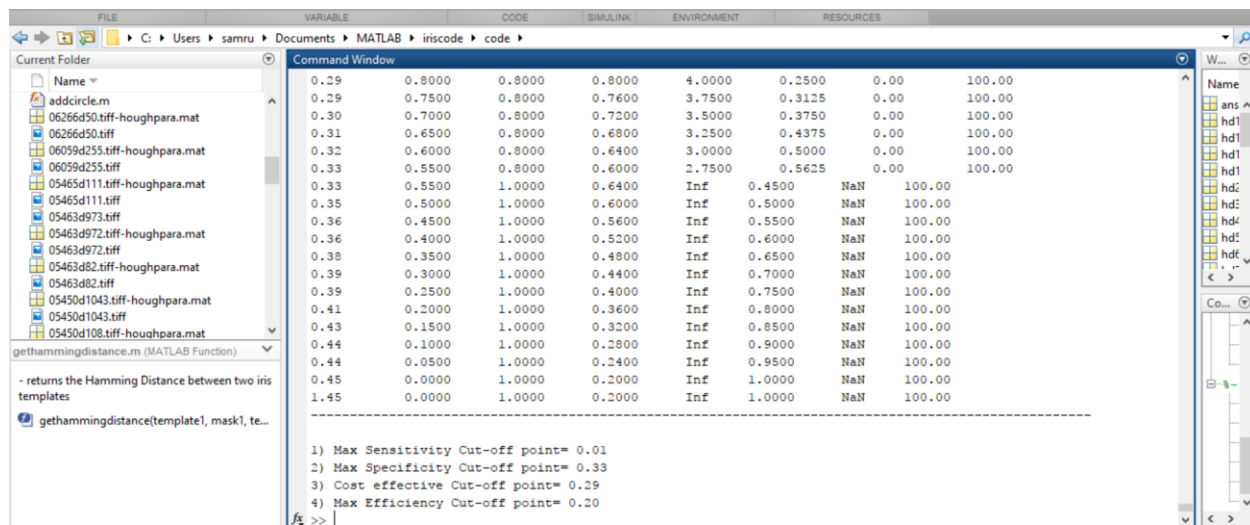
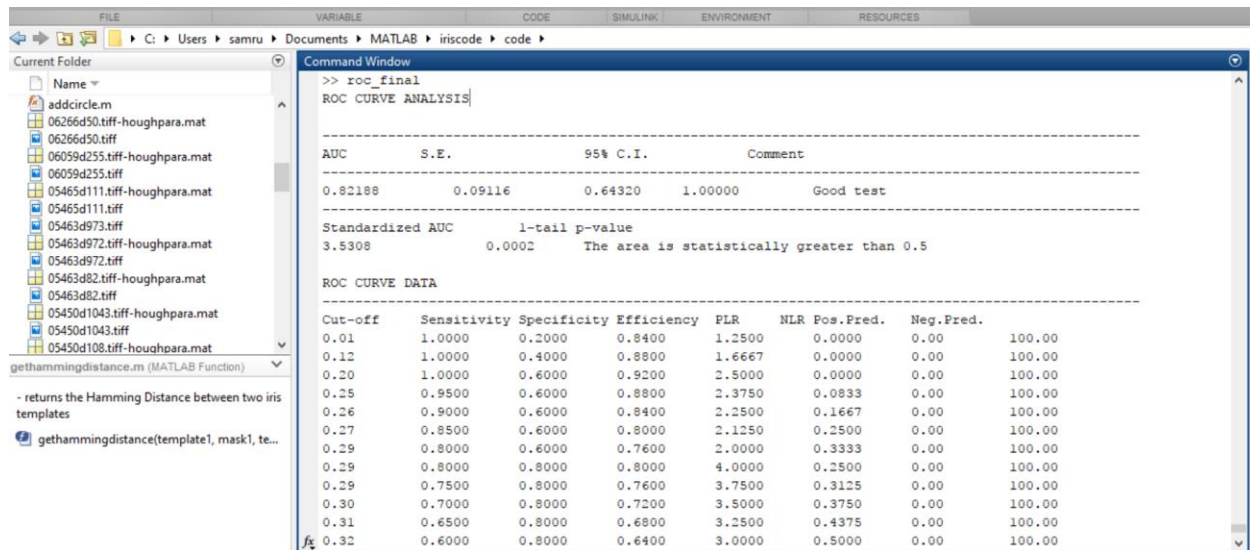
→ TPIR: Probability of observing the correct identity with top k ranks.

→ R_i is the rank number of the observation x_i and c indicates the serial number in the range of ascending data.

$$P_c = R_i / (CN + 1)$$







F) CONCLUSION AND FINDINGS

- Hence the data set are loaded as probe and gallery, and their templates were found and hamming distance was calculated for Matching
- From the above experiment, the test cases (25) showed good ROC and CMC curves
- It also has good AUC (Area of Under curve)
 $AUC = 0.82188$.
- And the standard. area of the error which is 0.09 which is a really good system
- Confidence interval ~~0.6820~~ = 0.64320, which makes it a good test
- Also the sensitivity, specificity and efficiency, PLR, NLR is calculated by varying the thresholds

NOTE : All of the above data are attached ~~in~~ as Screenshot ~~folder~~.