Question 3: Multimodal operation

The maximum marks for Question 3 is 4

One kind of multibiometric system is where two diffrent characteristics are used to verify an identity. Each charcteristic is often called a *mode*. Consider that a bimodal system using fingerprint and iris is to be deployed in a user verification process to *access government social security services*.

Let us construct this simulated bimodal system with fingerprint and iris.

Code | Start Over | Run Code

```
#copy the mated and non mated score distributions of the fingerprint system here
mated_scores_fp<-round(rnorm(20, mean=304.7143, sd=70.00948))
nonmated_scores_fp<-round(rnorm(20, mean=171.1143, sd=59.76019))

comparisons_col1<-c(rep("27_7_1", times =7), rep("47_7_1", times =7), rep("57_5_1", times=7),
rep("12_8_1", times=7), rep("76_7_1", times=7) )
comparisons_col2<-c("27_7_2", "27_7_3", "27_7_4", "27_7_5", "27_7_6", "27_7_7", "27_7_8",
"47_7_2", "47_7_3", "47_7_4", "47_7_5", "47_7_6", "47_7_7", "47_7_8", "57_5_2", "57_5_3",
"57_5_4", "57_5_5", "57_5_6", "57_5_7", "57_5_8", "12_8_2", "12_8_3", "12_8_4", "12_8_5","12_8_6"
"12_8_8","76_7_2","76_7_3","76_7_4","76_7_5","76_7_6","76_7_7","76_7_8")
comparisons_score<-c(249, 279, 223,352,263,285,190, 288, 302, 264,289,470,206,334,382,
259, 314,417,263,272,351, 386, 413, 363, 333, 379, 387, 376, 279, 287, 250, 319, 264, 196, 181 )

mated_database<-as.data.frame(cbind(comparisons_col1,comparisons_col2,comparisons_score))
mated_database

comparisons_col1<- c(rep("27_7_1", times =7), rep("47_7_1", times =7), rep("57_5_1", times=7),
rep("12_8_1", times=7), rep("76_7_1", times=7) )
comparisons_col2<- c("27_6_1" , "27_6_2", "27_6_3","27_6_4","27_6_5","27_6_6", "27_6_7","47_6_1","4
, "47_6_3","47_6_4","47_6_5","47_6_6","47_6_7","57_3_1","57_3_2","57_3_3","57_3_4","57_3_5","57_
"12_3_1", "12_3_2", "12_3_3" ,"12_3_4","12_3_5","12_3_6","12_3_7","76_8_1","76_8_2","76_8_3","76_8_
"76_8_5","76_8_6","76_8_7")
comparisons_score<-c(161, 131, 162,211,262,165,253, 121,64,148,70,277,216,250,139,201,162,248,16

nonmated_database<-as.data.frame(cbind(comparisons_col1,comparisons_col2,comparisons_score))
nonmated_database

#copy the mated and non mated score distributions of the iris system here



comparisons_col1<-c(rep("0001_L_000", times =4), rep("0001_R_000", times =4), rep("0002_L_000",
rep("0002_R_000", times=2), rep("0004_L_000", times=2), rep("0004_R_000", times=2), rep("0007_L_0
rep("0007_R_000", times=1), rep("0008_L_000", times=1), rep("0008_R_000", times=1) )
comparisons_col2<-c("0001_L_001", "0001_L_002", "0001_L_003", "0001_L_004", "0001_R_001", "0001_
"0001_R_003", "0001_R_004", "0002_L_001", "0002_L_002", "0002_R_001", "0002_R_002", "0004_L_001",
"0004_R_002", "0007_L_001", "0007_R_001", "0008_L_001", "0008_R_001")
comparisons_score<-c(791, 566, 746, 618, 589, 541, 612, 638, 482, 522, 693, 737, 503, 551, 443,

mated_scores_iris<-round(rnorm(20, mean= mean(comparisons_score), sd=50))
nonmated_scores_iris<-round(rnorm(20, mean=300, sd=50))


iris_mated_dataframe<-as.data.frame(cbind(comparisons_col1,comparisons_col2,comparisons_score))
iris_mated_dataframe
```

comparisons_col1 <chr>	comparisons_col2 <chr>	comparisons_score <chr>
27_7_1	27_7_2	249
27_7_1	27_7_3	279
27_7_1	27_7_4	223
27_7_1	27_7_5	352
27_7_1	27_7_6	263
27_7_1	27_7_7	285
27_7_1	27_7_8	190
47_7_1	47_7_2	288
47_7_1	47_7_3	302
47_7_1	47_7_4	264

1-10 of 35 rows | Previous 1 2 3 4 Next

comparisons_col1 <chr>	comparisons_col2 <chr>	comparisons_score <chr>
27_7_1	27_6_1	161
27_7_1	27_6_2	131
27_7_1	27_6_3	162
27_7_1	27_6_4	211
27_7_1	27_6_5	262
27_7_1	27_6_6	165
27_7_1	27_6_7	253
47_7_1	47_6_1	121
47_7_1	47_6_2	64
47_7_1	47_6_3	148

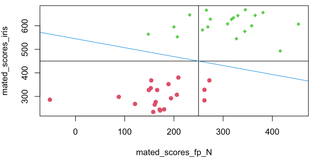
1-10 of 35 rows | Previous 1 2 3 4 Next

comparisons_col1 <chr>	comparisons_col2 <chr>	comparisons_score <chr>
0001_L_000	0001_L_001	791
0001_L_000	0001_L_002	566
0001_L_000	0001_L_003	746
0001_L_000	0001_L_004	618
0001_R_000	0001_R_001	589
0001_R_000	0001_R_002	541
0001_R_000	0001_R_003	612
0001_R_000	0001_R_004	638
0002_L_000	0002_L_001	482
0002_L_000	0002_L_002	522

1-10 of 20 rows | Previous 1 2 Next

comparisons_col1 <chr>	comparisons_col2 <chr>	comparisons_score <chr>
0001_L_000	0011_R_002	227
0001_L_000	0011_L_001	356
0001_L_000	0010_R_002	302
0001_L_000	0010_R_001	316
0001_R_000	0010_R_000	174
0001_R_000	0010_L_002	276
0001_R_000	0010_L_001	285
0001_R_000	0010_L_000	315
0002_L_000	0009_R_001	260
0002_L_000	0009_R_000	204

1-10 of 20 rows | Previous 1 2 Next



Decision Fusion

Decision Fusion is the process of combining the final verification decision by combining the outcomes of the two comparators (Fingerprint and Iris). The decisions are usually combined using a logical AND or OR operation.

Observe from the plot that the operating thresholds can break the space where the scores lie into 4 quadrants.

Can you identify the region where the fingerprint scores will cause a positive decision?

Can you identify the region where the iris scores will cause a positive decision?

These quadrants can be used to design a decision-fused system.

3a. If you were to design a decision fused comparator for the bimodal biometric system to access government services, explain the decision rule you would use to accept a user as genuine. Justify your choice.(1 mark)

3a. The decision rule for mated scores would need to be above the threshold for both iris and fingerprint (top right quadrant). Since the bimodal biometric system is used to access goevernment services it is preferable the system is of utmost security.

3b. False Match Rate = 0%, Genuine Acceptance Rate = (16/20)*100 = 80%. As there are zero non-mated pairs going into accepted quadrant therefore there is zero false matches. For the genuine users three of the 20 did not meet the threshold requirements for both iris and fingerprint therefore giving a genuine acceptance rate of 80%.

3b. What is the False Match Rate and Genuine Acceptance Rate of this data with your decision rule? Explain how you got your answers (1 mark)

Score Fusion

Score Fusion is the process of finding a linear combination of scores that would best separate the mated and non mated scores.

On the bimodal plot, draw a line that separates the mated scores from the non mated scores in the best way possible. This would form your score-fused threshold. (Note: the command `abline()` can be used to draw a line with your chosen slope and y-intercept on your plot)

3c. Write in the textbox below, what would the equation of that line be?(1 mark)

y = -0.38x + 545

3d. Based on your score-fused threshold what would be the False Match Rate and Genuine Acceptance Rate for the data? Explain how you got your answer.(1 mark)

False Match Rate = 0%, Genuine Acceptance Rate = 100%.
The area above the line y = -0.38x + 545 is the accepting region for the score fusion. All the mated pairs are above this line and all the non mated are below therefore giving 0% false match and 100% Genuine acceptance rate.