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CS286

Homework 2

Answer 8.1

a) Say we have 10 match scores (M = 10) and we use 5-fold validation for training. In the worst case, all the match scores will be part of a single fold. In this case, during training, for n-1 (4 in this case) fold will have no match scores as all the match scores are part of the training phase. In the last fold, the training phase will have no match score but, the test phase will generate 10 match scores. Thus, overall, we get exactly 10 (M) match scores.
This can be proved for all the other combinations of the fold.

b) N nomatch scores are computed. Similar to the above problem.

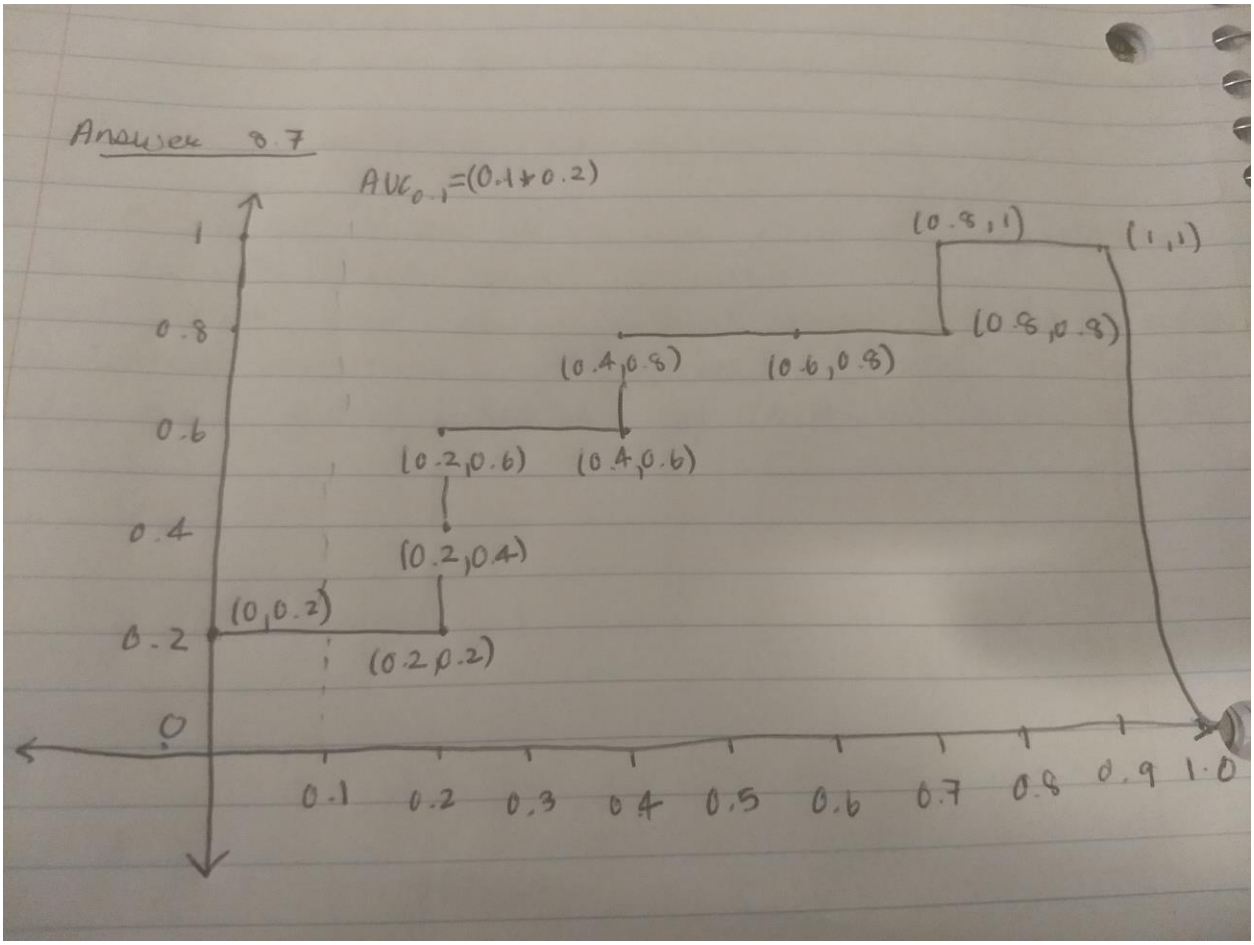
c) For 5-fold validation, the variance in the data would be less and the data will have more bias. The time required to train the model will be less than a 5-fold validation.
For 10-fold validation, the variance would be high while the bias in the dataset will be lower. But, the computation will take higher time than a 5-fold validation.

Answer 8.6:

Accuracy = (TP + FN) / (P + N)
= (TP + FN)/ (TP + FN + TN + FP)
= (98 + 8500) / (98 + 2 + 8500 + 1500)
= 8598/ 10100 = 85.12%

Balanced Accuracy = ½((TP/P) + (TN/N))
= 91.5%

Answer 8.7:



Answer 8.10:

It is given that 1 out of 1,000 is expected to be malign.
Total malign: 2,00,000 / 1,000 = 200
Total benign: 2,00,000 – 200 = 1,99,800
Total malign samples actually classified as malign = TPR * Total Malign = 0.95 * 200 = 190
Total malign samples classified as benign = 200 – 190 = 10
Total benign samples classified as malign = FPR * Total benign = 0.01 * 1,99,800 = 1,998
Total benign samples classified as benign = 1,99,800 – 1,998 = 1,97,612

a) fraction of benign = 1,97, 612 / (1,97,612 + 10) = 197612/ 197622

b) fraction of malign = 190 / (1998 + 190) = 190 / 2188

c) If we change the threshold to decrease the False Positive Rate, we are eventually increasing the false negative rate. Our model would then start leaving out samples that are actually malign. Thus, we need to find a balance of threshold so that minimum number of benign

samples are detected as malign. After this, we can apply secondary tests on these samples to actually see if they are malign.