Approach Advantages Disadvantages Assumptions In this particular example. The dis advantages of lising Naïve Bayes The primary It is sulfally be non the advantages of using the assumptions that are Nuive Bayés model would be I general made with the waive essentially that it is "baye's model are ble features versi to simple compared to the that the amplexity is greatly that the leatures ould he are independent of Bayosion Network model. more specified reduced in this example. Since there is not as much when selected each other. (This is equivolent to being an omputation needed and your midel For the <u>email</u> example, we would ossume that under (Heat model). would not be overfithed. note of inputs relate to each other The disadvantages of the The advantage of the Bayesian The assumption that Bayesian retwork would be Networks Bayosion Network would is mule w/ the nayesion Nelwones that it is amputationally Bayesian Network he that it is a complete would be more expensive and concul overfit the model. enitable ble model is that model. You could also detecting on amail or spam would mean the features are answer prohabalistic queries. that you would need - Being both over lit and advantage. departing on each to connect features What this mean is that in together. For instance, you green, we would be able the sentina structure other. With and to the example, With and to team to the example, this means to dependent on each other. and metadata of the to connect features together. email could be interpaneded

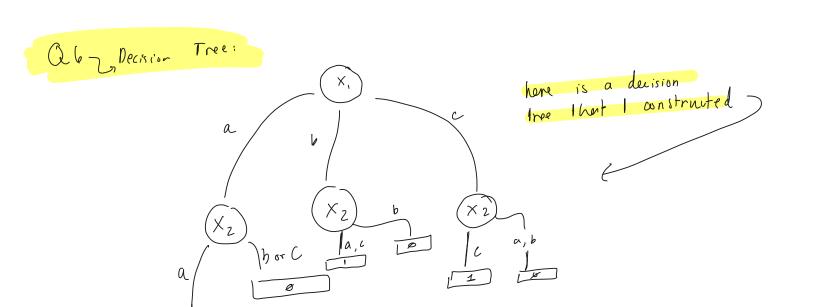
Question 5:  Test (feature)  X. > Positive  X. Negalive	Hos FW (1shel C1) Ø. 8	Healthy (label (2) 8.1 0.9	P(Heolity) = 0.2  P(Flu) = 1 - P(  P(Flu)	.5 Healthy) = 1-0.25 ) = 0.75
Trest Results )				
Build a M	aine Bay	e's classif	ier using the	L Discriminant ent is healthy

Build a naine Baye's classifier using the Discriminant Function. Can this classifier product if a patient is healthy function. Can this classifier product if a patient is healthy or nut-healthy based on the fest results?

Or nut-healthy based on the fest result indicate will high confidence (eg. can a positive test result indicate will high confidence that a patient has the flu?)

Then, we handle the regative case:

$$P(flu \mid x_1, x_2) \longrightarrow P(flu) \cdot \prod_{i=1}^{n} P(x_i \mid flu) \cdot P(x_2 \mid flu) \longrightarrow P(x_2 \mid flu)$$



Explanation:

First, we start with the fact that X, Can fake any of

the values, a, b, or C. After it takes A, B, or C,

the values, a, b, or C. After it takes A, B, or C,

then, we go into the X2 made when we go

then, we go into the x2 mide when we go

then, we go into the into either I

mto Xz, then we go alepending on certain values.

or & depending on certain values.

Nov, we calculate the entry of our 'Y' values We have a total of 12 y-volves. 6 can be - 10° 6 can go to --> 1'

Thus, the 
$$P(Y=0)=0.5$$
]
and, the probability of  $P(Y=1)=0.5$ ]

$$H(\gamma=\emptyset) = -\left(\emptyset.5 \times \log_2(\emptyset.5) + \emptyset.5 \log_2(\emptyset.5)\right)$$

$$H(\gamma=\emptyset) = -\left(0.5 \times \log_2(\emptyset.5) + 0.5 \log_2(\emptyset.5)\right)$$
this value is ho

this value is both for when the output is Ø and when the output is 1

Now, we calculate the values for entropy for the first feature X.

X, will work in the following way.

we can get any of the 2 values, a, b, or C.

We calculate the first  $p(a|a) = \frac{2}{4}$ ,  $p(1|a) = \frac{2}{4}$ 

value b:  $p(0|b) = \frac{0}{2}, p(1|b) = \frac{2}{2}$ 

Now, we use the Entropy formula

for each of these, and we see what we will get.

Entropy for values of 
$$X_i$$
:

$$H = \text{this is our entropy}$$

$$H(y|_{X_i} = a) = 1 \quad H(y|_{X_i} = c) = 1$$

$$H(y|_{X_i} = b) = 0, \quad H(y|_{X_i} = c) = 1$$

$$H(y|_{X_i} = b) = 0, \quad H(y|_{X_i} = c) = 1$$

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$$\lim_{k \to \infty} \sup_{x \to c} \sup_{$$

H(
$$y | x_1 = 0$$
) = 0.81, H( $y | y_1 = b$ ) = 0,  
H( $y | x_2 = 0$ ) = 0.81, H( $y | y_1 = b$ ) = 0,  
H( $y | x_1 = 0$ ) = 0.81, H( $y | y_1 = b$ ) = 0.71:

Now, we calculate the IG for both X, and Xc.

$$16(x_1) = H(y) - H(y|x_1) = 1.0 - \frac{2}{3}$$

$$16(x_2) = H(y) - H(y|x_2) = 1.0 - 0.54$$

$$16(x_2) = H(y) - H(y|x_2) = 1.0 - 0.54$$

What this means is that the feature X2 would be selected first.

First, we do something the pisterior called calculating the pisterior probabilities.

$$p(spam) = \frac{2}{5} (z spam files out of 5 total files).$$

Now, we calculate the words that appear in the spam emails (their prohabilities)

$$\rho\left(\rho_{r}:e\mid spam\right): \frac{2}{2} \rightarrow 1$$

The values for the probability

Thus, File G would he classified

as spown.