

INTRODUCTION TO ARTIFICIAL INTELLIGENCE

EXERCISE 7

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Introduction :

In this report, we show our work on Bayesian Modelling to predict the disease given the symptoms. We train our model with test data, and we evaluate it on test data.

Training :

The Bayes Theorem states:

$$P(A|B) = \frac{P(A) \cdot P(B|A)}{P(B)}$$

In our case we want to determine the disease given the symptoms, so A corresponds to the disease, and B corresponds to the set of the symptoms. In order to do that, we must calculate the probabilities of each disease - $P(A)$, the probability of each symptom - $P(B)$, and the conditional probabilities of each symptom - $P(B|A)$. Using Bayes' rule, we can incorporate the prior probability to calculate the actual probability that the person has a disease given a the symptoms and its presence in the other patient.

The above probabilities can be computed from the test data.

Testing:

For each set of symptoms, we compute the probabilities $P(A | \cap B_i)$, for each disease. To do

that, we treat symptoms, as if they are independent. That means that $P(\cap B_i) = \prod P(B_i)$.

After that, we predict the disease with 2 methods.

- Method 1: We predict that the disease is the one with the highest probability. In this case, our model will return the same disease for the same symptoms. In a larger data set to test this model would have more inaccuracies, than method 2, analysed below.
- Method 2. We predicted disease is selected randomly, with the distinct probabilities that were previously calculated. This way, our model won't necessarily return the same disease for the same set of symptoms. For example, if two diseases have similar symptoms, then if we want to predict the disease from those symptoms then the model will sometimes return the first, and sometimes the second disease.

Results:

The **accuracy** of the model with **method 1** is 95.12%, and with **method 2** is 95.12% - 100%. This happens because, as explained before, some of the diseases have similar symptoms, and thus the model may sometimes confuse them (The probabilities are really close and their difference is almost negligible in some cases so it is more correct to not just ignore the

second most possible disease). For example, the first method always gets wrong the Hepatitis D - it predicts that it is Hepatitis E which has very similar symptoms.

We also calculate **the mean expected disease probability** (the mean of the probabilities of the correct diseases) as a measure of **confidence**. We find it equal to 97.34%, which means our model is very confident most of the time, for the most diseases.

In addition, we calculate the **average square loss**(he loss is the mean overseen data of the squared differences between true and predicted values, or writing it as a formula.), which is 1.45%.

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Prediction accuracy using method 1: 0.9512195121951219
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Prediction accuracy using method 2: 0.975609756097561
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Mean square loss: 0.014533354593913616
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Mean expected disease probability (confidence measure): 0.9733764349547425
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Notes:

The testing data set, as well as the training data set, is small, and thus the calculated metrics may be a little misleading.