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CS 109

Section #9
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Section Solution 9: Final Review

Based on the work of many CS109 instructors and course staff members.

Welcome to the last 109 section! Thanks for sticking with us all quarter! The handout this week touches on various topics from the last three weeks that haven't yet been exercised in a section handout.

1. **Naïve Bayes (courtesy of David Varodayan and Lisa Yan)**

   Suppose we observe two discrete input variables X_1 and X_2 and want to predict a single binary output variable Y (which can have values 0 or 1). We know that the functional forms for the input variables are $(X_1|Y=0) \sim \text{Poi}(\lambda_0)$, $(X_1|Y=1) \sim \text{Poi}(\lambda_1)$, $(X_2|Y=0) \sim \text{Ber}(p_0)$, and $(X_2|Y=1) \sim \text{Ber}(p_1)$, but we don't know the optimal values of the parameters. We are, however, given a dataset of 9 training instances (shown at right.)

X_1	X_2	Y	X_1	X_2	Y
1	1	**0**	3	1	**1**
3	0	**0**	5	0	**1**
7	1	**0**	5	1	**1**
9	0	**0**	5	1	**1**
			7	1	**1**

   a. Use Maximum Likelihood Estimation to estimate the parameters λ_0, p_0, λ_1, and p_1.

$$\lambda_0 = \frac{1}{4}(1+3+7+9) = \frac{20}{4} = 5 \qquad p_0 = \frac{1}{4}(1+0+1+0) = \frac{1}{2}$$
$$\lambda_1 = \frac{1}{5}(3+5+5+5+7) = \frac{25}{5} = 5 \qquad p_1 = \frac{1}{5}(1+0+1+1+1) = \frac{4}{5}$$

   b. Use Maximum Likelihood Estimation to estimate the parameter p_y for $Y \sim Ber(p_y)$.

$$P(Y=1) = 5/9.$$

   c. You observe the following testing instance: $(X_1, X_2) = (2, 0)$. Using the Naïve Bayes assumption, predict the output Y for the testing instance. For this problem, showing how you computed your prediction is worth more points than the final answer.

We predict $Y = 0$ if the following Naïve Bayes inequality holds:

$$P(Y=1)P(X_1=2|Y=1)P(X_2=0|Y=1) \overset{?}{<} P(Y=0)P(X_1=2|Y=0)P(X_2=0|Y=0)$$

$$\frac{5}{9}\left(\frac{\lambda_1^2}{2!}e^{-\lambda_1}\right)\left(1-\frac{4}{5}\right) \overset{?}{<} \frac{4}{9}\left(\frac{\lambda_0^2}{2!}e^{-\lambda_0}\right)\left(1-\frac{1}{2}\right)$$

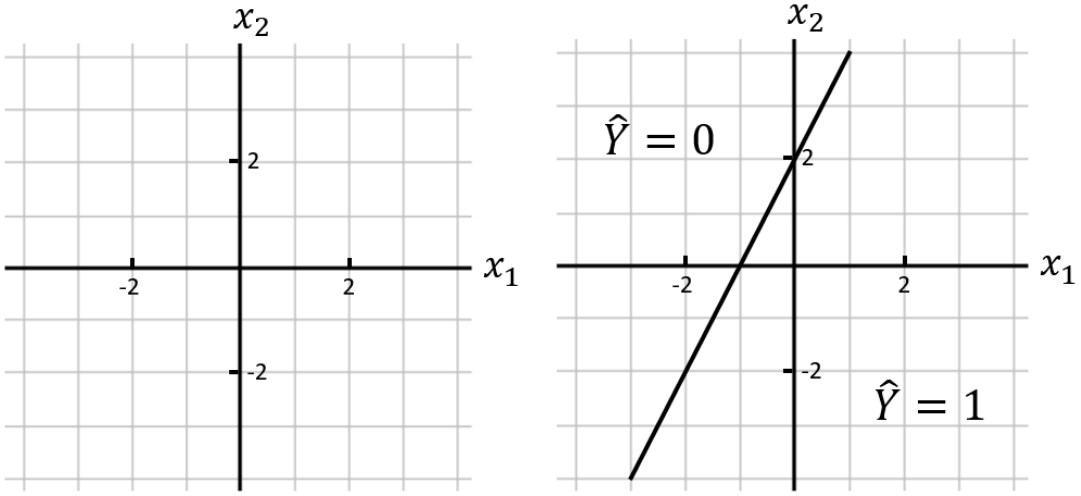
$$\frac{5}{9}\left(\frac{5^2}{2!}e^{-5}\right)\frac{1}{5} \overset{?}{<} \frac{4}{9}\left(\frac{5^2}{2!}e^{-5}\right)\frac{1}{2}$$

$$\frac{5}{9}\cdot\frac{1}{5} \overset{?}{<} \frac{4}{9}\cdot\frac{1}{2}$$

$$\frac{1}{9} < \frac{2}{9}$$

Since the last inequality is true, that means the first inequality was true, so we predict $Y = 0$.

2. **Logistic regression (courtesy of David Varodayan)**



The two parts of this problem are unrelated.

a. **Prediction.** Suppose you have trained a logistic regression classifier that accepts as input a data point (x_1, x_2) and predicts a class label $\hat{Y}$. The parameters of the model are $(\theta_0, \theta_1, \theta_2) = (2, 2, -1)$. On the axes, draw the decision boundary $\theta^T\mathbf{x} = 0$ and clearly mark which side of the boundary predicts $\hat{Y} = 0$ and which side predicts $\hat{Y} = 1$.

$\theta^T\mathbf{x}$ can be expanded as $2 + 2x_1 - x_2 = 0$ because $x_0 = 1$ by definition. The prediction is 1 when $\theta^T\mathbf{x} > 0$. For example, the origin $(x_1, x_2) = (0, 0)$ yields $\theta^T\mathbf{x} = 2$, which gives us the prediction $\hat{Y} = 1$.

See the graph above, to the right of the original.

b. **Training.** The logistic regression parameter update equation is

$$\theta_j^{\text{new}} = \theta_j^{\text{old}} + \eta \sum_{i=1}^{n} \left[y^{(i)} - \sigma\left(\theta^{\text{old}^T} \mathbf{x}^{(i)}\right) \right] x_j^{(i)}$$

Your training set consists of two data points $\left(x_1^{(1)}, y^{(1)}\right) = (1, 1)$ and $\left(x_1^{(2)}, y^{(2)}\right) = (-1, 0)$. Given $\left(\theta_0^{\text{old}}, \theta_1^{\text{old}}\right) = (0, 0)$ and $\eta = 0.1$, find $\left(\theta_0^{\text{new}}, \theta_1^{\text{new}}\right)$.

First notice that $\left(\theta_0^{\text{old}}, \theta_1^{\text{old}}\right) = (0, 0)$ implies that $\sigma\left(\theta^{\text{old}^T} \mathbf{x}^{(i)}\right) = \sigma(0) = 0.5$. Therefore,

$$\begin{aligned}
\theta_0^{\text{new}} &= 0 + 0.1\left([1 - 0.5]\,(1) + [0 - 0.5]\,(1)\right) \qquad \text{since } x_0^{(i)} = 1 \text{ by definition} \\
&= 0 + 0.1(0.5 - 0.5) = 0 \\
\theta_1^{\text{new}} &= 0 + 0.1\left([1 - 0.5]\,(1) + [0 - 0.5]\,(-1)\right) \\
&= 0 + 0.1(0.5 + 0.5) = 0.1
\end{aligned}$$

3. **Continuous Joint Distributions (courtesy of Oishi Banerjee)**

a. Let X, Y, and Z be independent Normal variables with means of $\mu_X = 4$, $\mu_Y = 5$, and $\mu_Z = 6$ and variances $\sigma_X^2 = 16$, $\sigma_Y^2 = 25$, and $\sigma_Z^2 = 36$. Let $A = X + Y$ and $B = Y + Z$. It can be shown that the joint distribution (A, B) is Bivariate Normal. What are the parameters of the joint distribution (A, B)?

$$(A, B) \sim N(\mu, \Sigma), \mu = \begin{bmatrix} \mu_X + \mu_Y \\ \mu_Y + \mu_Z \end{bmatrix}, \Sigma = \begin{bmatrix} Var(A) & Cov(A, B) \\ Cov(A, B) & Var(B) \end{bmatrix}$$

Now, $Var(A) = Var(X + Y)$, and because X and Y are independent, $Var(A) = Var(X + Y) = \sigma_X^2 + \sigma_Y^2$. Similarly, $Var(B) = Var(Y + Z) = \sigma_Y^2 + \sigma_Z^2$. Also, $Cov(A, B) = Cov(X + Y, Y + Z)$, but because X, Y, and Z are independent, $Cov(A, B) = Cov(X + Y, Y + Z) = Cov(Y, Y) = \sigma_Y^2$. Therefore,

$$\mu = \begin{bmatrix} \mu_X + \mu_Y \\ \mu_Y + \mu_Z \end{bmatrix} = \begin{bmatrix} 9 \\ 11 \end{bmatrix}$$
$$\Sigma = \begin{bmatrix} \sigma_X^2 + \sigma_Y^2 & \sigma_Y^2 \\ \sigma_Y^2 & \sigma_Y^2 + \sigma_Z^2 \end{bmatrix} = \begin{bmatrix} 41 & 25 \\ 25 & 61 \end{bmatrix}$$

b. Suppose hundreds of thousands (that is, a sufficiently large number) of student scores on a 150-question exam are distributed according to the following random variable:

$$R = \sum_{i=1}^{50} M_i + 0.5 \sum_{j=1}^{100} W_j \tag{1}$$

Each of the M_i are independent and identically distributed (IID) Beta random variables—yes, the questions are scored on a continuous scale from 0 to 1—and the W_j are separate IID Beta random variables, where all W_j are independent of all M_i. The Beta parameters are $\alpha_M = 10$, $\beta_M = 2$, $\alpha_W = 8$, and $\beta_W = 4$. If we sample 100 student scores $R_1, \ldots, R_n$ IID according to the distribution of R above, what is the distribution of the sample mean $\overline{R}$?

$$\begin{aligned} E[M_i] &= \tfrac{\alpha_M}{\alpha_M+\beta_M} = 0.83333 \\ E[W_i] &= \tfrac{\alpha_W}{\alpha_W+\beta_W} = 0.66667 \\ Var(M_i) &= \tfrac{\alpha_M\beta_M}{(\alpha_M+\beta_M)^2(\alpha_M+\beta_M+1)} = 0.01068 \\ Var(W_i) &= \tfrac{\alpha_W\beta_W}{(\alpha_W+\beta_W)^2(\alpha_W+\beta_W+1)} = 0.01709 \end{aligned}$$

We can compute R's expectation using linearity of expectation. Because R is a sum of independent RVs, we can compute R's variance by summing up the variance of the independent M_i and W_i's as below:

$$\begin{aligned} E[R] &= 50\,E[M_i] + 0.5 \cdot 100\,E[W_i] &&= 75 \\ \mathrm{Var}(R) &= 50\ \mathrm{Var}(M_i) + 0.25 \cdot 100\ \mathrm{Var}(W_i) &&= 0.961 \end{aligned}$$

As an aside, R can be approximated as $R \sim \mathrm{N}(75, 0.961)$, since the sums of both question types M_i and W_i respectively approach Normal distributions according to the Central Limit Theorem, and the sum of independent Normal distributions is itself a Normal distribution. The distribution of the sample mean $\overline{R}$ is then given by:

$$\begin{aligned} \overline{R} = \frac{1}{100}\sum_{i=1}^{100} R_i &\sim N(75, \frac{1}{100}0.961) \\ &\sim N(75, 0.0096) \end{aligned}$$

4. **Bootstrapping and Null Hypotheses (courtesy of Oishi Banerjee)**

While testing the efficacy of a new drug, Skylar Pharmaceuticals has collected 1000 data samples. Most of the samples came from patients who were treated with the drug, but the rest came from patients who received a placebo. Skylar observed that the sample mean blood pressure in the treated group was 80, while the sample mean blood pressure in the placebo group was 86. To demonstrate the difference is statistically significant, Skylar implemented the following to produce a p-value.

Data scientists at Skylar wrote the following bootstrapping code to arrive at a p-value to suggest

the difference isn't statistically significant. Unfortunately (or fortunately, depending on your point of view), their code is not right.

```
import numpy as np

def resample(whole,num_samples):
    return np.random.choice(whole, num_samples, replace=True)

# list_treat is an ordinary 1-d numpy array
# it contains all the diastolic blood pressures of
# each patient who was treated

# list_placebo is an ordinary 1-d numpy array
# it contains the diastolic blood pressures of each
# patient who received a placebo
def pvalue(list_treat, list_placebo):
    # np.concatenate will make a 1000-element array #containing the
       elements of both list_treat and list_placebo
    whole = np.concatenate([list_treat,list_placebo])
    threshold = np.mean(list_treat) - np.mean(list_placebo)
    counter, num_trials = 0, 100000
    for trial in range(num_trials):
        sample_treat = resample(list_treat, 500)
        sample_placebo = resample(list_placebo, 500)
        mean_treat = np.mean(sample_treat)
        mean_placebo = np.mean(sample_placebo)
        new_diff = np.abs(mean_treat - mean_placebo)
        if new_diff == threshold: counter += 1
    return counter/num_trials
```

Point out the algorithmic errors. Be clear what Skylar should do instead, explaining why each change you would make is necessary for correct bootstrapping.

- As written, the threshold will be -6, so new_diff can never be smaller than threshold! Because were really only concerned with magnitudes, Skylar should replace threshold with np.abs(threshold).
- To simulate the null hypothesis, we should sample from our new combined distribution. As a result both calls to resample should pass in whole, not list_treat or list_placebo.
- Though were now sampling from our new combined distribution, we want to stay true to the design of the original experiment in every other way. Therefore we should make sure sample_treat has as many elements as list_treat and sample_placebo has as many elements as list_placebo. The 500s should be replaced with len(list_treat) and len(list_placebo) respectively.
- When bootstrapping, we count up how many times we see a result as dramatic or more dramatic than ours under the null hypothesis. As a result, we should check if new_diff is greater than or equal to threshold.