DSAI 512 Fall 2025
HW #2

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I. Problem 1

Drawing marbles with replacement, where:

- μ: probability of drawing red
- $1-\mu$: probability of drawing green
- $N = 10$: sample size
- ν: fraction of red in sample
- $\mu \in \{0.05, 0.5, 0.8\}$
- $P(\nu = 0)$: the probability that no red marbles are drawn.

A. 1.a

Since draws are independent with replacement:

$$P(\nu = 0) = (1-\mu)^{10} \tag{1}$$

$$\begin{aligned}
\mu = 0.05: &\quad P(\nu = 0) = (1-0.05)^{10} \approx 0.5987\\
\mu = 0.5: &\quad P(\nu = 0) = (1-0.5)^{10} \approx 0.0010\\
\mu = 0.8: &\quad P(\nu = 0) = (1-0.8)^{10} \approx 1.024e-7
\end{aligned}$$

B. 1.b

Let event $\mathcal{B}$: at least one sample has $\nu = 0$
Let event $\overline{\mathcal{B}}$: none of the samples has $\nu = 0$
Using the complement rule:

$$P(\mathcal{B}) = 1 - P(\overline{\mathcal{B}}) = 1 - \left(1-(1-\mu)^{10}\right)^{1000} \tag{2}$$

$$\begin{aligned}
\mu = 0.05: &\quad 1-(1-0.5987)^{1000} \approx 1.0000\\
\mu = 0.5: &\quad 1-(1-0.0010)^{1000} \approx 0.6323\\
\mu = 0.8: &\quad 1-(1-1.024e-7)^{1000} \approx 0.0001
\end{aligned}$$

C. 1.c

Same calculation with $B =$ 1,000,000 experiments:

$$P(\mathcal{B}) = 1 - \left(1-(1-\mu)^{10}\right)^{1000000} \tag{3}$$

$$\begin{aligned}
\mu = 0.05: &\quad 1-(1-0.5987)^{1000000} \approx 1.0000\\
\mu = 0.5: &\quad 1-(1-0.0010)^{1000000} \approx 1.0000\\
\mu = 0.8: &\quad 1-(1-1.024e-7)^{1000000} \approx 0.0973
\end{aligned}$$

D. 1.d

When we observe the $\mu = 0.5$ case from 1.a, we can see the bad event ($\nu = 0$) is very unlikely to happen, with a probability of only 0.0010. This is similar to running a single train_test_split experiment with a fixed random_state from scikit-learn. However, when we increase the number of experiments or in other words try many hypotheses, we see the probability of at least one bad event occuring jumps to 0.6323 (for $B = 1000$) and then to 1.000 (for $B = 1,000,000$). This means as the number of hypotheses grows, it becomes almost certain that at least one of them will mislead us. Since we always look for the best hypothesis, we're very likely to get fooled by that one. To give a more vivid example, if our random_state in train_test_split gives us a misleading sample like 10 red marbles while the truth is $\mu = 0.5$, a hypothesis g that says 'always guess red' will get a perfect score ($E_{in} = 0$). This hypothesis will be chosen because it looks the best, leading us to be fooled. This is the essence of overfitting as in sample error (E_{in}) is low, but its true error (E_{out}) is much higher. This is why the Hoeffding inequality, by itself, isn't enough. It only defines the bound for one hypothesis. That's why introducing the Union Bound is necessary. It states that **the total probability of at least one of our many hypotheses being misleading is no more than the sum of all their individual probabilities.**

II. Problem 2

A. 2.a

No, it does not guarantee better performance. If we assume that our dataset is biased towards mostly low temperature like $\{1, -1, -1, \ldots, -1\}$, Algorithm A will choose h_2 as it will get the best score with 96% accuracy. However, in the real world if the true distribution is nearly balanced ($p \approx 0.5$), because of this biased distribution in D, our accuracy will fall to approximately 50% and since this is not better than random guessing, it is not guaranteed.

B. 2.b

If all samples have +1 results, then Algorithm A chooses h_1 as it yields the best result and Algorithm B chooses h_2. In a scenario where Algorithm B performs better in the real world, it is needed that $f(x) = -1$ probability should be greater than $f(x) = +1$:

$$\begin{aligned} 1 - p &> p \\ 1 &> 2p \\ 0.5 &> p \end{aligned}$$

In this specific case, if $0.5 > p$, then it is possible.

C. 2.c

For case 1 where $p = 0.9$, Algorithm A performs better if it selects h_1. For Algorithm A to choose h_1, the dataset D must observe that h_1 outperforms h_2, which occurs only when the number of $+1$ samples exceeds the number of -1 samples. We can express this probability as $P(k \geq 13)$, where k represents the number of $+1$ samples.

For case 2 where $p = 0.1$, Algorithm A performs better if it selects h_2. This occurs when the number of -1 samples exceeds the number of $+1$ samples. We can express this probability as $P(k < 13)$.

Since these show binomial distribution we can define and compute them:

$$P(k \geq 13) = \sum_{k=13}^{25} \binom{25}{k} (0.9)^k (1-0.9)^{25-k} \approx 1.0000$$

$$P(k < 13) = \sum_{k=0}^{12} \binom{25}{k} (0.1)^k (1-0.1)^{25-k} \approx 1.0000$$

D. 2.d

Let P_A be the probability that Algorithm A chooses the correct hypothesis and P_B be the probability that Algorithm B chooses the correct hypothesis. Since B always chooses the opposite of A, B is correct when A is wrong denoted by:

$$P_B = 1 - P_A$$

The condition for B to be more likely to perform better is $P_B > P_A$:

$$\begin{aligned} 1 - P_A &> P_A \\ 1 &> 2P_A \\ 0.5 &> P_A \end{aligned}$$

The problem is to find the range of p for which $P_A < 0.5$.

If $p > 0.5$: The correct hypothesis is h_1.

A chooses h_1 if $k \geq 13$. Thus, $P_A = P(k \geq 13)$. The mean of the distribution is $E[k] = np = 25p > 12.5$. Since the mean is greater than 12.5, the probability is concentrated on the right hand side, so $P(k \geq 13) > 0.5$.

If $p < 0.5$: The correct hypothesis is h_2.

A chooses h_2 if $k < 13$. Thus, $P_A = P(k < 13)$. The mean of the distribution is $E[k] = np = 25p < 12.5$. Since the mean is less than 12.5, the probability is concentrated on the left hand side, so $P(k < 13) > 0.5$.

If $p = 0.5$: Both hypotheses are equally correct.

$P_A = P(k < 13) = P(k \geq 13) = 0.5$.

The condition $P_A < 0.5$ is never met. Therefore, there is no solution for the case where B is more likely to perform better. This shows that Algorithm A is always a better (or equal) strategy than deliberately contradicting the result despite having limited data.

E. 2.e

Algorithm C chooses h_1 or h_2 with 50% probability regardless of the data D. Its expected accuracy is:

$$\begin{aligned} Acc_C &= P(h_1 \text{ wins}) \cdot \text{Acc}(h_1) + P(h_2 \text{ wins}) \cdot \text{Acc}(h_2) \\ Acc_C &= (0.5) \cdot (p) + (0.5) \cdot (1-p) \\ Acc_C &= 0.5p + 0.5 - 0.5p = 0.5 \end{aligned}$$

Algorithm C's accuracy is always 50%.

As p varies, accuracy of C is still constant at 0.5. From 2.d, we can derive Algorithm A's probability of being correct (P_A) is always ≥ 0.5, while (P_B) is always ≤ 0.5. This means A's expected accuracy will be ≥ 0.5 and B's will be ≤ 0.5. Thus, Algorithm A always performs better than or equal to Algorithm C. Algorithm C always performs better than or equal to Algorithm B.

A performs as well as C when $Acc_A = Acc_C = 0.5$. This happens only when the problem is also random at $p = 0.5$. In this case both h_1 and h_2 have 50% accuracy, so any choice yields the same 50% expected accuracy.

F. 2.f

It illustrates the danger of interpreting small datasets. The scenario in 2.b, where our dataset consists of 25 +1 samples, shows this perfectly. An algorithm learning from this data (Algorithm A in this case) would be 100% confident that h_1 is correct. However, if the true p is 0.1, this learned hypothesis is dangerously wrong. As shown in 2.c and 2.d, the success of Algorithm A (P_A) is a probability that depends on N and p. If $p = 0.9$, learning is almost guaranteed to succeed ($P_A \approx 1$). If $p = 0.5$, learning is no better than a coin flip ($P_A = 0.5$). Since learning can fail, we need tools to measure the risk of failure. A generalization bound (like Hoeffding inequality for single hypotheses or union bound for multiple) provides a mathematical notion between what we see in sample and what we can expect in the real world.

III. Code Repository

Computations will be available at *this GitHub repository* after the deadline.

IV. Acknowledgements

Gemini 2.5 Pro was used to assist in converting handwritten mathematical notation to LaTeX format and ensuring my analogies make sense within the context. Crucially, it helped build my intuition for question 2.d, specifically regarding the "probability mass" logic and its relationship to the expected value as well as noticing P_A and P_B boundaries in 2.e.