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ECE 1395

Homework 1

1) I could use regression to predict tumor size in radiology from Medical images.

- a) Some features I would use are pixel intensity values, shape features, and texture features.
- b) For labels, I would use tumor size and tumor volume.
- c) For data collection, I would find hospitals' datasets of radiology medical images and corresponding measurements in them.
- d) Some challenges are medical images are very noisy, the labeled data may have a lot of variance, and biological systems are complex to predict.

2) I could use classification to classify if a patient has a specific disease.

- a) Some features I would use are results from medical diagnostic tests, lab tests, and imaging studies, specifically blood pressure, heart rate, body temp, and respiratory rate.
- b) For labels, I would have either "has disease" or "no disease".
- c) For data, I would get datasets from hospitals and treatment centers.
- d) The data collected could all be from one place, which causes an imbalance and may not be diverse enough.

3c) Yes, the histogram for x does look like a gaussian distribution, and the histogram for z looks like a uniform distribution.

3e)

```
v/ps1.py
Time to run 3d: 1.94 seconds
Time to run 3e: 0.00024 seconds
(.venv) keshavshankar@Keshavs-MacBo
```

The Second way in 3e is more efficient, because numpy has a built in override operator to perform such a calculation.

3f)

```
v/ps1.py
Elements retrieved in 3f: 375588
(.venv) keshavshankar@Keshavs-MacBo
v/ps1.py"
Elements retrieved in 3f: 374844
(.venv) keshavshankar@Keshavs-MacBo
v/ps1.py"
Elements retrieved in 3f: 374233
(.venv) keshavshankar@Keshavs-MacBo
```

Yes, there is a difference. This is because we are generating random numbers for the "z" vector, thus the # of values btwn.

0 & 1.5 will always change.

4b)

```
v/ps1.py"
The resultant solution for 4b is:
[[ 0.3]
 [ 0.4]
 [-0. ]]
(.venv) keshavshankar@Keshavs-MacBo
```

4c)

$$x_1 = [-0.5 \quad 0 \quad 1.5] \Rightarrow (-0.5, 0, 1.5)^2 = (0.25, 0, 2.25) \\ = \sqrt{2.5} = \boxed{1.58} \quad \text{L1 norm}$$

$$x_2 = [-1 \quad -1 \quad 0] \Rightarrow (-1, -1, 0)^2 = (1, 1, 0) \\ = \sqrt{2} = \boxed{1.41} \quad \text{L2 norm}$$

```
v/ps1.py"
Norm of x1: 1.58
Norm of x2: 1.41
(.venv) keshavshankar@
```

The python solution verifies that the calculations are correct.

5a)

```
v/ps1.py"
x: [[ 1  1  1]
     [ 2  2  2]
     [ 3  3  3]
     [ 4  4  4]
     [ 5  5  5]
     [ 6  6  6]
     [ 7  7  7]
     [ 8  8  8]
     [ 9  9  9]
     [10 10 10]]
(.venv) keshavsh
```

5d)

```
v/ps1.py
-X train:
[[8 8 8]
 [6 6 6]
 [5 5 5]
 [3 3 3]
 [9 9 9]
 [2 2 2]
 [4 4 4]
 [7 7 7]]
-Y train:
[[8]
 [6]
 [5]
 [3]
 [9]
 [2]
 [4]
 [7]]
-X test:
[[10 10 10]
 [ 1  1  1]]
-Y test:
[[10]
 [ 1]]
(.venv) keshavshankar
```

trial 1

```
-X train:
[[ 7  7  7]
 [ 2  2  2]
 [ 1  1  1]
 [ 4  4  4]
 [ 9  9  9]
 [ 3  3  3]
 [ 8  8  8]
 [10 10 10]]
-Y train:
[[ 7]
 [ 2]
 [ 1]
 [ 4]
 [ 9]
 [ 3]
 [ 8]
 [10]]
-X test:
[[6 6 6]
 [5 5 5]]
-Y test:
[[6]
 [5]]
```

trial 2

```
-X train:
[[ 7  7  7]
 [ 6  6  6]
 [ 5  5  5]
 [ 1  1  1]
 [10 10 10]
 [ 9  9  9]
 [ 8  8  8]
 [ 2  2  2]]
-Y train:
[[ 7]
 [ 6]
 [ 5]
 [ 1]
 [10]
 [ 9]
 [ 8]
 [ 2]]
-X test:
[[4 4 4]
 [3 3 3]]
-Y test:
[[4]
 [3]]
```

trial 3

No, you do not get the same submatrices every time because you are using a random seed to shuffle the arrays every time.